

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 3, 2004, 20:29:27 ; Search time 17.4001 Seconds
(without alignments)
1525.031 Million cell updates/sec

Title: US-10-644-187-6

Sequence: 1 AAFPNCTMMQYFEWYLPDDG.....TTREWTGEFVWTEPRUAV 514

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: 1: /cgn2_6/prodata/2/1aa/5A COMB.pap:*
2: /cgn2_6/prodata/2/1aa/5B COMB.pap:*
3: /cgn2_6/prodata/2/1aa/6A COMB.pap:*
4: /cgn2_6/prodata/2/1aa/6B COMB.pap:*
5: /cgn2_6/prodata/2/1aa/6C COMB.pap:*
6: /cgn2_6/prodata/2/1aa/6D COMB.pap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2847	100.0	514	3	US-09-182-859-6
2	2847	100.0	514	3	US-09-264-097-8
3	2847	100.0	514	4	US-09-672-459-6
4	2847	100.0	514	4	US-10-186-042-6
5	2847	100.0	515	4	US-09-291-023A-17
6	2847	100.0	515	4	US-09-537-168-8
7	2847	100.0	515	4	US-09-540-715A-17
8	2847	100.0	549	1	US-08-459-610-6
9	2847	100.0	549	1	US-08-459-610-6
10	2847	100.0	549	2	US-08-459-610-6
11	2847	100.0	549	2	US-08-459-610-6
12	2847	100.0	549	2	US-08-459-610-6
13	2847	100.0	549	2	US-08-459-610-6
14	2847	100.0	549	2	US-08-459-610-6
15	2847	100.0	549	2	US-08-459-610-6
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18	2847	100.0	549	2	US-08-459-610-6
19	2847	100.0	549	2	US-08-459-610-6
20	2847	100.0	549	2	US-08-459-610-6
21	2847	100.0	549	2	US-08-459-610-6
22	2847	100.0	549	2	US-08-459-610-6
23	2847	100.0	549	2	US-08-459-610-6
24	2847	100.0	549	2	US-08-459-610-6
25	2847	100.0	549	2	US-08-459-610-6
26	2847	100.0	549	2	US-08-459-610-6

28	2720.5	95.6	548	2	US-08-704-706A-37	Sequence 37, Appl
29	2720.5	95.6	548	3	US-08-890-383-6	Sequence 6, Appl
30	2720.5	95.6	548	3	US-08-914-679A-6	Sequence 6, Appl
31	2720.5	95.6	548	3	US-08-965-659-38	Sequence 38, Appl
32	2720.5	95.6	548	3	US-08-194-664A-35	Sequence 35, Appl
33	2720.5	95.6	548	5	PCT-US94-01553A-35	Sequence 35, Appl
34	2720.5	95.6	548	5	PCT-US95-10426-35	Sequence 35, Appl
35	1915.5	67.3	485	4	US-09-291-023A-14	Sequence 4, Appl
36	1915.5	67.3	485	4	US-09-291-023A-14	Sequence 4, Appl
37	1915.5	67.3	485	4	US-09-540-715A-14	Sequence 4, Appl
38	1915.5	67.3	485	4	US-09-540-715A-14	Sequence 4, Appl
39	1910.5	67.1	485	4	US-09-291-023A-18	Sequence 18, Appl
40	1910.5	67.1	485	4	US-09-291-023A-18	Sequence 18, Appl
41	1910.5	67.1	485	4	US-09-381-687-1	Sequence 1, Appl
42	1910.5	67.1	485	4	US-09-381-687-1	Sequence 1, Appl
43	1909.5	67.1	485	2	US-08-446-803-1	Sequence 2, Appl
44	1909.5	67.1	485	2	US-08-446-803-1	Sequence 1, Appl
45	1909.5	67.1	485	2	US-08-600-908A-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1	US-09-182-859-6	Sequence 6, Application US/09182859
1	US-09-182-859-6	Sequence 6, Application US/09182859
2	US-09-182-859-6	Sequence 6, Application US/09182859
3	US-09-182-859-6	Sequence 6, Application US/09182859
4	US-09-182-859-6	Sequence 6, Application US/09182859
5	US-09-182-859-6	Sequence 6, Application US/09182859
6	US-09-182-859-6	Sequence 6, Application US/09182859
7	US-09-182-859-6	Sequence 6, Application US/09182859
8	US-09-182-859-6	Sequence 6, Application US/09182859
9	US-09-182-859-6	Sequence 6, Application US/09182859
10	US-09-182-859-6	Sequence 6, Application US/09182859
11	US-09-182-859-6	Sequence 6, Application US/09182859
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13	US-09-182-859-6	Sequence 6, Application US/09182859
14	US-09-182-859-6	Sequence 6, Application US/09182859
15	US-09-182-859-6	Sequence 6, Application US/09182859
16	US-09-182-859-6	Sequence 6, Application US/09182859
17	US-09-182-859-6	Sequence 6, Application US/09182859
18	US-09-182-859-6	Sequence 6, Application US/09182859
19	US-09-182-859-6	Sequence 6, Application US/09182859
20	US-09-182-859-6	Sequence 6, Application US/09182859
21	US-09-182-859-6	Sequence 6, Application US/09182859
22	US-09-182-859-6	Sequence 6, Application US/09182859
23	US-09-182-859-6	Sequence 6, Application US/09182859
24	US-09-182-859-6	Sequence 6, Application US/09182859
25	US-09-182-859-6	Sequence 6, Application US/09182859
26	US-09-182-859-6	Sequence 6, Application US/09182859

Db 241 FEFPPDMLSYVRSQTKPLFTVGEWYSYDINKLHNYITKTDGMSLFDAPLHNKFTYASK 300
 QY 301 SGGAFDMRLTMTNTLMKQDPTLAVTFVNDHDEPGQALQSWDPMFKPLAVALFILTREG 360
 Db 301 SGGAFDMRLTMTNTLMKQDPTLAVTFVNDHDEPGQALQSWDPMFKPLAVALFILTREG 360
 QY 361 YPCVFYGDYVGIPOYNIPLSKIDPLLIARDYAVGTQHDYLDHSDIIGWTRREGTEKP 420
 Db 361 YPCVFYGDYVGIPOYNIPLSKIDPLLIARDYAVGTQHDYLDHSDIIGWTRREGTEKP 420
 QY 421 GSGLAALITDGGGSKMYVKGQAHGKVFYDLTGNRSDTITNSDGWGEFKNVGSVSV 480
 Db 421 GSGLAALITDGGGSKMYVKGQAHGKVFYDLTGNRSDTITNSDGWGEFKNVGSVSV 480
 QY 481 VPKTTVSTIARPIITRPWTGSEFVWTEPRLYAM 514
 Db 481 VPKTTVSTIARPIITRPWTGSEFVWTEPRLYAM 514

RESULT 2

US-09-264-097-8
 ; Sequence 8, Application US/09264097
 ; Patent No. 6287826
 ; GENERAL INFORMATION:
 ; APPLICANT: Hendriksen, Barrie Edmund
 ; APPLICANT: Hendriksen, Hanne Vang
 ; TITLE OF INVENTION: Enzymatic Preparation of Glucose Syrup
 ; FILE REFERENCE: 5278.200-US
 ; CURRENT APPLICATION NUMBER: US/09/264,097
 ; CURRENT FILING DATE: 1999-03-08
 ; EARLIER APPLICATION NUMBER: PA 0321/98
 ; EARLIER FILING DATE: 1998-03-09
 ; EARLIER APPLICATION NUMBER: 60/079,209
 ; EARLIER FILING DATE: 1998-03-24
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO: 8
 ; LENGTH: 514
 ; TYPE: PRF
 ; ORGANISM: Bacillus
 US-09-264-097-8

Query Match

Best Local Similarity 100.0%; Score 2847; DB 3; Length 514;
 Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPFNGTMMQYFEWYLPDDGTLMTKVAEANNLSIGITLMLPWAYKTSRSDVGYGY 60
 Db 1 AAPFNGTMMQYFEWYLPDDGTLMTKVAEANNLSIGITLMLPWAYKTSRSDVGYGY 60
 QY 61 DLYDLGEFNOKGTVRKTYGTAQYLOAIQAHAAGQYADVFEHKGADGTEWDAVE 120
 Db 61 DLYDLGEFNOKGTVRKTYGTAQYLOAIQAHAAGQYADVFEHKGADGTEWDAVE 120
 QY 121 VNSDRNOEISGTYYQIOAWTKFDFPGRGNTYSSFKRWYHFGVWDESRKLSRIYKFRG 180
 Db 121 VNSDRNOEISGTYYQIOAWTKFDFPGRGNTYSSFKRWYHFGVWDESRKLSRIYKFRG 180
 QY 181 IGRAMDEVTENGNDYLMYADLMDHDEVTTELKMGKMYNTNIDGFLDAVKH 240
 Db 181 IGRAMDEVTENGNDYLMYADLMDHDEVTTELKMGKMYNTNIDGFLDAVKH 240
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 Db 241 FSEFPDMLSYVRSQTKPLFTVGEWYSYDINKLHNYITKTDGMSLFDAPLHNKFTYASK 300
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 Db 301 SGGAFDMRLTMTNTLMKQDPTLAVTFVNDHDEPGQALQSWDPMFKPLAVALFILTREG 360
 QY 361 YPCVFYGDYVGIPOYNIPLSKIDPLLIARDYAVGTQHDYLDHSDIIGWTRREGTEKP 420
 Db 361 YPCVFYGDYVGIPOYNIPLSKIDPLLIARDYAVGTQHDYLDHSDIIGWTRREGTEKP 420

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 QY 421 GSGLAALITDGGGSKMYVKGQAHGKVFYDLTGNRSDTITNSDGWGEFKNVGSVSV 480
 Db 421 GSGLAALITDGGGSKMYVKGQAHGKVFYDLTGNRSDTITNSDGWGEFKNVGSVSV 480
 QY 481 VPKTTVSTIARPIITRPWTGSEFVWTEPRLYAM 514
 Db 481 VPKTTVSTIARPIITRPWTGSEFVWTEPRLYAM 514

RESULT 3

US-09-672-459-6
 ; Sequence 6, Application US/09672459
 ; Patent No. 643688
 ; GENERAL INFORMATION:
 ; APPLICANT: Svendsen, Allan
 ; APPLICANT: Borchert, Torben
 ; APPLICANT: Bisgaard-Frantzen, Henrik
 ; TITLE OF INVENTION: Alpha-Amylase Mutants
 ; FILE REFERENCE: 4796.204-US
 ; CURRENT APPLICATION NUMBER: US/09/672,459
 ; CURRENT FILING DATE: 2000-09-28
 ; PRIOR APPLICATION NUMBER: 09/182,859
 ; PRIOR FILING DATE: 1998-10-29
 ; PRIOR APPLICATION NUMBER: 0515/96
 ; PRIOR FILING DATE: 1996-04-30
 ; PRIOR APPLICATION NUMBER: 0712/96
 ; PRIOR FILING DATE: 1996-06-28
 ; PRIOR APPLICATION NUMBER: 0775/96
 ; PRIOR FILING DATE: 1996-07-11
 ; PRIOR APPLICATION NUMBER: 1263/96
 ; PRIOR FILING DATE: 1996-11-08
 ; NUMBER OF SEQ ID NOS: 37
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO: 6
 ; LENGTH: 514
 ; TYPE: PRF
 ; ORGANISM: Bacillus stearothermophilus
 US-09-672-459-6

Query Match

Best Local Similarity 100.0%; Score 2847; DB 4; Length 514;
 Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPFNGTMMQYFEWYLPDDGTLMTKVAEANNLSIGITLMLPWAYKTSRSDVGYGY 60
 Db 1 AAPFNGTMMQYFEWYLPDDGTLMTKVAEANNLSIGITLMLPWAYKTSRSDVGYGY 60
 QY 61 DLYDLGEFNOKGTVRKTYGTAQYLOAIQAHAAGQYADVFEHKGADGTEWDAVE 120
 Db 61 DLYDLGEFNOKGTVRKTYGTAQYLOAIQAHAAGQYADVFEHKGADGTEWDAVE 120
 QY 121 VNSDRNOEISGTYYQIOAWTKFDFPGRGNTYSSFKRWYHFGVWDESRKLSRIYKFRG 180
 Db 121 VNSDRNOEISGTYYQIOAWTKFDFPGRGNTYSSFKRWYHFGVWDESRKLSRIYKFRG 180
 QY 181 IGRAMDEVTENGNDYLMYADLMDHDEVTTELKMGKMYNTNIDGFLDAVKH 240
 Db 181 IGRAMDEVTENGNDYLMYADLMDHDEVTTELKMGKMYNTNIDGFLDAVKH 240
 QY 241 FSEFPDMLSYVRSQTKPLFTVGEWYSYDINKLHNYITKTDGMSLFDAPLHNKFTYASK 300
 Db 241 FSEFPDMLSYVRSQTKPLFTVGEWYSYDINKLHNYITKTDGMSLFDAPLHNKFTYASK 300
 QY 301 SGGAFDMRLTMTNTLMKQDPTLAVTFVNDHDEPGQALQSWDPMFKPLAVALFILTREG 360
 Db 301 SGGAFDMRLTMTNTLMKQDPTLAVTFVNDHDEPGQALQSWDPMFKPLAVALFILTREG 360
 QY 361 YPCVFYGDYVGIPOYNIPLSKIDPLLIARDYAVGTQHDYLDHSDIIGWTRREGTEKP 420
 Db 361 YPCVFYGDYVGIPOYNIPLSKIDPLLIARDYAVGTQHDYLDHSDIIGWTRREGTEKP 420

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Page 3

QY 421 GSGLAALITDGGGSKMYVGVKQHAGKVFYDLTGNRSDVTITNSDGWGEFKYNGGSVSW 480
DB 421 GSGLAALITDGGGSKMYVGVKQHAGKVFYDLTGNRSDVTITNSDGWGEFKYNGGSVSW 480
QY 481 VPRKTTVSTIARPIITTRPMTGFEFVMTBRLVAM 514
DB 481 VPRKTTVSTIARPIITTRPMTGFEFVMTBRLVAM 514

RESULT 4
US-10-186-042-6
Sequence 6, Application US/10186042
Patent No. 6642044
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Borchert, Torben
APPLICANT: Bisgaard-Frantzen, Henrik
TITLE OF INVENTION: Alpha-Amylase Mutants
FILE REFERENCE: 4796.204-US
CURRENT APPLICATION NUMBER: US/10/186,042
PRIOR FILING DATE: 2002-06-28
PRIOR APPLICATION NUMBER: US/09/672,459
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: 09/182,859
PRIOR FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: 0515/96
PRIOR FILING DATE: 1996-04-30
PRIOR APPLICATION NUMBER: 0712/96
PRIOR FILING DATE: 1996-06-28
PRIOR APPLICATION NUMBER: 0775/96
PRIOR FILING DATE: 1996-07-11
PRIOR APPLICATION NUMBER: 1263/96
PRIOR FILING DATE: 1996-11-08
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 6
LENGTH: 514
TYPE: PRT
ORGANISM: Bacillus stearothermophilus
US-10-186-042-6

Query Match 100.0%; Score 2847; DB 4; Length 514;
Best Local Similarity 100.0%; Pred. No. 1.6e-245;
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAPNGTMMQYFEWYLPDDGTLMTKYANBANLSSIGITALLMPPAYKGTSRSDVGYGY 60
DB 1 AAPNGTMMQYFEWYLPDDGTLMTKYANBANLSSIGITALLMPPAYKGTSRSDVGYGY 60
QY 61 DLYDGEFNOKGIVRTKGYTKAQYLOAIQAAHAGQYADVDFHKGADGTEWDAVE 120
DB 61 DLYDGEFNOKGIVRTKGYTKAQYLOAIQAAHAGQYADVDFHKGADGTEWDAVE 120
QY 121 VNPSDRNOEISGTYQIOAWTKFDFPGKNTYSSFKRWYHFDGVWDESRKLSRIYKFRG 180
DB 121 VNPSDRNOEISGTYQIOAWTKFDFPGKNTYSSFKRWYHFDGVWDESRKLSRIYKFRG 180
QY 181 IGAWMDEVDTENGNDYLYMADLDMDHEVVTLEKNMGKMYNTNIDGFRDLDAVXHIX 240
DB 181 IGAWMDEVDTENGNDYLYMADLDMDHEVVTLEKNMGKMYNTNIDGFRDLDAVXHIX 240
QY 241 FSEFPDWLSYVRSGQTKPLFTVGEYMSYDINKLHNYITKTGMSLFDAPLHKKFYTASX 300
DB 241 FSEFPDWLSYVRSGQTKPLFTVGEYMSYDINKLHNYITKTGMSLFDAPLHKKFYTASX 300
QY 301 SGGAPEMRITLMTNLMKQDPTLAVTFVNDHDETEPGALOSWVDPWFKPLAYAFILTRQEG 360
DB 301 SGGAPEMRITLMTNLMKQDPTLAVTFVNDHDETEPGALOSWVDPWFKPLAYAFILTRQEG 360
QY 361 YPCVFGDYGYGIPQYNIPLSKSKIDPELLARDAVAGTQHDYLDHSDIIGWTRREGGTEKP 420
DB 361 YPCVFGDYGYGIPQYNIPLSKSKIDPELLARDAVAGTQHDYLDHSDIIGWTRREGGTEKP 420

QY 421 GSGLAALITDGGGSKMYVGVKQHAGKVFYDLTGNRSDVTITNSDGWGEFKYNGGSVSW 480
DB 421 GSGLAALITDGGGSKMYVGVKQHAGKVFYDLTGNRSDVTITNSDGWGEFKYNGGSVSW 480
QY 481 VPRKTTVSTIARPIITTRPMTGFEFVMTBRLVAM 514
DB 481 VPRKTTVSTIARPIITTRPMTGFEFVMTBRLVAM 514

RESULT 5
US-09-291-023A-17
Sequence 17, Application US/09291023A
Patent No. 6309871
GENERAL INFORMATION:
APPLICANT: Outtrup, Helle
APPLICANT: Borchert, Torben
APPLICANT: Nielsen, Bjarne
APPLICANT: Nielsen, Vibeke
TITLE OF INVENTION: Polypeptides Having Alkaline Alpha-amylase Activity And Nucleic A
FILE REFERENCE: 5821.010-US
CURRENT APPLICATION NUMBER: US/09/291,023A
PRIOR FILING DATE: 1999-04-13
PRIOR APPLICATION NUMBER: DK 1999 00438
PRIOR FILING DATE: 1999-03-31
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PatentIn version 3.0
SEQ ID NO 17
LENGTH: 515
TYPE: PRT
ORGANISM: Bacillus
US-09-291-023A-17

Query Match 100.0%; Score 2847; DB 4; Length 515;
Best Local Similarity 100.0%; Pred. No. 1.6e-245;
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAPNGTMMQYFEWYLPDDGTLMTKYANBANLSSIGITALLMPPAYKGTSRSDVGYGY 60
DB 1 AAPNGTMMQYFEWYLPDDGTLMTKYANBANLSSIGITALLMPPAYKGTSRSDVGYGY 60
QY 61 DLYDGEFNOKGIVRTKGYTKAQYLOAIQAAHAGQYADVDFHKGADGTEWDAVE 120
DB 61 DLYDGEFNOKGIVRTKGYTKAQYLOAIQAAHAGQYADVDFHKGADGTEWDAVE 120
QY 121 VNPSDRNOEISGTYQIOAWTKFDFPGKNTYSSFKRWYHFDGVWDESRKLSRIYKFRG 180
DB 121 VNPSDRNOEISGTYQIOAWTKFDFPGKNTYSSFKRWYHFDGVWDESRKLSRIYKFRG 180
QY 181 IGAWMDEVDTENGNDYLYMADLDMDHEVVTLEKNMGKMYNTNIDGFRDLDAVXHIX 240
DB 181 IGAWMDEVDTENGNDYLYMADLDMDHEVVTLEKNMGKMYNTNIDGFRDLDAVXHIX 240
QY 241 FSEFPDWLSYVRSGQTKPLFTVGEYMSYDINKLHNYITKTGMSLFDAPLHKKFYTASX 300
DB 241 FSEFPDWLSYVRSGQTKPLFTVGEYMSYDINKLHNYITKTGMSLFDAPLHKKFYTASX 300
QY 301 SGGAPEMRITLMTNLMKQDPTLAVTFVNDHDETEPGALOSWVDPWFKPLAYAFILTRQEG 360
DB 301 SGGAPEMRITLMTNLMKQDPTLAVTFVNDHDETEPGALOSWVDPWFKPLAYAFILTRQEG 360
QY 361 YPCVFGDYGYGIPQYNIPLSKSKIDPELLARDAVAGTQHDYLDHSDIIGWTRREGGTEKP 420
DB 361 YPCVFGDYGYGIPQYNIPLSKSKIDPELLARDAVAGTQHDYLDHSDIIGWTRREGGTEKP 420
QY 421 GSGLAALITDGGGSKMYVGVKQHAGKVFYDLTGNRSDVTITNSDGWGEFKYNGGSVSW 480
DB 421 GSGLAALITDGGGSKMYVGVKQHAGKVFYDLTGNRSDVTITNSDGWGEFKYNGGSVSW 480
QY 481 VPRKTTVSTIARPIITTRPMTGFEFVMTBRLVAM 514
DB 481 VPRKTTVSTIARPIITTRPMTGFEFVMTBRLVAM 514

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Page 4

RESULT 6
US-09-537-168-8
Sequence 8, Application US/09537168
Patent No. 6410295
GENERAL INFORMATION:
APPLICANT: Andersen, Carsten
APPLICANT: Jorgensen, Christel T.
APPLICANT: Bisgaard-Frantzen, Henrik
APPLICANT: Svendsen, Allan
APPLICANT: Kjaerulff, Soren
TITLE OF INVENTION: Alpha-Amylase Variants
FILE REFERENCE: 5886.200-US
CURRENT APPLICATION NUMBER: US/09/537,168
CURRENT FILING DATE: 2000-03-29
EARLIER APPLICATION NUMBER: PA 1999 00437
EARLIER FILING DATE: 1999-03-30
EARLIER APPLICATION NUMBER: 60/127,427
EARLIER FILING DATE: 1999-04-01
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8
LENGTH: 515
TYPE: PR1
ORGANISM: Bacillus stearothermophilus
US-09-537-168-8

Query Match 100.0%; Score 2847; DB 4; Length 515;
Best Local Similarity 100.0%; Pred. No. 1,66-245;
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPFNGTMQVFEWYLPDDGTLMTKVANEANNLSLIGITALMLPPAYKGTSRSDVGYGVY 60
DB 1 AAPFNGTMQVFEWYLPDDGTLMTKVANEANNLSLIGITALMLPPAYKGTSRSDVGYGVY 60
QY 61 DLYDGEFNQKGTVRKTKYTKAQYLOAIQAAHAGMOYADVDPHKGADTEWDAVE 120
DB 61 DLYDGEFNQKGTVRKTKYTKAQYLOAIQAAHAGMOYADVDPHKGADTEWDAVE 120
QY 121 VNPDRNOISGTYOIQAWTKFDPGRGNTYSSFKRMWHFPGVMDSEKLSRIYKRG 180
DB 121 VNPDRNOISGTYOIQAWTKFDPGRGNTYSSFKRMWHFPGVMDSEKLSRIYKRG 180
QY 121 VNPDRNOISGTYOIQAWTKFDPGRGNTYSSFKRMWHFPGVMDSEKLSRIYKRG 180
DB 121 VNPDRNOISGTYOIQAWTKFDPGRGNTYSSFKRMWHFPGVMDSEKLSRIYKRG 180
QY 181 IGRAMDWEVDTEGNVYDLYMADLDMDEBEVTELEKMGKMYVNTNIDGFLDAVKH1K 240
DB 181 IGRAMDWEVDTEGNVYDLYMADLDMDEBEVTELEKMGKMYVNTNIDGFLDAVKH1K 240
QY 241 FGFPPDMLSVRSQTKRPLFTVGEYWSYDINLHNYITKTDSMSLFDAPLHKKRYTASK 300
DB 241 FGFPPDMLSVRSQTKRPLFTVGEYWSYDINLHNYITKTDSMSLFDAPLHKKRYTASK 300
QY 301 SGGAFFMRTLMNTLMKQDPTLAVTFVDNHDTEPGQALQSWDPMFKPLAVAFILTRQEG 360
DB 301 SGGAFFMRTLMNTLMKQDPTLAVTFVDNHDTEPGQALQSWDPMFKPLAVAFILTRQEG 360
QY 361 YPCVFYGDYIGIPOYNIPLSKSIDPLLIARDDYAGTGHDLDSDIIGMREGTEKPE 420
DB 361 YPCVFYGDYIGIPOYNIPLSKSIDPLLIARDDYAGTGHDLDSDIIGMREGTEKPE 420
QY 421 GSGLAALITDGPGSKMVYKQAHAGKVFYDLTGNRSDVTITNSDGMGEFKVNGGSVSW 480
DB 421 GSGLAALITDGPGSKMVYKQAHAGKVFYDLTGNRSDVTITNSDGMGEFKVNGGSVSW 480
QY 481 VPKRTVSTIARPIITRRPWTGEFVWTEPRLVAM 514
DB 481 VPKRTVSTIARPIITRRPWTGEFVWTEPRLVAM 514

RESULT 7
US-09-540-715A-17
Sequence 17, Application US/09540715A
Patent No. 6623948

GENERAL INFORMATION:
APPLICANT: Outtrup, Helle
APPLICANT: Borchert, Torben
APPLICANT: Nielsen, Bjarne
APPLICANT: Nielsen, Vibeke
APPLICANT: Hoek, Lisbeth
TITLE OF INVENTION: Polypeptides Having Alkaline Alpha-amylase Activity And Nucleic A
FILE REFERENCE: 5821.010-US
CURRENT APPLICATION NUMBER: US/09/540,715A
CURRENT FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/291,023
PRIOR FILING DATE: 2001-08-14
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PatentIn version 3.0
SEQ ID NO 17
LENGTH: 515
TYPE: PR1
ORGANISM: Bacillus
US-09-540-715A-17

Query Match 100.0%; Score 2847; DB 4; Length 515;
Best Local Similarity 100.0%; Pred. No. 1,66-245;
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPFNGTMQVFEWYLPDDGTLMTKVANEANNLSLIGITALMLPPAYKGTSRSDVGYGVY 60
DB 1 AAPFNGTMQVFEWYLPDDGTLMTKVANEANNLSLIGITALMLPPAYKGTSRSDVGYGVY 60
QY 61 DLYDGEFNQKGTVRKTKYTKAQYLOAIQAAHAGMOYADVDPHKGADTEWDAVE 120
DB 61 DLYDGEFNQKGTVRKTKYTKAQYLOAIQAAHAGMOYADVDPHKGADTEWDAVE 120
QY 121 VNPDRNOISGTYOIQAWTKFDPGRGNTYSSFKRMWHFPGVMDSEKLSRIYKRG 180
DB 121 VNPDRNOISGTYOIQAWTKFDPGRGNTYSSFKRMWHFPGVMDSEKLSRIYKRG 180
QY 121 VNPDRNOISGTYOIQAWTKFDPGRGNTYSSFKRMWHFPGVMDSEKLSRIYKRG 180
DB 121 VNPDRNOISGTYOIQAWTKFDPGRGNTYSSFKRMWHFPGVMDSEKLSRIYKRG 180
QY 181 IGRAMDWEVDTEGNVYDLYMADLDMDEBEVTELEKMGKMYVNTNIDGFLDAVKH1K 240
DB 181 IGRAMDWEVDTEGNVYDLYMADLDMDEBEVTELEKMGKMYVNTNIDGFLDAVKH1K 240
QY 241 FGFPPDMLSVRSQTKRPLFTVGEYWSYDINLHNYITKTDSMSLFDAPLHKKRYTASK 300
DB 241 FGFPPDMLSVRSQTKRPLFTVGEYWSYDINLHNYITKTDSMSLFDAPLHKKRYTASK 300
QY 241 FGFPPDMLSVRSQTKRPLFTVGEYWSYDINLHNYITKTDSMSLFDAPLHKKRYTASK 300
DB 241 FGFPPDMLSVRSQTKRPLFTVGEYWSYDINLHNYITKTDSMSLFDAPLHKKRYTASK 300
QY 301 SGGAFFMRTLMNTLMKQDPTLAVTFVDNHDTEPGQALQSWDPMFKPLAVAFILTRQEG 360
DB 301 SGGAFFMRTLMNTLMKQDPTLAVTFVDNHDTEPGQALQSWDPMFKPLAVAFILTRQEG 360
QY 361 YPCVFYGDYIGIPOYNIPLSKSIDPLLIARDDYAGTGHDLDSDIIGMREGTEKPE 420
DB 361 YPCVFYGDYIGIPOYNIPLSKSIDPLLIARDDYAGTGHDLDSDIIGMREGTEKPE 420
QY 421 GSGLAALITDGPGSKMVYKQAHAGKVFYDLTGNRSDVTITNSDGMGEFKVNGGSVSW 480
DB 421 GSGLAALITDGPGSKMVYKQAHAGKVFYDLTGNRSDVTITNSDGMGEFKVNGGSVSW 480
QY 481 VPKRTVSTIARPIITRRPWTGEFVWTEPRLVAM 514
DB 481 VPKRTVSTIARPIITRRPWTGEFVWTEPRLVAM 514

RESULT 8
US-08-720-899-6
Sequence 6, Application US/08720899
Patent No. 5733460
GENERAL INFORMATION:
APPLICANT: Bisgaard-Frantzen, Henrik
APPLICANT: Borchert, Torben Vedel
APPLICANT: Svendsen, Allan
APPLICANT: Thellersen, Marianne
APPLICANT: Van der Zee, Pia
TITLE OF INVENTION: AMYLASE VARIANTS

NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 57534600 No. 5753460disk of No. 5753460th America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/720,899
FILING DATE: 10-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/343,804
FILING DATE: 22-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lowrey Dr., Karen A.
REGISTRATION NUMBER: 31,274
REFERENCE/DOCKET NUMBER: 4054,214-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 549 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-720-899-6

Query Match 100.0%; Score 2847; DB 1; Length 549;
Best Local Similarity 100.0%; Pred. No. 1,7e-245;
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAPFGTMMQYFEWYLPDDGTLMTKVAANEANNLSIGITALMLPPAYKSTSDVGYGY 60
DB 35 AAPFGTMMQYFEWYLPDDGTLMTKVAANEANNLSIGITALMLPPAYKSTSDVGYGY 94
QY 61 DLYDGEFNQKGTVRKYGKTAQYLOAIQAABAAGQYADVDFDKGADGTEWDAVE 120
DB 95 DLYDGEFNQKGTVRKYGKTAQYLOAIQAABAAGQYADVDFDKGADGTEWDAVE 154
QY 121 VNPSDRNOEISGTQYIOAWTKFDPGRGNTYSSFKRWYHFDGVMDSESRKLSRIYKFRG 180
DB 155 VNPSDRNOEISGTQYIOAWTKFDPGRGNTYSSFKRWYHFDGVMDSESRKLSRIYKFRG 214
QY 181 IGAAMDWEVDTENGYDYLMAVDLMDHPEVVELKMGKMYNTNIDGFRLDAYKIK 240
DB 215 IGAAMDWEVDTENGYDYLMAVDLMDHPEVVELKMGKMYNTNIDGFRLDAYKIK 274
QY 241 FSEFPDMLSYRSQGTGKPLFTVGEYWSYDINKLHNYITKDGTMSLFPAFLHNKFTYASK 300
DB 275 FSEFPDMLSYRSQGTGKPLFTVGEYWSYDINKLHNYITKDGTMSLFPAFLHNKFTYASK 334
QY 301 SGGAEDMRRLMTNTLMKQOPTLAVTFVDNHDTEPGQALQSWDPMFKELAYAFILTRQEG 360
DB 335 SGGAEDMRRLMTNTLMKQOPTLAVTFVDNHDTEPGQALQSWDPMFKELAYAFILTRQEG 394
QY 361 YECVPGDYVYGIPOYNIPELSKIDPLIARDYAYGCHDYLDSDIIGMREGTEKXP 420
DB 395 YECVPGDYVYGIPOYNIPELSKIDPLIARDYAYGCHDYLDSDIIGMREGTEKXP 454
QY 421 GSGALALITDGGSGKMTYVGRKQAGKVFYDLTGNRSDVTIINSQWGEFFKUNGGSVSW 480
DB 455 GSGALALITDGGSGKMTYVGRKQAGKVFYDLTGNRSDVTIINSQWGEFFKUNGGSVSW 514
QY 481 VPRKTVSTIARPIITRPWTGFEVWRTERLVAM 514

DB 515 VPRKTVSTIARPIITRPWTGFEVWRTERLVAM 548
RESULT 9
US-08-459-610-6
Sequence 6, Application US/08459610
Patent No. 5801043
GENERAL INFORMATION:
APPLICANT: Bisgaard-Frantzen, Henrik
APPLICANT: Borchert, Torden Vedel
APPLICANT: Svendsen, Allan
APPLICANT: Thellersen, Marianne
APPLICANT: Van der Zee, Pia
TITLE OF INVENTION: AMYLASE VARIANTS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 58010430 No. 5801043disk of No. 5801043th America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,610
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/343,804
FILING DATE: 22-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lowrey Dr., Karen A.
REGISTRATION NUMBER: 31,274
REFERENCE/DOCKET NUMBER: 4054,214-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 549 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-610-6

Query Match 100.0%; Score 2847; DB 1; Length 549;
Best Local Similarity 100.0%; Pred. No. 1,7e-245;
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAPFGTMMQYFEWYLPDDGTLMTKVAANEANNLSIGITALMLPPAYKSTSDVGYGY 60
DB 35 AAPFGTMMQYFEWYLPDDGTLMTKVAANEANNLSIGITALMLPPAYKSTSDVGYGY 94
QY 61 DLYDGEFNQKGTVRKYGKTAQYLOAIQAABAAGQYADVDFDKGADGTEWDAVE 120
DB 95 DLYDGEFNQKGTVRKYGKTAQYLOAIQAABAAGQYADVDFDKGADGTEWDAVE 154
QY 121 VNPSDRNOEISGTQYIOAWTKFDPGRGNTYSSFKRWYHFDGVMDSESRKLSRIYKFRG 180
DB 155 VNPSDRNOEISGTQYIOAWTKFDPGRGNTYSSFKRWYHFDGVMDSESRKLSRIYKFRG 214
QY 181 IGAAMDWEVDTENGYDYLMAVDLMDHPEVVELKMGKMYNTNIDGFRLDAYKIK 240
DB 215 IGAAMDWEVDTENGYDYLMAVDLMDHPEVVELKMGKMYNTNIDGFRLDAYKIK 274
QY 241 FSEFPDMLSYRSQGTGKPLFTVGEYWSYDINKLHNYITKDGTMSLFPAFLHNKFTYASK 300
DB 275 FSEFPDMLSYRSQGTGKPLFTVGEYWSYDINKLHNYITKDGTMSLFPAFLHNKFTYASK 334

QY 301 SGGAEDKRTLTMTNTLMKDQPLTAVTFVNDHTEPGQALQSVNDPWFKEFLAYAFILTRQEG 360
DB 335 SGGAEDKRTLTMTNTLMKDQPLTAVTFVNDHTEPGQALQSVNDPWFKEFLAYAFILTRQEG 394
QY 361 YPCVFYGDYVGIPOYNIPSLKSKIDPLLIARDYAVGTQHDYLDHSDIIGWTRGGTEKP 420
DB 395 YPCVFYGDYVGIPOYNIPSLKSKIDPLLIARDYAVGTQHDYLDHSDIIGWTRGGTEKP 454
QY 421 GSGLAALITDGPGGSKMYYVKGQAKVFDLTGNRSPTVTINSDDGGEFFVNGGSYSVM 480
DB 455 GSGLAALITDGPGGSKMYYVKGQAKVFDLTGNRSPTVTINSDDGGEFFVNGGSYSVM 514
QY 481 VPRKTTVSTIARPIITRPWTGEFVWTEPRLVAM 514
DB 515 VPRKTTVSTIARPIITRPWTGEFVWTEPRLVAM 548

RESULT 10

US-08-343-804-6
Sequence 6, Application US/08343804

Patent No. 5830837

GENERAL INFORMATION:

APPLICANT: Bisgaard-Frantzen, Henrik

APPLICANT: Borchert, Torben Vedel

APPLICANT: Svendsen, Allan

APPLICANT: Thelliesen, Marianne

APPLICANT: Van der Zee, Pia

TITLE OF INVENTION: AMYLASE VARIANTS

NUMBER OF SEQUENCES: 38

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 5830837disk of No. 5830837th America, Inc.

STREET: 405 Lexington Avenue, 64th Floor

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10174-6401

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/343,804

FILING DATE: 22-NOV-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Lowmey Dr., Karen A.

REGISTRATION NUMBER: 31,274

REFERENCE/DOCKET NUMBER: 4054.214-US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-867-0123

TELEFAX: 212-878-9655

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 549 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-343-804-6

Query Match

Best Local Similarity 100.0%; Score 2847; DB 2; Length 549;

Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPENGTMVQFEWYIPDQGLTMTKYANANNLSSIGTALMLPAPYAGTSSDVGYVY 60

DB 35 AAPENGTMVQFEWYIPDQGLTMTKYANANNLSSIGTALMLPAPYAGTSSDVGYVY 94

QY 61 DLYDLGEFNQKGVTRTKYTKAQYLOAIOAAHAGQVYADVDPHKGADGTEWDAVE 120

DB 95 DLYDLGEFNQKGVTRTKYTKAQYLOAIOAAHAGQVYADVDPHKGADGTEWDAVE 154

QY 121 VNPSDNGEISGTVOIQAMTKFDPFGKNTYSSFKRWYHPQGVMDSEKLSRIYXRG 180

DB 155 VNPSDNGEISGTVOIQAMTKFDPFGKNTYSSFKRWYHPQGVMDSEKLSRIYXRG 214
QY 181 ICKAMDWEVDTENGNYDYLMYADLDMDHEVYVTELRWGWKYVATTNIDGRDLAVGHIX 240
DB 215 ICKAMDWEVDTENGNYDYLMYADLDMDHEVYVTELRWGWKYVATTNIDGRDLAVGHIX 274
QY 241 RSEFPDMLSYVRSQTKGLFTVGEWYSYDINKLHNYITKTGDTMSLFPAPLHNFYXSK 300
DB 275 RSEFPDMLSYVRSQTKGLFTVGEWYSYDINKLHNYITKTGDTMSLFPAPLHNFYXSK 334
QY 301 SGGAEDKRTLTMTNTLMKDQPLTAVTFVNDHTEPGQALQSVNDPWFKEFLAYAFILTRQEG 360
DB 335 SGGAEDKRTLTMTNTLMKDQPLTAVTFVNDHTEPGQALQSVNDPWFKEFLAYAFILTRQEG 394
QY 361 YPCVFYGDYVGIPOYNIPSLKSKIDPLLIARDYAVGTQHDYLDHSDIIGWTRGGTEKP 420
DB 395 YPCVFYGDYVGIPOYNIPSLKSKIDPLLIARDYAVGTQHDYLDHSDIIGWTRGGTEKP 454
QY 421 GSGLAALITDGPGGSKMYYVKGQAKVFDLTGNRSPTVTINSDDGGEFFVNGGSYSVM 480
DB 455 GSGLAALITDGPGGSKMYYVKGQAKVFDLTGNRSPTVTINSDDGGEFFVNGGSYSVM 514
QY 481 VPRKTTVSTIARPIITRPWTGEFVWTEPRLVAM 514
DB 515 VPRKTTVSTIARPIITRPWTGEFVWTEPRLVAM 548

RESULT 11

US-08-687-399-6

Sequence 6, Application US/08687399

Patent No. 5928381

GENERAL INFORMATION:

APPLICANT: Toft, Annette H.

APPLICANT: Marcher, Dorte

APPLICANT: Pedersen, Hanne H.

APPLICANT: Nilsen, Thomas E.

TITLE OF INVENTION: A Combined Desizing and Bleaching

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 5928381disk of No. 5928381th America, Inc.

STREET: 405 Lexington Avenue, 64th Floor

CITY: New York

STATE: New York

COUNTRY: United States of America

ZIP: 10174-6401

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/687,399

FILING DATE:

CLASSIFICATION: 008

ATTORNEY/AGENT INFORMATION:

NAME: Lambiris, Elias J.

REGISTRATION NUMBER: 33,728

REFERENCE/DOCKET NUMBER: 4127.204-US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-867-0123

TELEFAX: 212-878-9655

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 549 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-687-399-6

Query Match

Best Local Similarity 100.0%; Score 2847; DB 2; Length 549;

Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Tue May 4 14:34:49 2004

us-10-644-187-6.ra1

Page 7

Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 AAPENGTMQYFEMWLPDDGTLMTKYANFANNLSSIGITALLPAPYKGTSSDVGYY 60
DB 35 AAPENGTMQYFEMWLPDDGTLMTKYANFANNLSSIGITALLPAPYKGTSSDVGYY 94
QY 61 DLYDLGEFNQKGTVRTKYGKAYLOAIQAAHAGQVADVFDPHKGADGTEWDAVE 120
DB 95 DLYDLGEFNQKGTVRTKYGKAYLOAIQAAHAGQVADVFDPHKGADGTEWDAVE 154
QY 121 VNPSDRNOEISGTYQIQAMTKFDPFGKNTYSSFKRWYHFDGVDMDESKLSRIYKFRG 180
DB 155 VNPSDRNOEISGTYQIQAMTKFDPFGKNTYSSFKRWYHFDGVDMDESKLSRIYKFRG 214
QY 181 IGRAMDWEVDTEGNVDYLMYADLDMDHPEVTELKNMGKMYNTNIDGFRLDAYKHK 240
DB 215 IGRAMDWEVDTEGNVDYLMYADLDMDHPEVTELKNMGKMYNTNIDGFRLDAYKHK 274
QY 241 FSPFPDMLSVRSQGTGKPLFTVEGYSYDINKLHNYITKTGMSLFDAPLHKKFYTASK 300
DB 275 FSPFPDMLSVRSQGTGKPLFTVEGYSYDINKLHNYITKTGMSLFDAPLHKKFYTASK 334
QY 301 SGCAFPMRTLMTNTLTKDOPTLAVFDVNDHTEPGQALOSWVDPWFKPLAYAFILTRQEG 360
DB 335 SGCAFPMRTLMTNTLTKDOPTLAVFDVNDHTEPGQALOSWVDPWFKPLAYAFILTRQEG 394
QY 361 YPCVFYGDYIGIPQYNIPSLKSKIDPLLIARDYAGTQHDYLDHSDIIGMTREGGTEKP 420
DB 395 YPCVFYGDYIGIPQYNIPSLKSKIDPLLIARDYAGTQHDYLDHSDIIGMTREGGTEKP 454
QY 421 GSGLAALITDGPSSKMYVKGOKHAKVFYDLTGNNSDTVTINSDDGGEFKVNGSSVSW 480
DB 455 GSGLAALITDGPSSKMYVKGOKHAKVFYDLTGNNSDTVTINSDDGGEFKVNGSSVSW 514
QY 481 VPRKTVSTIARPIITRPWTGEFVRWTEBRLVAM 514
DB 515 VPRKTVSTIARPIITRPWTGEFVRWTEBRLVAM 548
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RESULT 12

US-08-600-908A-6
Sequence 6, Application US/08600908A

GENERAL INFORMATION:

APPLICANT: Svendsen, Allan
APPLICANT: Bisg rd-Franzen, Henrik
APPLICANT: Borchert, Torden Vedel
TITLE OF INVENTION: '-Amylase Mutants'
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESS: No. 59891690 No. 59891690disk of No. 59891690h America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6401

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/600, 908A
FILING DATE: 13-FEB-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Green, Reza

REGISTRATION NUMBER: 38,475
REFERENCE/DOCKET NUMBER: 4394.204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:
LENGTH: 549 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-600-908A-6

Query Match 100.0%; Score 2847; DB 2; Length 549;
Best Local Similarity 100.0%; Pred. No. 1.7e-245;
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 AAPENGTMQYFEMWLPDDGTLMTKYANFANNLSSIGITALLPAPYKGTSSDVGYY 60
DB 35 AAPENGTMQYFEMWLPDDGTLMTKYANFANNLSSIGITALLPAPYKGTSSDVGYY 94
QY 61 DLYDLGEFNQKGTVRTKYGKAYLOAIQAAHAGQVADVFDPHKGADGTEWDAVE 120
DB 95 DLYDLGEFNQKGTVRTKYGKAYLOAIQAAHAGQVADVFDPHKGADGTEWDAVE 154
QY 121 VNPSDRNOEISGTYQIQAMTKFDPFGKNTYSSFKRWYHFDGVDMDESKLSRIYKFRG 180
DB 155 VNPSDRNOEISGTYQIQAMTKFDPFGKNTYSSFKRWYHFDGVDMDESKLSRIYKFRG 214
QY 181 IGRAMDWEVDTEGNVDYLMYADLDMDHPEVTELKNMGKMYNTNIDGFRLDAYKHK 240
DB 215 IGRAMDWEVDTEGNVDYLMYADLDMDHPEVTELKNMGKMYNTNIDGFRLDAYKHK 274
QY 241 FSPFPDMLSVRSQGTGKPLFTVEGYSYDINKLHNYITKTGMSLFDAPLHKKFYTASK 300
DB 275 FSPFPDMLSVRSQGTGKPLFTVEGYSYDINKLHNYITKTGMSLFDAPLHKKFYTASK 334
QY 301 SGCAFPMRTLMTNTLTKDOPTLAVFDVNDHTEPGQALOSWVDPWFKPLAYAFILTRQEG 360
DB 335 SGCAFPMRTLMTNTLTKDOPTLAVFDVNDHTEPGQALOSWVDPWFKPLAYAFILTRQEG 394
QY 361 YPCVFYGDYIGIPQYNIPSLKSKIDPLLIARDYAGTQHDYLDHSDIIGMTREGGTEKP 420
DB 395 YPCVFYGDYIGIPQYNIPSLKSKIDPLLIARDYAGTQHDYLDHSDIIGMTREGGTEKP 454
QY 421 GSGLAALITDGPSSKMYVKGOKHAKVFYDLTGNNSDTVTINSDDGGEFKVNGSSVSW 480
DB 455 GSGLAALITDGPSSKMYVKGOKHAKVFYDLTGNNSDTVTINSDDGGEFKVNGSSVSW 514
QY 481 VPRKTVSTIARPIITRPWTGEFVRWTEBRLVAM 514
DB 515 VPRKTVSTIARPIITRPWTGEFVRWTEBRLVAM 548
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RESULT 13

US-08-683-838A-6
Sequence 6, Application US/08683838A

GENERAL INFORMATION:

APPLICANT: Svendsen, Allan
APPLICANT: Bisg rd-Franzen, Henrik
APPLICANT: Borchert, Torden Vedel
TITLE OF INVENTION: '-Amylase Mutants'
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESS: No. 60227240 No. 60227240disk of No. 60227240h America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6401

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/683, 838A
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/600,908
FILING DATE: 13-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Green, Reza
REGISTRATION NUMBER: 38,475
REFERENCE/DOCKET NUMBER: 4394,204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 549 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-683-838A-6

Query Match 100.0%; Score 2847; DB 3; Length 549;
Best Local Similarity 100.0%; Pred. No. 1,7e-245;
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 AAPFGTMMQYFENWLPDDGTLMTKVAANEANLSSIGITLALMPAYKGTSRSDVGYGY 60
DB 35 AAPFGTMMQYFENWLPDDGTLMTKVAANEANLSSIGITLALMPAYKGTSRSDVGYGY 94
QY 61 DLYDGEFNQKGTATKTKGTAKQYLOAIQAAHAAQYADVPDHKGADGTEWDAVE 120
DB 95 DLYDGEFNQKGTATKTKGTAKQYLOAIQAAHAAQYADVPDHKGADGTEWDAVE 154
QY 121 VNPSDRNCEISGTQIOAMTKDFPGRGNTYSSFKRWYHFDGVDMDSRLSLRYKRG 180
DB 155 VNPSDRNCEISGTQIOAMTKDFPGRGNTYSSFKRWYHFDGVDMDSRLSLRYKRG 214
QY 181 IGRAMDWEVDTENGNYDYLMYADLMDHPEVYTELKMGKMYVNTNIDGRDLDAVKAHK 240
DB 215 IGRAMDWEVDTENGNYDYLMYADLMDHPEVYTELKMGKMYVNTNIDGRDLDAVKAHK 274
QY 241 FSEFPDMISYVSQTKPLFTVGEYWSYDINKLHNYITKTGMSLFPAPLHNKFTYASK 300
DB 275 FSEFPDMISYVSQTKPLFTVGEYWSYDINKLHNYITKTGMSLFPAPLHNKFTYASK 334
QY 301 SGGAFDMRTLMTNTLMKQOPTLAVTFVNDHDEPQALQSWDPMFKFLAFAFILTRQEG 360
DB 335 SGGAFDMRTLMTNTLMKQOPTLAVTFVNDHDEPQALQSWDPMFKFLAFAFILTRQEG 394
QY 361 YPCVFYGDYGGIPQYNIPSLKSKIDPLLIARDVAYGTOHDLHSDIIGWTRREGTEKP 420
DB 395 YPCVFYGDYGGIPQYNIPSLKSKIDPLLIARDVAYGTOHDLHSDIIGWTRREGTEKP 454
QY 421 GSGALALITDGGSGKMYVKGQAHGKVFYDLTGNRSDVTIINSQGWGEFFKNGGSVAV 480
DB 455 GSGALALITDGGSGKMYVKGQAHGKVFYDLTGNRSDVTIINSQGWGEFFKNGGSVAV 514
QY 481 VPKRTTVSTIARPIITRPWTGFEFVWTEPRIVAM 514
DB 515 VPKRTTVSTIARPIITRPWTGFEFVWTEPRIVAM 548
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RESULT 14

US-09-636-252A-6
Sequence 6, Application US/09636252A
Patent No. 6440716
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Bisgard-Frantzen, Henrik
APPLICANT: Borcherdt, Torben Vedel
TITLE OF INVENTION: Alpha-Amylase Mutants
FILE REFERENCE: 0776/1F216-US2
CURRENT APPLICATION NUMBER: US/09/636,252A
CURRENT FILING DATE: 2000-08-10
PRIOR APPLICATION NUMBER: 08/683,838

PRIOR FILING DATE: 1996-07-18
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 6
LENGTH: 549
TYPE: PRT
ORGANISM: B. steatothermophilus
US-09-636-252A-6

Query Match 100.0%; Score 2847; DB 4; Length 549;
Best Local Similarity 100.0%; Pred. No. 1,7e-245;
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 AAPFGTMMQYFENWLPDDGTLMTKVAANEANLSSIGITLALMPAYKGTSRSDVGYGY 60
DB 35 AAPFGTMMQYFENWLPDDGTLMTKVAANEANLSSIGITLALMPAYKGTSRSDVGYGY 94
QY 61 DLYDGEFNQKGTATKTKGTAKQYLOAIQAAHAAQYADVPDHKGADGTEWDAVE 120
DB 95 DLYDGEFNQKGTATKTKGTAKQYLOAIQAAHAAQYADVPDHKGADGTEWDAVE 154
QY 121 VNPSDRNCEISGTQIOAMTKDFPGRGNTYSSFKRWYHFDGVDMDSRLSLRYKRG 180
DB 155 VNPSDRNCEISGTQIOAMTKDFPGRGNTYSSFKRWYHFDGVDMDSRLSLRYKRG 214
QY 181 IGRAMDWEVDTENGNYDYLMYADLMDHPEVYTELKMGKMYVNTNIDGRDLDAVKAHK 240
DB 215 IGRAMDWEVDTENGNYDYLMYADLMDHPEVYTELKMGKMYVNTNIDGRDLDAVKAHK 274
QY 241 FSEFPDMISYVSQTKPLFTVGEYWSYDINKLHNYITKTGMSLFPAPLHNKFTYASK 300
DB 275 FSEFPDMISYVSQTKPLFTVGEYWSYDINKLHNYITKTGMSLFPAPLHNKFTYASK 334
QY 301 SGGAFDMRTLMTNTLMKQOPTLAVTFVNDHDEPQALQSWDPMFKFLAFAFILTRQEG 360
DB 335 SGGAFDMRTLMTNTLMKQOPTLAVTFVNDHDEPQALQSWDPMFKFLAFAFILTRQEG 394
QY 361 YPCVFYGDYGGIPQYNIPSLKSKIDPLLIARDVAYGTOHDLHSDIIGWTRREGTEKP 420
DB 395 YPCVFYGDYGGIPQYNIPSLKSKIDPLLIARDVAYGTOHDLHSDIIGWTRREGTEKP 454
QY 421 GSGALALITDGGSGKMYVKGQAHGKVFYDLTGNRSDVTIINSQGWGEFFKNGGSVAV 480
DB 455 GSGALALITDGGSGKMYVKGQAHGKVFYDLTGNRSDVTIINSQGWGEFFKNGGSVAV 514
QY 481 VPKRTTVSTIARPIITRPWTGFEFVWTEPRIVAM 514
DB 515 VPKRTTVSTIARPIITRPWTGFEFVWTEPRIVAM 548
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RESULT 15

US-09-381-687-7
Sequence 7, Application US/09381687
Patent No. 6486113
GENERAL INFORMATION:
APPLICANT: HARADA, Yuji
APPLICANT: IKAMA, Kaori
APPLICANT: ITO, Susumu
APPLICANT: IGARASHI, Kazuaki
APPLICANT: HAGIHARA, Hiroshi
APPLICANT: HAYASHI, Yasuhiko
APPLICANT: ARAKI, Hiroyuki
APPLICANT: OZAKI, Katsuya
TITLE OF INVENTION: MUTANT ALPHA-AMYLASES
FILE REFERENCE: 2173-0115P
CURRENT APPLICATION NUMBER: US/09/381,687
CURRENT FILING DATE: 1999-09-23
SOFTWARE: PatentIn version 3.0
SEQ ID NO 7
LENGTH: 515
TYPE: PRT
ORGANISM: B. steatothermophilus

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US-09-381-687-7

Query Match 98.5%; Score 2805; DB 4; Length 515;
Best Local Similarity 98.8%; Pred. No. 8,9e-242;
Matches 508; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

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QY 1 AAFNGTMMQYFEMYLPPDGLTMTKVANEANNLSLGIITLMLPPAYKGISRSVDYGVY 60
DB 1 AAFNGTMMQYFEMYLPPDGLTMTKVANEANNLSLGIITLMLPPAYKGISRSVDYGVY 60
QY 61 DLYDGEFNQKGTATKXGTAQYLOAIOAAHAGMOYADVFPDHKGADGTEWDAVE 120
DB 61 DLYDGEFNQKGTATKXGTAQYLOAIOAAHAGMOYADVFPDHKGADGTEWDAVE 120
QY 121 VNPSDRNOEISGTYOIOAWTKFDPGRGNTYSSFKRWYHFDGVWDESRKLSRIYKRG 180
DB 121 VNPSDRNOEISGTYOIOAWTKFDPGRGNTYSSFKRWYHFDGVWDESRKLSRIYKRG 180
QY 181 IGAAMDVEYDTENGNYDILMTADLMDHPEVYTELKNMGKYYVNTNIDGRFLDAYKIK 240
DB 181 IGAAMDVEYDTENGNYDILMTADLMDHPEVYTELKNMGKYYVNTNIDGRFLDAYKIK 240
QY 241 FSFFPDWLSYVRSQTKPLFTVGEYMSYDINKLHNYITKTDGTMSLPDAPLHNKFTASK 300
DB 241 FSFFPDWLSYVRSQTKPLFTVGEYMSYDINKLHNYITKTDGTMSLPDAPLHNKFTASK 300
QY 301 SGGAFTDMRTLMTNTLMKDOPTLAVTFVNDHTEPGQALQSWVDPWFKPLAYAFILTRQEG 360
DB 301 SGGAFTDMRTLMTNTLMKDOPTLAVTFVNDHTEPGQALQSWVDPWFKPLAYAFILTRQEG 360
QY 361 YPCVFYGDYVGIPOXNIPSLKSKIDPLIARRDYAVGTQHDYLDHSDIIGWTREGTEKP 420
DB 361 YPCVFYGDYVGIPOXNIPSLKSKIDPLIARRDYAVGTQHDYLDHSDIIGWTREGTEKP 420
QY 421 GSGLAALITDGPQSSKMTVQKQHAKVYDITGNRSDDVTINSDMGSEFKVNGSVSVW 480
DB 421 GSGLAALITDGPQSSKMTVQKQHAKVYDITGNRSDDVTINSDMGSEFKVNGSVSVW 480
QY 481 VPRKTTVSTIARPIITRRPWTGEFVWTEBRLVAM 514
DB 481 VPRKTTVSTIARPIITRRPWTGEFVWTEBRLVAM 514
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Search completed: May 3, 2004, 20:35:57
Job time : 18.4001 secs

QY 61 DLYDGEFNQKGTARTKTKGTAKQYLQAIQAHAAGMÖVYADVDFHKGAGDTEWDAVE 120
DB 61 DLYDGEFNQKGTARTKTKGTAKQYLQAIQAHAAGMÖVYADVDFHKGAGDTEWDAVE 120
QY 121 VNPSDRNOEISGTQYQIQAMTKFDFPGRGNTYSSFKRMWYHFDGVDMDSRKLSTIYKFRG 180
DB 121 VNPSDRNOEISGTQYQIQAMTKFDFPGRGNTYSSFKRMWYHFDGVDMDSRKLSTIYKFRG 180
QY 181 IKGAMDEVDTEENGNVYDIAMADLMDHPEVYTELKNMGKRYVNTTINDGRDLAVAHIK 240
DB 181 IKGAMDEVDTEENGNVYDIAMADLMDHPEVYTELKNMGKRYVNTTINDGRDLAVAHIK 240
QY 241 FSPFPDWLSYVRSQTKGKPLFTVGEYWSYDINKLHNYITKTDGTMSLFDAPLHNFYTAASK 300
DB 241 FSPFPDWLSYVRSQTKGKPLFTVGEYWSYDINKLHNYITKTDGTMSLFDAPLHNFYTAASK 300
QY 301 SGCAFDMETLMTNTLMKQOPTLAVTFVNDHDEBGOALQSVDMWDFKPLAFAFLITRQEG 360
DB 301 SGCAFDMETLMTNTLMKQOPTLAVTFVNDHDEBGOALQSVDMWDFKPLAFAFLITRQEG 360
QY 361 YPCVFYGDYGIPOYNIPSLKSKIDPLLIARDYAAGTQHDYLDHSDIIGMTREBGTETKP 420
DB 361 YPCVFYGDYGIPOYNIPSLKSKIDPLLIARDYAAGTQHDYLDHSDIIGMTREBGTETKP 420
QY 421 GSGLAALITDGPQSGKMYVKGQAHGKVFYDLTGNSRDTVTINDSGGEFRKNGGSVSW 480
DB 421 GSGLAALITDGPQSGKMYVKGQAHGKVFYDLTGNSRDTVTINDSGGEFRKNGGSVSW 480
QY 481 VPKTIVSTIARPIITRPMTGEPVWTEPRLVAV 514
DB 481 VPKTIVSTIARPIITRPMTGEPVWTEPRLVAV 514

RESULT 2

US-10-186-042-6
Sequence 6, Application US/10186042
Publication No. US20030171236A1
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Borchert, Torben
APPLICANT: Bisgaard-Franzen, Henrik
TITLE OF INVENTION: Alpha-Amylase Mutants
FILE REFERENCE: 4796.204-US
CURRENT APPLICATION NUMBER: US/10/186.042
CURRENT FILING DATE: 2002-06-28
PRIOR APPLICATION NUMBER: US/09/672.459
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: 09/182.859
PRIOR FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: 0515/96
PRIOR FILING DATE: 1996-04-30
PRIOR APPLICATION NUMBER: 0712/96
PRIOR FILING DATE: 1996-06-28
PRIOR APPLICATION NUMBER: 0775/96
PRIOR FILING DATE: 1996-07-11
PRIOR APPLICATION NUMBER: 1263/96
PRIOR FILING DATE: 1996-11-08
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 6
LENGTH: 514
TYPE: PRT
ORGANISM: Bacillus stearothermophilus
US-10-186-042-6

Query Match 100.0%; Score 2847; DB 14; Length 514;
Best Local Similarity 100.0%; Pred. No. 5e-256;
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPFGTMMQYFEWYLPDDGTLMTKVANEANNLSLIGITALMLPFAKGTSRSDVGYGVY 60
DB 1 AAPFGTMMQYFEWYLPDDGTLMTKVANEANNLSLIGITALMLPFAKGTSRSDVGYGVY 60

QY 61 DLYDGEFNQKGTARTKTKGTAKQYLQAIQAHAAGMÖVYADVDFHKGAGDTEWDAVE 120
DB 61 DLYDGEFNQKGTARTKTKGTAKQYLQAIQAHAAGMÖVYADVDFHKGAGDTEWDAVE 120
QY 121 VNPSDRNOEISGTQYQIQAMTKFDFPGRGNTYSSFKRMWYHFDGVDMDSRKLSTIYKFRG 180
DB 121 VNPSDRNOEISGTQYQIQAMTKFDFPGRGNTYSSFKRMWYHFDGVDMDSRKLSTIYKFRG 180
QY 181 IKGAMDEVDTEENGNVYDIAMADLMDHPEVYTELKNMGKRYVNTTINDGRDLAVAHIK 240
DB 181 IKGAMDEVDTEENGNVYDIAMADLMDHPEVYTELKNMGKRYVNTTINDGRDLAVAHIK 240
QY 241 FSPFPDWLSYVRSQTKGKPLFTVGEYWSYDINKLHNYITKTDGTMSLFDAPLHNFYTAASK 300
DB 241 FSPFPDWLSYVRSQTKGKPLFTVGEYWSYDINKLHNYITKTDGTMSLFDAPLHNFYTAASK 300
QY 301 SGCAFDMETLMTNTLMKQOPTLAVTFVNDHDEBGOALQSVDMWDFKPLAFAFLITRQEG 360
DB 301 SGCAFDMETLMTNTLMKQOPTLAVTFVNDHDEBGOALQSVDMWDFKPLAFAFLITRQEG 360
QY 361 YPCVFYGDYGIPOYNIPSLKSKIDPLLIARDYAAGTQHDYLDHSDIIGMTREBGTETKP 420
DB 361 YPCVFYGDYGIPOYNIPSLKSKIDPLLIARDYAAGTQHDYLDHSDIIGMTREBGTETKP 420
QY 421 GSGLAALITDGPQSGKMYVKGQAHGKVFYDLTGNSRDTVTINDSGGEFRKNGGSVSW 480
DB 421 GSGLAALITDGPQSGKMYVKGQAHGKVFYDLTGNSRDTVTINDSGGEFRKNGGSVSW 480
QY 481 VPKTIVSTIARPIITRPMTGEPVWTEPRLVAV 514
DB 481 VPKTIVSTIARPIITRPMTGEPVWTEPRLVAV 514

RESULT 3

US-09-854-346-6
Sequence 6, Application US/09854346
Patent No. US2002068352A1
GENERAL INFORMATION:
APPLICANT: No. US2002068352A1ozymes A/S
APPLICANT: Svendsen, Allan
APPLICANT: Jorgensen, Christel Thea
APPLICANT: Nielsen, Bjarne Ronfeldt
TITLE OF INVENTION: Alpha-amylase variants with altered i.6 activity
FILE REFERENCE: 6140.200-US
CURRENT APPLICATION NUMBER: US/09/854.346
CURRENT FILING DATE: 2001-05-11
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
LENGTH: 515
TYPE: PRT
ORGANISM: Bacillus stearothermophilus
US-09-854-346-6

Query Match 100.0%; Score 2847; DB 9; Length 515;
Best Local Similarity 100.0%; Pred. No. 5e-256;
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPFGTMMQYFEWYLPDDGTLMTKVANEANNLSLIGITALMLPFAKGTSRSDVGYGVY 60
DB 1 AAPFGTMMQYFEWYLPDDGTLMTKVANEANNLSLIGITALMLPFAKGTSRSDVGYGVY 60
QY 61 DLYDGEFNQKGTARTKTKGTAKQYLQAIQAHAAGMÖVYADVDFHKGAGDTEWDAVE 120
DB 61 DLYDGEFNQKGTARTKTKGTAKQYLQAIQAHAAGMÖVYADVDFHKGAGDTEWDAVE 120
QY 121 VNPSDRNOEISGTQYQIQAMTKFDFPGRGNTYSSFKRMWYHFDGVDMDSRKLSTIYKFRG 180
DB 121 VNPSDRNOEISGTQYQIQAMTKFDFPGRGNTYSSFKRMWYHFDGVDMDSRKLSTIYKFRG 180
QY 181 IKGAMDEVDTEENGNVYDIAMADLMDHPEVYTELKNMGKRYVNTTINDGRDLAVAHIK 240
DB 181 IKGAMDEVDTEENGNVYDIAMADLMDHPEVYTELKNMGKRYVNTTINDGRDLAVAHIK 240

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QY 241 FSEFPDMLSVRSQCKPLFTVGEVWSYDINKLHNYITKTGDMTSLPDAPLHNKPYTASK 300
DB 241 FSEFPDMLSVRSQCKPLFTVGEVWSYDINKLHNYITKTGDMTSLPDAPLHNKPYTASK 300
QY 301 SGGAPEMTLMTNTLMKQPTLAFTVFNHDEPBGALQSWDPMFKPLAVALITRQEG 360
DB 301 SGGAPEMTLMTNTLMKQPTLAFTVFNHDEPBGALQSWDPMFKPLAVALITRQEG 360
QY 361 YPCVFGDYGGIPQYNIPLSKIDPLIARRDYAGTQHDYLDHSDIIGMTREGTEKP 420
DB 361 YPCVFGDYGGIPQYNIPLSKIDPLIARRDYAGTQHDYLDHSDIIGMTREGTEKP 420
QY 421 GSGLAALITDGPSSKMYVKGQHAGKVFYDLTGNSDVTITNSDGMGEFKVNGSVSVW 480
DB 421 GSGLAALITDGPSSKMYVKGQHAGKVFYDLTGNSDVTITNSDGMGEFKVNGSVSVW 480
QY 481 VPKRTVSTIARPIITRPWTGSEFVRWTEBRLVAM 514
DB 481 VPKRTVSTIARPIITRPWTGSEFVRWTEBRLVAM 514

RESULT 4

US-09-918-543-6
Sequence 6, Application US/09918543
Patent No. US2002015574A1
GENERAL INFORMATION:
APPLICANT: NO. US2002015574A1ozymes A/S
APPLICANT: Thisted, Thomas
APPLICANT: Kjaerulf, Soren
APPLICANT: Andersen, Carsten
APPLICANT: Fuglsang, Claus Crome
TITLE OF INVENTION: Alpha-amylase mutants with altered properties
FILE REFERENCE: 10062.200-US
CURRENT APPLICATION NUMBER: US/09/918,543
CURRENT FILING DATE: 2001-07-31
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin version 3.1
SEQ ID NO 6
LENGTH: 515
TYPE: PRF
ORGANISM: Bacillus stearothermophilus
US-09-918-543-6

Query Match 100.0%; Score 2847; DB 9; Length 515;
Best Local Similarity 100.0%; Pred. No. Se-256;
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAFNGTMMQYFEMWLPDDGTLMTKVAEANNLSIGITATLWLPAYKGTSRSDVGYGY 60
DB 1 AAFNGTMMQYFEMWLPDDGTLMTKVAEANNLSIGITATLWLPAYKGTSRSDVGYGY 60
QY 61 DLYDLGEFNQKGTVRKTKYGTQAQYLOAIOAAHAGQVADYVFDHKGADGTEWDAVE 120
DB 61 DLYDLGEFNQKGTVRKTKYGTQAQYLOAIOAAHAGQVADYVFDHKGADGTEWDAVE 120
QY 121 VNPSDRNOEISGTYOQAWTKFDPGRGNTYSSFKRWTHFDGVMDSESKLSRIYKFRG 180
DB 121 VNPSDRNOEISGTYOQAWTKFDPGRGNTYSSFKRWTHFDGVMDSESKLSRIYKFRG 180
QY 181 IGAAMDVEVDTEGNANDYLMYADLMDHDEVTTELKMGKMYVNTNIDGFRIDAVKHIK 240
DB 181 IGAAMDVEVDTEGNANDYLMYADLMDHDEVTTELKMGKMYVNTNIDGFRIDAVKHIK 240
QY 241 FSEFPDMLSVRSQCKPLFTVGEVWSYDINKLHNYITKTGDMTSLPDAPLHNKPYTASK 300
DB 241 FSEFPDMLSVRSQCKPLFTVGEVWSYDINKLHNYITKTGDMTSLPDAPLHNKPYTASK 300
QY 301 SGGAPEMTLMTNTLMKQPTLAFTVFNHDEPBGALQSWDPMFKPLAVALITRQEG 360
DB 301 SGGAPEMTLMTNTLMKQPTLAFTVFNHDEPBGALQSWDPMFKPLAVALITRQEG 360
QY 361 YPCVFGDYGGIPQYNIPLSKIDPLIARRDYAGTQHDYLDHSDIIGMTREGTEKP 420
DB 361 YPCVFGDYGGIPQYNIPLSKIDPLIARRDYAGTQHDYLDHSDIIGMTREGTEKP 420

DB 361 YPCVFGDYGGIPQYNIPLSKIDPLIARRDYAGTQHDYLDHSDIIGMTREGTEKP 420
QY 421 GSGLAALITDGPSSKMYVKGQHAGKVFYDLTGNSDVTITNSDGMGEFKVNGSVSVW 480
DB 421 GSGLAALITDGPSSKMYVKGQHAGKVFYDLTGNSDVTITNSDGMGEFKVNGSVSVW 480
QY 481 VPKRTVSTIARPIITRPWTGSEFVRWTEBRLVAM 514
DB 481 VPKRTVSTIARPIITRPWTGSEFVRWTEBRLVAM 514

RESULT 5

US-09-925-576C-6
Sequence 6, Application US/09925576C
Publication No. US20030129718A1
GENERAL INFORMATION:
APPLICANT: Andersen, Carsten
APPLICANT: Borchert, Torben Vedel
APPLICANT: Nielsen, Bjarne Ronfeldt
TITLE OF INVENTION: Amylase Variants
FILE REFERENCE: 10004.204-US
CURRENT APPLICATION NUMBER: US/09/925,576C
CURRENT FILING DATE: 2001-08-09
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.1
SEQ ID NO 6
LENGTH: 515
TYPE: PRF
ORGANISM: Bacillus stearothermophilus
US-09-925-576C-6

Query Match 100.0%; Score 2847; DB 10; Length 515;
Best Local Similarity 100.0%; Pred. No. Se-256;
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAFNGTMMQYFEMWLPDDGTLMTKVAEANNLSIGITATLWLPAYKGTSRSDVGYGY 60
DB 1 AAFNGTMMQYFEMWLPDDGTLMTKVAEANNLSIGITATLWLPAYKGTSRSDVGYGY 60
QY 61 DLYDLGEFNQKGTVRKTKYGTQAQYLOAIOAAHAGQVADYVFDHKGADGTEWDAVE 120
DB 61 DLYDLGEFNQKGTVRKTKYGTQAQYLOAIOAAHAGQVADYVFDHKGADGTEWDAVE 120
QY 121 VNPSDRNOEISGTYOQAWTKFDPGRGNTYSSFKRWTHFDGVMDSESKLSRIYKFRG 180
DB 121 VNPSDRNOEISGTYOQAWTKFDPGRGNTYSSFKRWTHFDGVMDSESKLSRIYKFRG 180
QY 181 IGAAMDVEVDTEGNANDYLMYADLMDHDEVTTELKMGKMYVNTNIDGFRIDAVKHIK 240
DB 181 IGAAMDVEVDTEGNANDYLMYADLMDHDEVTTELKMGKMYVNTNIDGFRIDAVKHIK 240
QY 241 FSEFPDMLSVRSQCKPLFTVGEVWSYDINKLHNYITKTGDMTSLPDAPLHNKPYTASK 300
DB 241 FSEFPDMLSVRSQCKPLFTVGEVWSYDINKLHNYITKTGDMTSLPDAPLHNKPYTASK 300
QY 301 SGGAPEMTLMTNTLMKQPTLAFTVFNHDEPBGALQSWDPMFKPLAVALITRQEG 360
DB 301 SGGAPEMTLMTNTLMKQPTLAFTVFNHDEPBGALQSWDPMFKPLAVALITRQEG 360
QY 361 YPCVFGDYGGIPQYNIPLSKIDPLIARRDYAGTQHDYLDHSDIIGMTREGTEKP 420
DB 361 YPCVFGDYGGIPQYNIPLSKIDPLIARRDYAGTQHDYLDHSDIIGMTREGTEKP 420
QY 421 GSGLAALITDGPSSKMYVKGQHAGKVFYDLTGNSDVTITNSDGMGEFKVNGSVSVW 480
DB 421 GSGLAALITDGPSSKMYVKGQHAGKVFYDLTGNSDVTITNSDGMGEFKVNGSVSVW 480
QY 481 VPKRTVSTIARPIITRPWTGSEFVRWTEBRLVAM 514
DB 481 VPKRTVSTIARPIITRPWTGSEFVRWTEBRLVAM 514

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RESULT 6
US-10-146-327-8
; Sequence 8, Application US/10146327
; Publication No. US20030044954A1
; GENERAL INFORMATION:
; APPLICANT: Andersen, Carsten
; APPLICANT: Jorgensen, Christel T.
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Svendsen, Allan
; APPLICANT: Kjaerulf, Soren
; TITLE OF INVENTION: Alpha-Amylase Variants
; FILE REFERENCE: 5886.200-US
; CURRENT APPLICATION NUMBER: US/10/146,327
; CURRENT FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: US/09/537,168
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: PA 1999 00437
; PRIOR FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: 60/127,427
; PRIOR FILING DATE: 1999-04-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 515
; TYPE: prt
; ORGANISM: Bacillus stearothermophilus
US-10-146-327-8

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Query Match	Similarity	100.0%	Score 2847	DB 14	Length 515
Best Local	Similarity	100.0%	Pred. No. 5e-256		
Match	514	Conservative	0	Mismatches	0
				Indels	0
				Gaps	0
Qy	1	AAPFNGTMMQYFEWYLPPDGGTLMTKVANEANNLSGLGITATMLPRAYKGTSPSDYGVGY	60		
Db	1	AAPFNGTMMQYFEWYLPPDGGTLMTKVANEANNLSGLGITATMLPRAYKGTSPSDYGVGY	60		
Qy	61	DLVDGEENOKCTVETKTKGKQAYIOAIOAAHAAAGQVADYVFPHKGGADGETEWADAVE	120		
Db	61	DLVDGEENOKCTVETKTKGKQAYIOAIOAAHAAAGQVADYVFPHKGGADGETEWADAVE	120		
Qy	121	VNPSDRNOEISGTYOIOAWTKFDFPGRGNTYTSFKRWYTHFPGVMDSESRKLSRTYKBERG	180		
Db	121	VNPSDRNOEISGTYOIOAWTKFDFPGRGNTYTSFKRWYTHFPGVMDSESRKLSRTYKBERG	180		
Qy	181	IGKADMEWDTEENGVDYLYMTADLDMDDHEVYTELKMGKMWVNTTNIIDGFRLDAVKAIX	240		
Db	181	IGKADMEWDTEENGVDYLYMTADLDMDDHEVYTELKMGKMWVNTTNIIDGFRLDAVKAIX	240		
Qy	241	BSFPFDMULSYVRSQTKPLFTYGEKWSYDINKLHNYITTDGTMSLFDAPLINKFPTASK	300		
Db	241	BSFPFDMULSYVRSQTKPLFTYGEKWSYDINKLHNYITTDGTMSLFDAPLINKFPTASK	300		
Qy	301	SGGAFDMRLTNLTMLTKDQPTLAVTFVNDHDEPGQALQSWVDPMKPPLAVAFILTRQEG	360		
Db	301	SGGAFDMRLTNLTMLTKDQPTLAVTFVNDHDEPGQALQSWVDPMKPPLAVAFILTRQEG	360		
Qy	361	YSCVFPGDYVGGIPQNYIPLSKSKIDPLLARPYAAGTQHDYLDHSDIIGMREGTEKRP	420		
Db	361	YSCVFPGDYVGGIPQNYIPLSKSKIDPLLARPYAAGTQHDYLDHSDIIGMREGTEKRP	420		
Qy	421	GGGIALITDDPGGSKMYGVKQAHAKVFPYDLTGNPSDVTYINSDDGWGEFKNGGGSVYW	480		
Db	421	GGGIALITDDPGGSKMYGVKQAHAKVFPYDLTGNPSDVTYINSDDGWGEFKNGGGSVYW	480		
Qy	481	VPRKTVSTIARPIITRRPWTGEFVWTEPRVLAM	514		
Db	481	VPRKTVSTIARPIITRRPWTGEFVWTEPRVLAM	514		

```

GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Bisgard-Frantzen, Henrik
APPLICANT: Borchert, Torben Vogel
TITLE OF INVENTION: Alpha-Amylase Mutants
FILE REFERENCE: 0776/1P216-US2
CURRENT APPLICATION NUMBER: US/10/184,771
CURRENT FILING DATE: 2002-06-28
PRIOR APPLICATION NUMBER: US/09/636,252
PRIOR FILING DATE: 2000-08-10
PRIOR APPLICATION NUMBER: 08/683,838
PRIOR FILING DATE: 1996-07-18
NUMBER OF SEQ. ID NOS: 16
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 6
LENGTH: 549
TYPE: PRT
ORGANISM: B. stearothermophilus
US-10-184-771-6

Query March 100.0% Score 2847; DB 14; Length 549;
Best Local Similarity 100.0%; Pred. No. 5, 5e-256;
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0

```

```

0Y      1  AAFPNCTMOCYEWMLPDDGLMTKRVANEANNUSLSLITLMLPPEAKVGRSDVGY 60
Db      35  AAFPNGTMOQYEWMLPDDGLMTKRVANEANNUSLSLITLMLPPEAKVGRSDVGY 94
0Y      61  DLYDLGEFNQCKGTVTKYGTAKYQLQALQAAHAAQWVADVVPDHKGADGTEWDAVE 120
Db      95  DLYDLGEFNQCKGTVTKYGTAKYQLQALQAAHAAQWVADVVPDHKGADGTEWDAVE 154
0Y      121  VMSPDNQEISGTYQIQAWTKFDPFGRGNTYSSFRKMWHPDDVMDDESKLSRIYKFRG 180
Db      155  VMSPDNQEISGTYQIQAWTKFDPFGRGNTYSSFRKMWHPDDVMDDESKLSRIYKFRG 214
0Y      181  IGRAMDWEVDTENGNNDYLMADLMDHPEVYTELKMGKMYVNTTINDGFRDLAVKHIT 240
Db      215  IGRAMDWEVDTENGNNDYLMADLMDHPEVYTELKMGKMYVNTTINDGFRDLAVKHIT 274
0Y      241  FSFPFDMLSYRSQCKPLFTVGEWASDINLKNYTLTKDGMSTLEDAHLHKFTASK 300
Db      275  FSFPFDMLSYRSQCKPLFTVGEWASDINLKNYTLTKDGMSTLEDAHLHKFTASK 334
0Y      301  SGGAFDMRLMTTLTKDQPLTAVFVNNDHTEPQALQSWDWEFKPLAYAFILTRQEG 360
Db      335  SGGAFDMRLMTTLTKDQPLTAVFVNNDHTEPQALQSWDWEFKPLAYAFILTRQEG 394
0Y      361  YPCVFYDYGITQYNIPELSKIDPLIARDVAYGQHUYLDHSDIIGMTREGGREXP 420
Db      395  YPCVFYDYGITQYNIPELSKIDPLIARDVAYGQHUYLDHSDIIGMTREGGREXP 454
0Y      421  GSGAALITDPGSGKMYVGVKQAHAKFYDITGRSDVTIINSDGWGEFKNVGSVW 480
Db      455  GSGAALITDPGSGKMYVGVKQAHAKFYDITGRSDVTIINSDGWGEFKNVGSVW 514
0Y      481  VPRKTVSTIARPIITRPMTGEFVKTRELVAM 514
Db      515  VPRKTVSTIARPIITRPMTGEFVKTRELVAM 548

RESULT 8
US-10-081-872-104
/ Sequence 104, Application US/10081872
/ Publication No. US20030125341
/ GENERAL INFORMATION:
/ APPLICANT: Callen, Walter
/ APPLICANT: Richardson, Toby
/ APPLICANT: Frey, Gerhard
/ APPLICANT: Short, Jay M.
/ APPLICANT: Machur, Eric J.
/ APPLICANT: Gray, Kevin A. S.
/ APPLICANT: Ketovuo, Jannie S.

```

```
APPLICANT: Slupska, Malgorzata
TITLE OF INVENTION: ENZYMES HAVING ALPHA AMYLASE ACTIVITY
FILE REFERENCE: 09010-108001
CURRENT APPLICATION NUMBER: US/10/081,872
CURRENT FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: US 60/270,495
PRIOR FILING DATE: 2001-02-21
PRIOR APPLICATION NUMBER: US 60/270,496
PRIOR FILING DATE: 2001-02-21
PRIOR APPLICATION NUMBER: US 60/291,122
PRIOR FILING DATE: 2001-05-14
NUMBER OF SEQ ID NOS: 321
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 104
LENGTH: 549
TYPE: PRT
ORGANISM: Environmental
US-10-081-872-104
```

```
Query Match          99.4%; Score 2829; DB 14; Length 549;
Best Local Similarity 99.4%; Pred. No. 2.6e-254;
Matches 511; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 AAFNGTMMQYFEMWLPDDGTLMTKYANBANNLSLIGITALMLPAYKGTSSSDVGYGY 60
DB 35 AAFNGTMMQYFEMWLPDDGTLMTKYANBANNLSLIGITALMLPAYKGTSSSDVGYGY 94
QY 61 DLYDGEFNOKGVTRKYGTAKQYLOAIOAAAGQYADVPFHKGAGDTEWDAVE 120
DB 95 DLYDGEFNOKGVTRKYGTAKQYLOAIOAAAGQYADVPFHKGAGDTEWDAVE 154
QY 121 VNPSDRNOEISGTQYIOAWTKDFPGRGNTYSSFKRWYHFDGVWDESRKLSRIYKFRG 180
DB 155 VNPSDRNOEISGTQYIOAWTKDFPGRGNTYSSFKRWYHFDGVWDESRKLSRIYKFRG 214
QY 181 IGAAMDWEVDTENGNDYLYMADLMDHREVTTELKMGKMYVNTNIDGRDLAVKHIX 240
DB 215 IGAAMDWEVDTENGNDYLYMADLMDHREVTTELKMGKMYVNTNIDGRDLAVKHIX 274
QY 241 FSFFPDMLSYVRSQTKPLFTVGEYWSYDINKLHNYITKTGMSLFDAPLHNKFTYASK 300
DB 275 FSFFPDMLSYVRSQTKPLFTVGEYWSYDINKLHNYITKTGMSLFDAPLHNKFTYASK 334
QY 301 SSGAFDMRTLMTNTLMKQOPTLAVTFVDNHDTEPGQALQSWDPMFKPLAYAFILTRQEG 360
DB 335 SSGAFDMRTLMTNTLMKQOPTLAVTFVDNHDTEPGQALQSWDPMFKPLAYAFILTRQEG 394
QY 361 YPCVFYGDYVGIPOYNIPLSKSIDPLLIARDYAVGTQHDYLDHSDIIGWREGGTEKP 420
DB 395 YPCVFYGDYVGIPOYNIPLSKSIDPLLIARDYAVGTQHDYLDHSDIIGWREGGTEKP 454
QY 421 GSGLAALITDGGGSKMYVKGQAHGKVFYDLTGKRSPTVTIINSOGWGEFFKYNNGSVSW 480
DB 455 GSGLAALITDGGGSKMYVKGQAHGKVFYDLTGKRSPTVTIINSOGWGEFFKYNNGSVSW 514
QY 481 VPKRTVSTIARPIITRPWTGFEFVWTEPRLVAM 514
DB 515 VPKRTVSTIARPIITRPWTGFEFVWTEPRLVAM 548
```

RESULT 9
US-10-385-305-104
Sequence 104, Application US/10385305
Publication No. US20040018607A1
GENERAL INFORMATION:
APPLICANT: Callien, Walter
APPLICANT: Richardson, Toby
APPLICANT: Frey, Gerhard
APPLICANT: Short, Jay M.
APPLICANT: Mathur, Eric J.
APPLICANT: Gray, Kevin A.
APPLICANT: Kerovuo, Janne S.

```
APPLICANT: Slupska, Malgorzata
TITLE OF INVENTION: ENZYMES HAVING ALPHA AMYLASE ACTIVITY
FILE REFERENCE: 09010-108001
CURRENT APPLICATION NUMBER: US/10/385,305
CURRENT FILING DATE: 2003-03-06
PRIOR APPLICATION NUMBER: US/10/081,872
PRIOR FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: US 60/270,495
PRIOR FILING DATE: 2001-02-21
PRIOR APPLICATION NUMBER: US 60/270,496
PRIOR FILING DATE: 2001-02-21
PRIOR APPLICATION NUMBER: US 60/291,122
PRIOR FILING DATE: 2001-05-14
NUMBER OF SEQ ID NOS: 321
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 104
LENGTH: 549
TYPE: PRT
ORGANISM: Environmental
US-10-385-305-104
```

```
Query Match          99.4%; Score 2829; DB 15; Length 549;
Best Local Similarity 99.4%; Pred. No. 2.6e-254;
Matches 511; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 AAFNGTMMQYFEMWLPDDGTLMTKYANBANNLSLIGITALMLPAYKGTSSSDVGYGY 60
DB 35 AAFNGTMMQYFEMWLPDDGTLMTKYANBANNLSLIGITALMLPAYKGTSSSDVGYGY 94
QY 61 DLYDGEFNOKGVTRKYGTAKQYLOAIOAAAGQYADVPFHKGAGDTEWDAVE 120
DB 95 DLYDGEFNOKGVTRKYGTAKQYLOAIOAAAGQYADVPFHKGAGDTEWDAVE 154
QY 121 VNPSDRNOEISGTQYIOAWTKDFPGRGNTYSSFKRWYHFDGVWDESRKLSRIYKFRG 180
DB 155 VNPSDRNOEISGTQYIOAWTKDFPGRGNTYSSFKRWYHFDGVWDESRKLSRIYKFRG 214
QY 181 IGAAMDWEVDTENGNDYLYMADLMDHREVTTELKMGKMYVNTNIDGRDLAVKHIX 240
DB 215 IGAAMDWEVDTENGNDYLYMADLMDHREVTTELKMGKMYVNTNIDGRDLAVKHIX 274
QY 241 FSFFPDMLSYVRSQTKPLFTVGEYWSYDINKLHNYITKTGMSLFDAPLHNKFTYASK 300
DB 275 FSFFPDMLSYVRSQTKPLFTVGEYWSYDINKLHNYITKTGMSLFDAPLHNKFTYASK 334
QY 301 SSGAFDMRTLMTNTLMKQOPTLAVTFVDNHDTEPGQALQSWDPMFKPLAYAFILTRQEG 360
DB 335 SSGAFDMRTLMTNTLMKQOPTLAVTFVDNHDTEPGQALQSWDPMFKPLAYAFILTRQEG 394
QY 361 YPCVFYGDYVGIPOYNIPLSKSIDPLLIARDYAVGTQHDYLDHSDIIGWREGGTEKP 420
DB 395 YPCVFYGDYVGIPOYNIPLSKSIDPLLIARDYAVGTQHDYLDHSDIIGWREGGTEKP 454
QY 421 GSGLAALITDGGGSKMYVKGQAHGKVFYDLTGKRSPTVTIINSOGWGEFFKYNNGSVSW 480
DB 455 GSGLAALITDGGGSKMYVKGQAHGKVFYDLTGKRSPTVTIINSOGWGEFFKYNNGSVSW 514
QY 481 VPKRTVSTIARPIITRPWTGFEFVWTEPRLVAM 514
DB 515 VPKRTVSTIARPIITRPWTGFEFVWTEPRLVAM 548
```

RESULT 10
US-10-081-872-92
Sequence 92, Application US/10081872
Publication No. US20030125534A1
GENERAL INFORMATION:
APPLICANT: Callien, Walter
APPLICANT: Richardson, Toby
APPLICANT: Frey, Gerhard
APPLICANT: Short, Jay M.
APPLICANT: Mathur, Eric J.

APPLICANT: Gray, Kevin A.
APPLICANT: Kerovo, Jeanne S.
APPLICANT: Slupeka, Malgorzata
TITLE OF INVENTION: ENZYMES HAVING ALPHA AMYLASE ACTIVITY
FILE REFERENCE: 09010-108001
CURRENT APPLICATION NUMBER: US/10/081,872
CURRENT FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: US 60/270,495
PRIOR FILING DATE: 2001-02-21
PRIOR APPLICATION NUMBER: US 60/270,496
PRIOR FILING DATE: 2001-02-21
PRIOR APPLICATION NUMBER: US 60/291,122
PRIOR FILING DATE: 2001-05-14
SOFTWARE: FastSeq for Windows Version 4.0
SEQUENCE ID NO: 92
LENGTH: 549
TYPE: PRT
ORGANISM: Bacterial
US-10-081-872-92

Query Match 99.2%; Score 2825; DB 14; Length 549;
Best Local Similarity 99.4%; Pred. No. 6.1e-254;

Matches 511; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

1 AAFNGTMMQYFEMWIPDDGTMTKVAANEANNISLIGITALMLPPAYKTSRSDVGYVY 60
35 AAFNGTMMQYFEMWIPDDGTMTKVAANEANNISLIGITALMLPPAYKTSRSDVGYVY 94
61 DLYDLGEFNOKGVTRKRYGKAYLOAIOAAHAGQYADVPFHKGAGDTEWDAVE 120
95 DLYDLGEFNOKGVTRKRYGKAYLOAIOAAHAGQYADVPFHKGAGDTEWDAVE 154
121 VNPSDRNOEISGTYYQIOAWTKFDPGRGNTYSSFKRWYHFDGVWDESRKLSRIYKFRG 180
155 VNPSDRNOEISGTYYQIOAWTKFDPGRGNTYSSFKRWYHFDGVWDESRKLSRIYKFRG 214
181 IGRAMWEVDTEGNANDYLMYADLDMDHBEVYTELKNWKMVNTNIDGFLDAVKHK 240
215 IGRAMWEVDTEGNANDYLMYADLDMDHBEVYTELKNWKMVNTNIDGFLDAVKHK 274
241 FSEFFPDLISYRSQTKPLFTVGEYWSYDINKLHNYITKTDGMSLFDAPLNKRYTASK 300
275 FSEFFPDLISYRSQTKPLFTVGEYWSYDINKLHNYITKTDGMSLFDAPLNKRYTASK 334
301 SGGAFFMRITMTNTLMKDOPTLAFTVDNHDTEPGQALOSWDPMFKPLAFAFILTRREG 360
335 SGGAFFMRITMTNTLMKDOPTLAFTVDNHDTEPGQALOSWDPMFKPLAFAFILTRREG 394
361 YPCVFYGDYIGIPOYNIPLSKSIDPLLIARRDYAGTQHDYLDHSDIIGWREGTEKRP 420
395 YPCVFYGDYIGIPOYNIPLSKSIDPLLIARRDYAGTQHDYLDHSDIIGWREGTEKRP 454
421 GSGIALIITDGPQSGSKMYVKQKQAKVYDILGNRSDVTYINSOGMGEFKNGGVSVM 480
455 GSGIALIITDGPQSGSKMYVKQKQAKVYDILGNRSDVTYINSOGMGEFKNGGVSVM 514
481 VPRKTIYSTIARPIITRPWTGEFVRWTEBRLVAM 514
515 VPRKTIYSTIARPIITRPWTGEFVRWTEBRLVAM 548

RESULT 11

US-10-385-305-92
Sequence 32, Application US/10385305
Publication No. US20040018607A1
GENERAL INFORMATION:
APPLICANT: Callen, Walter
APPLICANT: Richardson, Toby
APPLICANT: Frey, Gerhard
APPLICANT: Short, Jay M.
APPLICANT: Mathur, Eric J.

APPLICANT: Gray, Kevin A.
APPLICANT: Kerovo, Jeanne S.
APPLICANT: Slupeka, Malgorzata
TITLE OF INVENTION: ENZYMES HAVING ALPHA AMYLASE ACTIVITY
FILE REFERENCE: 09010-108001
CURRENT APPLICATION NUMBER: US/10/385,305
CURRENT FILING DATE: 2003-03-06
PRIOR APPLICATION NUMBER: US/10/081,872
PRIOR FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: US 60/270,495
PRIOR FILING DATE: 2001-02-21
PRIOR APPLICATION NUMBER: US 60/270,496
PRIOR FILING DATE: 2001-02-21
PRIOR APPLICATION NUMBER: US 60/291,122
PRIOR FILING DATE: 2001-05-14
SOFTWARE: FastSeq for Windows Version 4.0
SEQUENCE ID NO: 92
LENGTH: 549
TYPE: PRT
ORGANISM: Bacterial
US-10-385-305-92

Query Match 99.2%; Score 2825; DB 15; Length 549;
Best Local Similarity 99.4%; Pred. No. 6.1e-254;

Matches 511; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

1 AAFNGTMMQYFEMWIPDDGTMTKVAANEANNISLIGITALMLPPAYKTSRSDVGYVY 60
35 AAFNGTMMQYFEMWIPDDGTMTKVAANEANNISLIGITALMLPPAYKTSRSDVGYVY 94
61 DLYDLGEFNOKGVTRKRYGKAYLOAIOAAHAGQYADVPFHKGAGDTEWDAVE 120
95 DLYDLGEFNOKGVTRKRYGKAYLOAIOAAHAGQYADVPFHKGAGDTEWDAVE 154
121 VNPSDRNOEISGTYYQIOAWTKFDPGRGNTYSSFKRWYHFDGVWDESRKLSRIYKFRG 180
155 VNPSDRNOEISGTYYQIOAWTKFDPGRGNTYSSFKRWYHFDGVWDESRKLSRIYKFRG 214
181 IGRAMWEVDTEGNANDYLMYADLDMDHBEVYTELKNWKMVNTNIDGFLDAVKHK 240
215 IGRAMWEVDTEGNANDYLMYADLDMDHBEVYTELKNWKMVNTNIDGFLDAVKHK 274
241 FSEFFPDLISYRSQTKPLFTVGEYWSYDINKLHNYITKTDGMSLFDAPLNKRYTASK 300
275 FSEFFPDLISYRSQTKPLFTVGEYWSYDINKLHNYITKTDGMSLFDAPLNKRYTASK 334
301 SGGAFFMRITMTNTLMKDOPTLAFTVDNHDTEPGQALOSWDPMFKPLAFAFILTRREG 360
335 SGGAFFMRITMTNTLMKDOPTLAFTVDNHDTEPGQALOSWDPMFKPLAFAFILTRREG 394
361 YPCVFYGDYIGIPOYNIPLSKSIDPLLIARRDYAGTQHDYLDHSDIIGWREGTEKRP 420
395 YPCVFYGDYIGIPOYNIPLSKSIDPLLIARRDYAGTQHDYLDHSDIIGWREGTEKRP 454
421 GSGIALIITDGPQSGSKMYVKQKQAKVYDILGNRSDVTYINSOGMGEFKNGGVSVM 480
455 GSGIALIITDGPQSGSKMYVKQKQAKVYDILGNRSDVTYINSOGMGEFKNGGVSVM 514
481 VPRKTIYSTIARPIITRPWTGEFVRWTEBRLVAM 514
515 VPRKTIYSTIARPIITRPWTGEFVRWTEBRLVAM 548

RESULT 12

US-09-769-864-3
Sequence 3, Application US/09769864
Patent No. US20010039253A1
GENERAL INFORMATION:
APPLICANT: Borchert, Torben V.
APPLICANT: Svendsen, Allan
APPLICANT: Andersen, Carsten

APPLICANT: Nielsen, Bjarne
 APPLICANT: Nissen, Torden L.
 APPLICANT: Kjaerulff, Soren
 TITLE OF INVENTION: Alpha-Amulase Mutants
 FILE REFERENCES: 5368.200-US
 CURRENT APPLICATION NUMBER: US/09/769,864
 PRIOR FILING DATE: 2001-01-25
 PRIOR APPLICATION NUMBER: 09/183,412
 NUMBER OF SEQ ID NOS: 58
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO: 3
 LENGTH: 514
 TYPE: PRT
 ORGANISM: Bacillus stearothermophilus
 US-09-769-864-3

Query Match 97.6%; Score 2780; DB 9; Length 514;
 Best Local Similarity 98.1%; Pred. No. 8.6e-250;
 Matches 504; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

1 AAFNGTMMQYFEMYLPPDDGLMTKVNANNNLSLIGITALMPPAYKTSRSDVGYGY 60
 1 AAFNGTMMQYFEMYLPPDDGLMTKVNANNNLSLIGITALMPPAYKTSRSDVGYGY 60
 61 DLYDLEFNGKGVTRTKYGAQYLQAIQAHAAGQYADVDFDHKGADGTEWDAVE 120
 61 DLYDLEFNGKGVTRTKYGAQYLQAIQAHAAGQYADVDFDHKGADGTEWDAVE 120
 121 VNPSDRNOEISGTYQIQAMTKFPPGRGNTYSSFKRWTHFPGVMDSEKLSRIYKFRG 180
 121 VNPSDRNOEISGTYQIQAMTKFPPGRGNTYSSFKRWTHFPGVMDSEKLSRIYKFRG 180
 121 VNPSDRNOEISGTYQIQAMTKFPPGRGNTYSSFKRWTHFPGVMDSEKLSRIYKFRG 180
 121 VNPSDRNOEISGTYQIQAMTKFPPGRGNTYSSFKRWTHFPGVMDSEKLSRIYKFRG 180
 181 IGAAMDWEVDTEGNNDYLAADLMDHPEVTELKMGKMYNTNINIGFRIDAVALHIK 240
 181 IGAAMDWEVDTEGNNDYLAADLMDHPEVTELKMGKMYNTNINIGFRIDAVALHIK 240
 181 IGAAMDWEVDTEGNNDYLAADLMDHPEVTELKMGKMYNTNINIGFRIDAVALHIK 240
 241 FSEFPDMLSVRSQGTGKPLFTVGEYWSYDINKLHNTYTKDGTMSLPDAPLHKKFYTASK 300
 241 FSEFPDMLSVRSQGTGKPLFTVGEYWSYDINKLHNTYTKDGTMSLPDAPLHKKFYTASK 300
 241 FSEFPDMLSVRSQGTGKPLFTVGEYWSYDINKLHNTYTKDGTMSLPDAPLHKKFYTASK 300
 301 SGAPDMRILMTNTLMKDQPTLAVTFVNDHTEBGAALQSWDPWFKPLAVAFILTRQEG 360
 301 SGAPDMRILMTNTLMKDQPTLAVTFVNDHTEBGAALQSWDPWFKPLAVAFILTRQEG 360
 301 SGAPDMRILMTNTLMKDQPTLAVTFVNDHTEBGAALQSWDPWFKPLAVAFILTRQEG 360
 361 YPCVFYGYGIPQYNIPSLKSKIDPLLIARDVAYGTOHLYLDHSDIIGWTEEGTEKP 420
 361 YPCVFYGYGIPQYNIPSLKSKIDPLLIARDVAYGTOHLYLDHSDIIGWTEEGTEKP 420
 361 YPCVFYGYGIPQYNIPSLKSKIDPLLIARDVAYGTOHLYLDHSDIIGWTEEGTEKP 420
 421 GSGLAALITDGGGSKMYVGKQAHGKVFYDLTGNSDVTITNSDGMGEFKVNGGSVAV 480
 421 GSGLAALITDGGGSKMYVGKQAHGKVFYDLTGNSDVTITNSDGMGEFKVNGGSVAV 480
 421 GSGLAALITDGGGSKMYVGKQAHGKVFYDLTGNSDVTITNSDGMGEFKVNGGSVAV 480
 481 VPKRTVSTIARPIITRPWTGEFVWTEPRLVAM 514
 481 VPKRTVSTIARPIITRPWTGEFVWTEPRLVAM 514
 481 VPKRTVSTIARPIITRPWTGEFVWTEPRLVAM 514

RESULT 13

US-09-902-188A-3
 Sequence 3, Application US/09902188A
 Patent No. US2002009896A1

GENERAL INFORMATION:

APPLICANT: Bisgaard-Frantzen, Henrik
 Svendsen, Allan
 Borchert, Torden Vedel
 TITLE OF INVENTION: AMYLASE VARIANTS
 NUMBER OF SEQUENCES: 32
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: No. US2002009896A10 No. US2002009896A1disk of No. US200200989
 STREET: 405 Lexington Avenue, Suite 6400
 CITY: New York
 STATE: New York

COUNTRY: U.S.A.
 ZIP: 10174-6401
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25 (BPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/902,188A
 FILING DATE: 10-Jul-2001
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/354,191
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Lambiris, Elias J.
 REGISTRATION NUMBER: 33,728
 REFERENCE/DOCKET NUMBER: 4318.204-US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212 867 0123
 TELEFAX: 212 867 0298
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 514 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULAR TYPE: peptide
 SEQUENCE DESCRIPTION: SEQ ID NO: 3:
 US-09-902-188A-3

Query Match 97.6%; Score 2780; DB 9; Length 514;
 Best Local Similarity 98.1%; Pred. No. 8.6e-250;
 Matches 504; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

1 AAFNGTMMQYFEMYLPPDDGLMTKVNANNNLSLIGITALMPPAYKTSRSDVGYGY 60
 1 AAFNGTMMQYFEMYLPPDDGLMTKVNANNNLSLIGITALMPPAYKTSRSDVGYGY 60
 61 DLYDLEFNGKGVTRTKYGAQYLQAIQAHAAGQYADVDFDHKGADGTEWDAVE 120
 61 DLYDLEFNGKGVTRTKYGAQYLQAIQAHAAGQYADVDFDHKGADGTEWDAVE 120
 121 VNPSDRNOEISGTYQIQAMTKFPPGRGNTYSSFKRWTHFPGVMDSEKLSRIYKFRG 180
 121 VNPSDRNOEISGTYQIQAMTKFPPGRGNTYSSFKRWTHFPGVMDSEKLSRIYKFRG 180
 121 VNPSDRNOEISGTYQIQAMTKFPPGRGNTYSSFKRWTHFPGVMDSEKLSRIYKFRG 180
 121 VNPSDRNOEISGTYQIQAMTKFPPGRGNTYSSFKRWTHFPGVMDSEKLSRIYKFRG 180
 181 IGAAMDWEVDTEGNNDYLAADLMDHPEVTELKMGKMYNTNINIGFRIDAVALHIK 240
 181 IGAAMDWEVDTEGNNDYLAADLMDHPEVTELKMGKMYNTNINIGFRIDAVALHIK 240
 181 IGAAMDWEVDTEGNNDYLAADLMDHPEVTELKMGKMYNTNINIGFRIDAVALHIK 240
 241 FSEFPDMLSVRSQGTGKPLFTVGEYWSYDINKLHNTYTKDGTMSLPDAPLHKKFYTASK 300
 241 FSEFPDMLSVRSQGTGKPLFTVGEYWSYDINKLHNTYTKDGTMSLPDAPLHKKFYTASK 300
 241 FSEFPDMLSVRSQGTGKPLFTVGEYWSYDINKLHNTYTKDGTMSLPDAPLHKKFYTASK 300
 301 SGAPDMRILMTNTLMKDQPTLAVTFVNDHTEBGAALQSWDPWFKPLAVAFILTRQEG 360
 301 SGAPDMRILMTNTLMKDQPTLAVTFVNDHTEBGAALQSWDPWFKPLAVAFILTRQEG 360
 301 SGAPDMRILMTNTLMKDQPTLAVTFVNDHTEBGAALQSWDPWFKPLAVAFILTRQEG 360
 361 YPCVFYGYGIPQYNIPSLKSKIDPLLIARDVAYGTOHLYLDHSDIIGWTEEGTEKP 420
 361 YPCVFYGYGIPQYNIPSLKSKIDPLLIARDVAYGTOHLYLDHSDIIGWTEEGTEKP 420
 361 YPCVFYGYGIPQYNIPSLKSKIDPLLIARDVAYGTOHLYLDHSDIIGWTEEGTEKP 420
 421 GSGLAALITDGGGSKMYVGKQAHGKVFYDLTGNSDVTITNSDGMGEFKVNGGSVAV 480
 421 GSGLAALITDGGGSKMYVGKQAHGKVFYDLTGNSDVTITNSDGMGEFKVNGGSVAV 480
 421 GSGLAALITDGGGSKMYVGKQAHGKVFYDLTGNSDVTITNSDGMGEFKVNGGSVAV 480
 481 VPKRTVSTIARPIITRPWTGEFVWTEPRLVAM 514
 481 VPKRTVSTIARPIITRPWTGEFVWTEPRLVAM 514
 481 VPKRTVSTIARPIITRPWTGEFVWTEPRLVAM 514

RESULT 14

US-10-665-667-3
 ; Sequence 3, Application US/1065667
 ; Publication No. US20040038368A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Borchert, Torben V.
 ; APPLICANT: Svendsen, Allan
 ; APPLICANT: Andersen, Carsten
 ; APPLICANT: Nielsen, Bjarne
 ; APPLICANT: Nissen, Torben L.
 ; APPLICANT: Kjaerulf, Søren
 ; TITLE OF INVENTION: Alpha-Amylase Mutants
 ; FILE REFERENCE: 5368.200-US
 ; CURRENT APPLICATION NUMBER: US/10/665,667
 ; CURRENT FILING DATE: 2003-09-19
 ; PRIOR APPLICATION NUMBER: US/09/769,864
 ; PRIOR FILING DATE: 2001-01-25
 ; PRIOR APPLICATION NUMBER: 09/183,412
 ; PRIOR FILING DATE: 1998-10-30
 ; NUMBER OF SEQ ID NOS: 58
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO: 3
 ; LENGTH: 514
 ; TYPE: PRT
 ; ORGANISM: Bacillus stearothermophilus
 ; US-10-665-667-3

Query Match 97.6%; Score 2780; DB 12; Length 514;
 Best Local Similarity 98.1%; Pred. No. 8.6e-250;
 Matches 504; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

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QY 1 AAFNGTMMQYFEWYLPDDGTLMTKVNANNNLSLIGITLMLPRAKGTSRSDVGYYV 60
DB 1 AAFNGTMMQYFEWYLPDDGTLMTKVNANNNLSLIGITLMLPRAKGTSRSDVGYYV 60
QY 61 DLYDGEFNQKGTATKTKGTATQAYLOAIQAAHAAQVYADVVDHKGADGTEWDAVE 120
DB 61 DLYDGEFNQKGTATKTKGTATQAYLOAIQAAHAAQVYADVVDHKGADGTEWDAVE 120
QY 121 VNPSPRNOEISGTQIOAWTKFDFPGKNTYSSFFKRWYHFDGVDMDESKLSRIYKFRG 180
DB 121 VNPSPRNOEISGTQIOAWTKFDFPGKNTYSSFFKRWYHFDGVDMDESKLSRIYKFRG 180
QY 121 VNPSPRNOEISGTQIOAWTKFDFPGKNTYSSFFKRWYHFDGVDMDESKLSRIYKFRG 180
DB 121 VNPSPRNOEISGTQIOAWTKFDFPGKNTYSSFFKRWYHFDGVDMDESKLSRIYKFRG 180
QY 181 IGAAMDWEVDTENGNVDYLMATADLMDHPEVYTELKSGKMYVNTTINDGRDLDAVGHK 240
DB 181 IGAAMDWEVDTENGNVDYLMATADLMDHPEVYTELKSGKMYVNTTINDGRDLDAVGHK 240
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DB 241 FSEFPDMLSYRSQTKPLFTVGEYWSYDINKLHNYITKTGTMSLFPAFLHNKFTYASK 300
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QY 361 YPCVFYGYGIPQVNIPLSKSKIDPLIARRDYAVGQHDYLDHSDIIGWTRREGTEKP 420
DB 361 YPCVFYGYGIPQVNIPLSKSKIDPLIARRDYAVGQHDYLDHSDIIGWTRREGTEKP 420
QY 421 GSGALALITDGPQSGKMYVKGQAHAKVFDLTGNRSDVTITNSDGWGEFKNVGSVSW 480
DB 421 GSGALALITDGPQSGKMYVKGQAHAKVFDLTGNRSDVTITNSDGWGEFKNVGSVSW 480
QY 481 VPRKTVSTIARPIITTRPWTGEPFWRTEPRILVAM 514
DB 481 VPRKTVSTIARPIITTRPWTGEPFWRTEPRILVAM 514

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RESULT 15
 US-10-025-648-3
 ; Sequence 3, Application US/10025648
 ; Publication No. US20030064908A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bisgaard-Frantzen, Henrik

Svendsen, Allan
 Borchert, Torben Vedel
 TITLE OF INVENTION: AMYLASE VARIANTS
 NUMBER OF SEQUENCES: 32
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Novo Nordisk of North America, Inc.
 STREET: 405 Lexington Avenue, Suite 6400
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10174-6401
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25 (EFO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/025,648
 FILING DATE: 19-Dec-2001
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/600,656
 FILING DATE: 13-FEB-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Lambiris, Elias J.
 REGISTRATION NUMBER: 33,728
 REFERENCE/DOCKET NUMBER: 4318.204-US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212 867 0123
 TELEFAX: 212 867 0298
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 514 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 SEQUENCE DESCRIPTION: SEQ ID NO: 3:

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QY 1 AAFNGTMMQYFEWYLPDDGTLMTKVNANNNLSLIGITLMLPRAKGTSRSDVGYYV 60
DB 1 AAFNGTMMQYFEWYLPDDGTLMTKVNANNNLSLIGITLMLPRAKGTSRSDVGYYV 60
QY 61 DLYDGEFNQKGTATKTKGTATQAYLOAIQAAHAAQVYADVVDHKGADGTEWDAVE 120
DB 61 DLYDGEFNQKGTATKTKGTATQAYLOAIQAAHAAQVYADVVDHKGADGTEWDAVE 120
QY 121 VNPSPRNOEISGTQIOAWTKFDFPGKNTYSSFFKRWYHFDGVDMDESKLSRIYKFRG 180
DB 121 VNPSPRNOEISGTQIOAWTKFDFPGKNTYSSFFKRWYHFDGVDMDESKLSRIYKFRG 180
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DB 121 VNPSPRNOEISGTQIOAWTKFDFPGKNTYSSFFKRWYHFDGVDMDESKLSRIYKFRG 180
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DB 181 IGAAMDWEVDTENGNVDYLMATADLMDHPEVYTELKSGKMYVNTTINDGRDLDAVGHK 240
QY 241 FSEFPDMLSYRSQTKPLFTVGEYWSYDINKLHNYITKTGTMSLFPAFLHNKFTYASK 300
DB 241 FSEFPDMLSYRSQTKPLFTVGEYWSYDINKLHNYITKTGTMSLFPAFLHNKFTYASK 300
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DB 301 SGGAFDMRTLMTNTLMKQOPTLAATFVNDHDEPQALQSWDVPFKPLAYAFILTRQEG 360
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DB 361 YPCVFYGYGIPQVNIPLSKSKIDPLIARRDYAVGQHDYLDHSDIIGWTRREGTEKP 420
QY 421 GSGALALITDGPQSGKMYVKGQAHAKVFDLTGNRSDVTITNSDGWGEFKNVGSVSW 480
DB 421 GSGALALITDGPQSGKMYVKGQAHAKVFDLTGNRSDVTITNSDGWGEFKNVGSVSW 480

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Tue May 4 14:34:49 2004

us-10-644-187-6.rapb

Page 9

Db 421 GSGLAALITDGPQSKMYGKQKAGKVFYDLTGNSDPTTINSDDGMEFKVNGGSVSW 480
Qy 481 VPKTTVSTIARPIITRPMTGSEVWTEPRLVW 514
Db 481 VPKTTVSTIAMSITTRPMTDEFWTEPRLVW 514

Search completed: May 3, 2004, 20:47:47
Job time : 41.0203 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 3, 2004, 20:45:43 ; Search time 14.6161 Seconds
(without alignments)
3382.735 Million cell updates/sec

Title: US-10-644-187-6

Perfect score: 2847
Sequence: 1 AAPNGTMMQYFEWYLPDDG.....TTRPWGTGEPYKWTPEPLVAM 514

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 9651526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2847	100.0	549	1 A54541	alpha-amylase (BC
2	2805	98.5	549	1 A24549	alpha-amylase (BC
3	2780	97.6	549	1 A24436	alpha-amylase (BC
4	2720.5	95.6	548	1 A1ASPF	alpha-amylase (BC
5	1874.5	65.8	518	1 A27705	alpha-amylase (BC
6	1794.5	63.0	512	1 ALBSL	alpha-amylase (BC
7	1773.5	62.3	514	1 ALBSN	alpha-amylase (EC
8	1345.5	47.3	492	2 AH2079	alpha-amylase (lmp
9	1315	46.2	484	2 G95160	alpha-amylase (lmp
10	1311	46.0	484	2 F98026	alpha-amylase (EC
11	1278.5	44.9	493	2 S15713	alpha-amylase (EC
12	1229	43.2	491	2 C66781	alpha-amylase (lmp
13	1112.5	39.1	494	1 B45738	alpha-amylase (BC
14	1101.5	38.7	494	2 AD0751	cytoplasmic alpha-
15	1078.5	37.9	495	2 AD3038	alpha-amylase amYA
16	1078.5	37.9	506	2 G98247	cytoplasmic alpha-
17	1074.5	37.7	495	1 A45738	alpha-amylase (BC
18	1074.5	37.7	495	2 B90962	cytoplasmic alpha-
19	1055.5	37.1	495	2 B65810	cytoplasmic alpha-
20	354.5	12.5	217	2 A19506	alpha-amylase (EC
21	326.5	11.5	482	2 S31478	alpha-amylase (BC
22	313	11.0	713	1 ALBSG7	cytoplasmic alpha-
23	307	10.8	826	2 E96720	probable alpha-amy
24	307	10.8	1196	2 A29130	beta-amylase (EC 3
25	302.5	10.6	713	2 S14958	alpha-amylase (EC
26	302	10.6	440	2 S09196	cyclomalto-dextrin
27	300	10.5	713	2 A58800	cyclomalto-dextrin
28	286	10.4	423	2 T09942	alpha-amylase (EC
29	295	10.4	428	2 T05521	alpha-amylase (EC

30	286.5	10.1	712	1 ALBSG3	cyclomalto-dextrin
31	286	10.0	718	1 ALBSMX	cyclomalto-dextrin
32	284.5	10.0	713	1 ALBSG1	cyclomalto-dextrin
33	283	9.9	421	2 S10514	alpha-amylase (EC
34	282	9.9	718	1 ALBSG6	cyclomalto-dextrin
35	280	9.8	413	1 ALMT3	alpha-amylase (EC
36	279.5	9.8	504	2 A55861	alpha-amylase (BC
37	278	9.8	718	1 ALBSG3	cyclomalto-dextrin
38	277.5	9.7	439	2 T02956	alpha-amylase (EC
39	275.5	9.7	564	2 T41503	alpha-amylase (BC
40	274.5	9.6	438	2 S14957	alpha-amylase (BC
41	274.5	9.6	528	1 ALBSK	alpha-amylase (EC
42	273	9.6	710	2 S63598	cyclomalto-dextrin
43	272.5	9.6	428	2 S10013	alpha-amylase (EC
44	272.5	9.6	434	2 S12775	alpha-amylase (EC
45	271.5	9.5	437	2 S14956	alpha-amylase (EC

ALIGNMENTS

RESULT 1

A54541
alpha-amylase (EC 3.2.1.1) precursor - *Bacillus stearothermophilus* (strain DN1792)
N/Alternate names: 1,4-alpha-D-glucan glucanohydrolase
C/Species: *Bacillus stearothermophilus*
C/Date: 28-Oct-1994 #sequence_revision 18-Aug-1995 #text_change 13-Jun-1997
C/Accession: A54541
R/Jorgensen, P.L.; Poulsen, G.B.; Diderichsen, B.
FEMS Microbiol. Lett. 77, 271-276, 1991
A/Title: Cloning of a chromosomal alpha-amylase gene from *Bacillus stearothermophilus*.
A/Reference number: A54541
A/Accession: A54541
A/Molecule type: DNA
A/Residues: 1-549 <OR>
A/Cross-references: GB:X59476
A/Experimental source: chromosomal DNA of strain DN1792
C/Comment: Alpha-amylase genes have been found on plasmids and in multiple copies on the
C/Genetics:
A/Start codon: GTG
C/Function:
A/Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A/Pathway: glycogen/starch degradation
C/Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology
C/Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; polysac
F/1-34/Domain: signal sequence #status predicted <Sig>
F/35-549/Product: alpha-amylase #status predicted <MAT>
F/235-368/Domain: alpha-amylase core homology <MAT>
F/119-237/Binding site: calcium (Asp, Asp, His) #status predicted
F/266,268,365/Active site: Asp, Glu, Asp #status predicted

Query Match 100.0%; Score 2847; DB 1; Length 549;
Best local similarity 100.0%; Pred. No. 5.5e-198;

Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	AAPNGTMMQYFEWYLPDDGTLMTKYANEANNLSIGITLMPAYKGTSRSDVGYGY	60
DB	35	AAPNGTMMQYFEWYLPDDGTLMTKYANEANNLSIGITLMPAYKGTSRSDVGYGY	94
QY	61	DLVLDGFNKGKTVRTKYGKQYLOAIQAAAGAGQVADVFDKGGADGTEWDAVE	120
DB	95	DLVLDGFNKGKTVRTKYGKQYLOAIQAAAGAGQVADVFDKGGADGTEWDAVE	154
QY	121	VNPSDRNOEISGTYQIAQWTKFPDPGGNGTYSFFKRWYFPDGVDMDESKLSRIYKFRG	180
DB	155	VNPSDRNOEISGTYQIAQWTKFPDPGGNGTYSFFKRWYFPDGVDMDESKLSRIYKFRG	214
QY	181	IGKAMDVEVDTEGNGYDLYADLDMDHPEVVELKNGKMYNTNTNIDGFRLDAYKHK	240
DB	215	IGKAMDVEVDTEGNGYDLYADLDMDHPEVVELKNGKMYNTNTNIDGFRLDAYKHK	274
QY	241	PSFPPDLSTYRSGTGKPLFTVGEYWSYDINKLHANYTTKTDGMSLFDALHKFYSK	300

Db 275 FSPFPDMLSYRSQGRKPLFTVGEYWSYDINKLHNYITKTGTSLEFADLHNKFTYASK 334
Qy 301 SGGAFFDMRTMTNTLMKDQPTLAATFVNDHDEPGQALQSWDPWFKPLAYAFILTRQEG 360
Db 335 SGGAFFDMRTMTNTLMKDQPTLAATFVNDHDEPGQALQSWDPWFKPLAYAFILTRQEG 394
Qy 361 YPCVFYGDYVGIPOYNISLSKSIDPILLIARDVAYGTQHDYLDHSDIIGWTRBGGTEKP 420
Db 395 YPCVFYGDYVGIPOYNISLSKSIDPILLIARDVAYGTQHDYLDHSDIIGWTRBGGTEKP 454
Qy 421 GSGLAALITDGPQSKMVMYVQKQAGKVFYDLTGNSDPTVINSDDGGEFFKNGGSYSVM 480
Db 455 GSGLAALITDGPQSKMVMYVQKQAGKVFYDLTGNSDPTVINSDDGGEFFKNGGSYSVM 514
Qy 481 VPRKTVSTIARPIITRPMTGEFVWTEPRLVAM 514
Db 515 VPRKTVSTIARPIITRPMTGEFVWTEPRLVAM 548

RESULT 2

A24549
alpha-amylase (EC 3.2.1.1) precursor - Bacillus stearothermophilus (strain NZ-3)
N:Alternate names: 1,4-alpha-D-glucan glucanohydrolase
C:Species: Bacillus stearothermophilus
C>Date: 30-Jun-1998 #sequence revision 18-Aug-1995 #text_change 18-Jun-1999
C:Accession: A24549; 139501; 139770
R:Gray, G.L.; Mainzer, S.B.; Rey, M.W.; Jamsa, M.H.; Kindle, K.L.; Carmona, C.; Reguad, J.
J: Bacteriol. 166, 635-643, 1986
A:Title: Structural genes encoding the thermophilic alpha-amylases of Bacillus stearothermophilus
A:Reference number: A91817; PMID:86195857; PMID:3009417
A:Accession: A24549
A:Molecule type: DNA
A:Residues: 1-549 <GRS>
A:Cross-references: GB:M13255; NID:G142512; PIDN:AAA22241.1; PID:G142513
A:Experimental source: genomic DNA of strain NZ-3
J: Satoch, H.; Nishida, H.; Isono, K.
J: Bacteriol. 170, 1034-1040, 1988
A:Title: Evidence for movement of the alpha-amylase gene into two phylogenetically distinct
A:Reference number: 139501; PMID:86193156; PMID:3257753
A:Accession: 139501
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 536-549 <RES>
A:Cross-references: GB:M29577; NID:G142476; PIDN:AAA22225.1; PID:G142478
A:Experimental source: strain DY-5
A:Accession: 139770
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 536-549 <RES>
A:Cross-references: GB:M29578; NID:G142484; PIDN:AAA22228.1; PID:G142486
A:Experimental source: strain 799
C:Comment: Alpha-amylase genes have been found on plasmids and in multiple copies on the
C:Genetics:
A:Start codon: GTG
C:Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology
C:Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; polysac
F:1-34/Domain: signal sequence #status predicted <Sig>
F:35-549/Product: alpha-amylase #status predicted <AMY>
F:235-368/Domain: alpha-amylase core homology <AMY>
F:139, 237, 272/Binding site: calcium (Asp, Asp, His) #status predicted
F:168, 298, 365/Active site: Asp, Glu, Asp #status predicted

Qy 61 DLYDGEFNQKQVTKTKYTAQYLQALQAAHAGMOTVADVFVDHKGADGTEWDAVE 120
Db 95 DLYDGEFNQKQVTKTKYTAQYLQALQAAHAGMOTVADVFVDHKGADGTEWDAVE 154
Qy 121 VNPSDRNOEISGTQIOAMTKFDPFGKNTYSSEFKWMEHEDGVWDSEKRLSIRYFERG 180
Db 155 VNPSDRNOEISGTQIOAMTKFDPFGKNTYSSEFKWMEHEDGVWDSEKRLSIRYFERG 214
Qy 181 ICKAWDEVDTEENGVYDLYMADLMDHPEVYTELKNWKKYVNTNIDGRDLAVYKIK 240
Db 215 ICKAWDEVDTEENGVYDLYMADLMDHPEVYTELKNWKKYVNTNIDGRDLAVYKIK 274
Qy 241 FSPFPDMLSYRSQGRKPLFTVGEYWSYDINKLHNYITKTGTSLEFADLHNKFTYASK 300
Db 275 FSPFPDMLSYRSQGRKPLFTVGEYWSYDINKLHNYITKTGTSLEFADLHNKFTYASK 334
Qy 301 SGGAFFDMRTMTNTLMKDQPTLAATFVNDHDEPGQALQSWDPWFKPLAYAFILTRQEG 360
Db 335 SGGAFFDMRTMTNTLMKDQPTLAATFVNDHDEPGQALQSWDPWFKPLAYAFILTRQEG 394
Qy 361 YPCVFYGDYVGIPOYNISLSKSIDPILLIARDVAYGTQHDYLDHSDIIGWTRBGGTEKP 420
Db 395 YPCVFYGDYVGIPOYNISLSKSIDPILLIARDVAYGTQHDYLDHSDIIGWTRBGGTEKP 454
Qy 421 GSGLAALITDGPQSKMVMYVQKQAGKVFYDLTGNSDPTVINSDDGGEFFKNGGSYSVM 480
Db 455 GSGLAALITDGPQSKMVMYVQKQAGKVFYDLTGNSDPTVINSDDGGEFFKNGGSYSVM 514
Qy 481 VPRKTVSTIARPIITRPMTGEFVWTEPRLVAM 514
Db 515 VPRKTVSTIARPIITRPMTGEFVWTEPRLVAM 548

RESULT 3

A24436
alpha-amylase (EC 3.2.1.1) precursor - Bacillus stearothermophilus plasmid pAT5
N:Alternate names: 1,4-alpha-D-glucan glucanohydrolase
C:Species: Bacillus stearothermophilus
C>Date: 05-Jun-1987 #sequence revision 18-Aug-1995 #text_change 18-Jun-1999
C:Accession: A24436; 139777
R:Nakajima, R.; Imanaka, T.; Aiba, S.
J: Bacteriol. 163, 401-406, 1985
A:Reference number: A24436; PMID:85234394; PMID:3924897
A:Accession: A24436
A:Molecule type: DNA
A:Residues: 1-549 <NAX>
A:Cross-references: GB:M11450
A:Experimental source: plasmid pAT5
A:Note: amino end of the mature protein also determined
R:Jorgensen, P.L.; Hansen, C.K.; Poulsen, G.B.; Didrichsen, B.
Gene 96, 37-41, 1990
A:Title: In vivo genetic engineering: homologous recombination as a tool for plasmid con
A:Reference number: 139772; PMID:91092499; PMID:2265757
A:Accession: 139777
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-45 <RES>
A:Cross-references: GB:M62638; NID:G142514; PIDN:AAA22242.1; PID:G142515
C:Comment: Alpha-amylase genes have been found on plasmids and in multiple copies on the
C:Genetics:
A:Gene: amyS
A:Genome: Plasmid
A:Start codon: GTG
C:Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology
C:Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; polysac
F:1-34/Domain: signal sequence #status predicted <Sig>
F:35-549/Product: alpha-amylase #status experimental <MAN>
F:235-368/Domain: alpha-amylase core homology <AMY>
F:139, 237, 272/Binding site: calcium (Asp, Asp, His) #status predicted
F:168, 298, 365/Active site: Asp, Glu, Asp #status predicted

Query Match 97.6%; Score 2780; DB 1; Length 549;
 Best Local Similarity 98.1%; Pred. No. 3.8e-193;
 Matches 504; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 AAPNGTMMQYFEMYLPPDDGLMTKVAANEANNTLSLGLTALMLPAPYKGRSDVGVGY 60
 DB 35 AAPNGTMMQYFEMYLPPDDGLMTKVAANEANNTLSLGLTALMLPAPYKGRSDVGVGY 94
 QY 61 DLYDLGEFNQKGTATKTKGTAQYLOAIQAHAAGMUYADVDPDHKGADGTEWDAVE 120
 DB 95 DLYDLGEFNQKGTATKTKGTAQYLOAIQAHAAGMUYADVDPDHKGADGTEWDAVE 154
 QY 121 VNBSDRNOEISGTQIOAWTKFDFPGRGNNTYSSFKRWYHFDGVDMDSRKLRIYKRG 180
 DB 155 VNPSDRNOEISGTQIOAWTKFDFPGRGNNTYSSFKRWYHFDGVDMDSRKLRIYKRG 214
 QY 181 IKGAMDEVDTENGNYDYLMADLMDHPEVYTELKMGMKYVNTTINDGFRDLDAVGHK 240
 DB 215 IKGAMDEVDTENGNYDYLMADLMDHPEVYTELKMGMKYVNTTINDGFRDLDAVGHK 274
 QY 241 FSPFPDMLSYRSQTKPLFTVGEYWSYDINKLHNYITKTDGMSLFDAPLHKKFYTAK 300
 DB 275 FSPFPDMLSYRSQTKPLFTVGEYWSYDINKLHNYITKTDGMSLFDAPLHKKFYTAK 334
 QY 301 SGGAFDMRTLTMTLTKDQPTLAVTFVNDHDEPGALQSWVDPFMRPLAFAFILLTREG 360
 DB 335 SGGAFDMRTLTMTLTKDQPTLAVTFVNDHDEPGALQSWVDPFMRPLAFAFILLTREG 394
 QY 361 YPCVFYGDYGIPOYNIPSLKSKIDPLIARDYAVGTQHDYLDHSDIIGWREGTEKP 420
 DB 395 YPCVFYGDYGIPOYNIPSLKSKIDPLIARDYAVGTQHDYLDHSDIIGWREGTEKP 454
 QY 421 GSGIALITDGPGRSKMYVQKHAKGYFDLTGNRSDVTITNSDGWGEFKNKGSVSVW 480
 DB 455 GSGIALITDGPGRSKMYVQKHAKGYFDLTGNRSDVTITNSDGWGEFKNKGSVSVW 514
 QY 481 VPKRTVSTIARPIITRPMTGEFVWTEPRLVAV 514
 DB 515 VPKRTVSTIARPIITRPMTGEFVWTEPRLVAV 548

RESULT 4

ALBSP
 alpha-amyase (EC 3.2.1.1) precursor - *Bacillus stearothermophilus* (strain DY-5) plasmid
 N:Alternate names: 1,4-alpha-D-glucan glucanohydrolase
 C:Species: *Bacillus stearothermophilus*
 C>Date: 30-Jun-1987 #sequence revision 30-Jun-1987 #text_change 16-Feb-1997
 C:Accession: A21999; E91999; A91804; A00845
 R:Inara, H.; Sasaki, T.; Tsudoi, A.; Yamagata, H.; Tsukagoshi, N.; Uda, S.
 J: Biochem. 98, 95-103, 1985
 A:Title: Complete nucleotide sequence of a thermophilic alpha-amyase gene: homology bet
 A:Reference number: A91999; MUID:86008166; PMID:3876333
 A:Accession: A91999
 A:Molecule type: DNA
 A:Residues: 1-548 <1H>
 A:Cross-references: GB:X02769
 A:Experimental source: plasmid PH1300 from strain DY-5
 A:Accession: B91999
 A:Molecule type: protein
 A:Residues: 35-48 <1H2>
 R:Experimental source: strain DY-5
 R:Tsukagoshi, N.; Inara, H.; Sasaki, T.; Takemura, T.; Ihara, H.; Idota, Y.; Yamagata,
 U: Biochem. 164, 1182-1187, 1985
 A:Title: Efficient synthesis and secretion of a thermophilic alpha-amyase by protein-pr
 A:Reference number: A91804; MUID:86059211; PMID:2990773
 A:Contents: PBAM101
 A:Accession: A91804
 A:Molecule type: DNA
 A:Residues: 1-29, 'Q', 31-75, 'W', 77-122 <TSU>
 C:Comment: Alpha-amyase genes have been found on plasmids and in multiple copies on the
 C:Genetics:
 A:Genome: plasmid

A:Start codon: GTG

C:Function: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
 A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
 A:Pathway: glycoen/starch degradation
 C:Superfamily: alpha-amyase, amyloliquefactors type; alpha-amyase core homology
 C:Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; polysacc
 F:1-33/Domain: signal sequence #status predicted <SIG>
 F:35-548/Product: alpha-amyase #status experimental <MAT>
 F:235-366/Domain: alpha-amyase core homology <AMY>
 F:139,237,272/Binding site: calcium (Asp, Asp, His) #status predicted
 F:268,298,365/Active site: Asp, Glu, Asp #status predicted

Query Match 95.6%; Score 2720.5; DB 1; Length 548;
 Best Local Similarity 96.7%; Pred. No. 7.6e-189;
 Matches 497; Conservative 3; Mismatches 13; Indels 1; Gaps 1;

QY 1 AAPNGTMMQYFEMYLPPDDGLMTKVAANEANNTLSLGLTALMLPAPYKGRSDVGVGY 60
 DB 35 AAPNGTMMQYFEMYLPPDDGLMTKVAANEANNTLSLGLTALMLPAPYKGRSDVGVGY 94
 QY 61 DLYDLGEFNQKGTATKTKGTAQYLOAIQAHAAGMUYADVDPDHKGADGTEWDAVE 120
 DB 95 DLYDLGEFNQKGTATKTKGTAQYLOAIQAHAAGMUYADVDPDHKGADGTEWDAVE 154
 QY 121 VNPSDRNOEISGTQIOAWTKFDFPGRGNNTYSSFKRWYHFDGVDMDSRKLRIYKRG 180
 DB 155 VNPSDRNOEISGTQIOAWTKFDFPGRGNNTYSSFKRWYHFDGVDMDSRKLRIYKRG 214
 QY 181 IKGAMDEVDTENGNYDYLMADLMDHPEVYTELKMGMKYVNTTINDGFRDLDAVGHK 240
 DB 215 IKGAMDEVDTENGNYDYLMADLMDHPEVYTELKMGMKYVNTTINDGFRDLDAVGHK 274
 QY 241 FSPFPDMLSYRSQTKPLFTVGEYWSYDINKLHNYITKTDGMSLFDAPLHKKFYTAK 300
 DB 275 FSPFPDMLSYRSQTKPLFTVGEYWSYDINKLHNYITKTDGMSLFDAPLHKKFYTAK 334
 QY 301 SGGAFDMRTLTMTLTKDQPTLAVTFVNDHDEPGALQSWVDPFMRPLAFAFILLTREG 360
 DB 335 SGGAFDMRTLTMTLTKDQPTLAVTFVNDHDEPGALQSWVDPFMRPLAFAFILLTREG 393
 QY 361 YPCVFYGDYGIPOYNIPSLKSKIDPLIARDYAVGTQHDYLDHSDIIGWREGTEKP 420
 DB 394 YPCVFYGDYGIPOYNIPSLKSKIDPLIARDYAVGTQHDYLDHSDIIGWREGTEKP 453
 QY 421 GSGIALITDGPGRSKMYVQKHAKGYFDLTGNRSDVTITNSDGWGEFKNKGSVSVW 480
 DB 454 GSGIALITDGPGRSKMYVQKHAKGYFDLTGNRSDVTITNSDGWGEFKNKGSVSVW 513
 QY 481 VPKRTVSTIARPIITRPMTGEFVWTEPRLVAV 514
 DB 514 VPKRTVSTIARPIITRPMTGEFVWTEPRLVAV 547

RESULT 5

A27705
 alpha-amyase (EC 3.2.1.1) precursor - *Bacillus* sp.
 N:Alternate names: 1,4-alpha-D-glucan glucanohydrolase; G6-amyase
 C:Species: *Bacillus* sp.
 C>Date: 31-Mar-1989 #sequence revision 18-Aug-1995 #text_change 18-Jun-1999
 C:Accession: A27705
 R:Tsukamoto, A.; Kimura, K.; Ishii, Y.; Takano, T.; Yamane, K.
 Biochem. Biophys. Res. Commun. 151, 25-31, 1988
 A:Title: Nucleotide sequence of the maltohexase-producing amyase gene from an alkaloph
 A:Reference number: A27705; MUID:88162814; PMID:3258152
 A:Accession: A27705
 A:Molecule type: DNA
 A:Residues: 1-518 <TSU>
 A:Cross-references: GB:M18862; NID:g142496; PID:AAA22231.1; PID:g142497
 A:Experimental source: chromosomal DNA of strain 707
 A>Note: amino end of mature protein also determined
 C:Comment: This is the smallest of five starch-hydrolyzing enzymes from this organism.
 C:Function: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds

A:Pathway: glycogen/starch degradation
C:Superfamily: alpha-amylase, amyloliquefaciens type, alpha-amylase core homology
C:Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation
F:1-33/Domains: signal sequence #status predicted <SIG>
F:34-518/Product: alpha-amylase #status experimental <MAM>
F:236-369/Domains: alpha-amylase core homology <AMY>
F:139,238,273/Binding site: calcium (asn, asp, his) #status predicted
F:269,289,366/Active site: Asp, Glu, Asp #status predicted

Query Match 65.8%; Score 1874.5; DB 1; Length 518;
Best Local Similarity 67.2%; Pred. No. 9,4e-128;
Matches 321; Conservative 76; Mismatches 80; Indels 1; Gaps 1;

QY 5 NGTMMQYFEMVLPDGLMTKRVANEANNSLSLGTALMLPPAYKGRSRDPVGYDLYD 64
DB 39 NGTMMQYFEMVLPDGLMTKRVANEANNSLSLGTALMLPPAYKGRSRDPVGYDLYD 98
QY 65 LGFENQKGTATKTKYKTAQYLQALQAAHAAQVYADVDFHKGADGTEWDAVEVNS 124
DB 99 LGFENQKGTATKTKYKTAQYLQALQAAHAAQVYADVDFHKGADGTEWDAVEVNS 158
QY 125 DRNCEISGTQIQMTKFPDPGRCNTYSSFRKRYHEDGVDMDSRRL-SRIKFKGICK 183
DB 159 NRNCEVGEYTEMTKFPDPGRCNTYSSFRKRYHEDGVDMDSRRL-SRIKFKGICK 218
QY 184 AMDVEVDTENGNYDLYADLDMDHPEVTELEKMGKMYNTTINIDGFRDAVAKHIFSF 243
DB 219 AMDVEVDTENGNYDLYADLDMDHPEVTELEKMGKMYNTTINIDGFRDAVAKHIFSF 278
QY 244 FPDMLSTVRSQGTGKPLTVGEGYNSYDINKLHNTTKDGMSLPDALHAKFTASKSG 303
DB 279 TRDWINHVRSTYGMKVAVEFMWINDGALENYLOKNNHNSYFVDFLHNLNASKSG 338
QY 304 AFDRTMTNTIMDQPLATFVNDHDEFGALQGVDPWFPEPLAVALILTROGEPYC 363
DB 339 NYDRKRNIFNGVGRHPSHATFVNDHDEFGALQGVDPWFPEPLAVALILTROGEPYC 398
QY 364 VFYGDYIGIPQYNTPLSKLTDPLILARDVAYGTQDYDHDSDITWTEGTEKPGSG 423
DB 399 VFYGDYIGIPQYNTPLSKLTDPLILARDVAYGTQDYDHDSDITWTEGTEKPGSG 458
QY 424 LAALITGPGGSKMYVGVKQAGKVFYDLTGNSRDYTLNSDGEKFGVGSVYV 481
DB 459 LATIMSDAGGSKMFGVGRNKGAGVMDITGNRGITVTLNADGNGNSVNGGSISIV 516

RESULT 6

ALBBL
alpha-amylase (EC 3.2.1.1) precursor [validated] - Bacillus licheniformis
N:Alternate names: 1,4-alpha-D-glucan glucanohydrolase
C:Species: Bacillus licheniformis
C:Date: 30-Jun-1997 #sequence revision 24-Apr-1998 #text change 15-Sep-2000
C:Accession: A01997; B24549; A21663; I39774; A26151; S53788; A00844
R:Yukki, T.; Nomura, T.; Tetsuka, H.; Tsuboi, A.; Yamagata, H.; Tsukagoshi, N.; Uchida, S.
J. Biochem. 98, 1147-1156, 1985
A:Title: Complete nucleotide sequence of a gene coding for heat- and pH-stable alpha-amylase deduced from the DNA sequences.
A:Reference number: A01997; PMID:86111694; PMID:2418011
A:Accession: A01997
A:Molecule type: DNA
A:Residues: 1-162, 'R', 164-512 <YU>
A:Cross-references: GB:X03236; NID:G39551; PIDN:CAA26981.1; PID:G39552
A:Experimental source: ATCC 27811
R:Gray, G.L.; Mainzer, S.E.; Rey, M.M.; Lamsa, M.H.; Kandle, K.L.; Carmona, C.; Reguadt, J. Bacteriol. 166, 635-643, 1986
A:Title: Structural genes encoding the thermophilic alpha-amylases of Bacillus stearothermophilus
A:Reference number: A01817; PMID:86195857; PMID:3009417
A:Accession: B24549
A:Molecule type: DNA
A:Residues: 1-338, 'G', 340-348, 'S', 350-512 <GRA>
A:Cross-references: GB:M13256; NID:G142510; PIDN:AAA22240.1; PID:G142511
A:Experimental source: NCIB 8061
R:Stephens, M.A.; Ortlepp, S.A.; Ollington, J.F.; McConnell, D.C.

J. Bacteriol. 158, 369-372, 1994
A:Title: Nucleotide sequence of the 5' region of the Bacillus licheniformis alpha-amylase
A:Reference number: A01786; PMID:84185455; PMID:6609154
A:Accession: A01786
A:Molecule type: DNA
A:Residues: 1-104 <ST>
A:Cross-references: GB:X01984; NID:G142432; PIDN:AAA22193.1; PID:G142433
R:Shakoy, M.; Palva, I.
J. Biochem. 145, 567-572, 1994
A:Title: Isolation and the 5' end nucleotide sequence of Bacillus licheniformis alpha-amylase
A:Reference number: A21663; PMID:85076554; PMID:6334606
A:Accession: A21663
A:Molecule type: DNA
A:Residues: 1-3, 'H', 5-12, 'P', 14-47, 'R', 49-61, 'V', 63, 'D', 65-67, 'VA', 70-71, 'S', 73-80, 'D', 82
A:Experimental source: chromosomal DNA of ATCC 14580
A:Note: the authors translated the codon CGT for residue 48 as Gly and GAC for residue 64
R:bioide, B.M.; Chambliss, G.H.; McConnell, D.J.
J. Bacteriol. 171, 2435-2442, 1989
A:Title: Bacillus licheniformis alpha-amylase gene, amyL, is subject to promoter-independent
A:Reference number: I39773; PMID:89213924; PMID:2540150
A:Accession: I39774
A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA
A:Residues: 1-29 <LMO>
A:Cross-references: GB:M26412; NID:G341477; PIDN:AAA22237.1; PID:G516590
R:Jorgensen, P.L.; Hansen, C.K.; Poulsen, G.B.; Diderichsen, B.
Gene 96, 37-41, 1990
A:Title: In vivo genetic engineering: homologous recombination as a tool for plasmid construction
A:Reference number: I39772; PMID:91092499; PMID:2265757
A:Accession: I39772
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-32, 'I' <CJR>
A:Cross-references: GB:M2637; NID:G142498; PIDN:AAA22232.1; PID:G142499
R:Kuhn, H.; Fietzek, P.P.; Lampen, J.O.
J. Bacteriol. 149, 372-373, 1982
A:Title: N-terminal amino acid sequence of Bacillus licheniformis alpha-amylase: comparison
A:Reference number: A26151; PMID:82098050; PMID:6172418
A:Accession: A26151
A:Molecule type: protein
A:Residues: 30-37, 'E', 39-41, 'X', 43-47 <KUH>
R:Maciunas, M.; Wiegand, G.; Huber, R.
J. Mol. Biol. 246, 545-559, 1995
A:Title: Crystal structure of calcium-depleted Bacillus licheniformis alpha-amylase at 2.0 Å
A:Reference number: S53788; PMID:95182462; PMID:7877175
A:Accession: S53788
A:Molecule type: protein
A:Residues: 1-220-227 <MAC>
A:Note: sequence represents amino end of an internal fragment created by a single enzymatic
R:Maciunas, M.; Wiegand, G.; Huber, R.
submitted to the Brookhaven Protein Data Bank, July 1995
A:Reference number: A65206; PDB:1BPL
A:Contents: annotation; X-ray crystallography, 2.2 angstroms, residues 32-210, 222-511
A:Note: these structural studies suggest 163 is less rather than Arg
R:Song, H.K.; Huang, K.Y.; Chang, C.; Sun, S.W.
submitted to the Brookhaven Protein Data Bank, October 1996
A:Reference number: A68860; PDB:1IVS
A:Contents: annotation; X-ray crystallography, 1.7 angstroms, residues 32-210, 222-511
C:Genetics:
A:Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology
C:Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; polysaccharide degradation
F:1-29/Domains: signal sequence #status predicted <SIG>
F:30-512/Product: alpha-amylase #status experimental <MAM>
F:227-260/Domains: alpha-amylase core homology <AMY>
F:103, 229, 264/Binding site: calcium (asn, asp, his) #status experimental
F:260, 290, 357/Active site: Asp, Glu, Asp #status experimental

Query Match 63.0%; Score 1794.5; DB 1; Length 512;
Best Local Similarity 65.0%; Pred. No. 5.6e-122;

A:Molecule type: DNA
 A:Residues: 1-492 <KUR>
 A:Cross-references: GB:BA000019; PIDN:BA073889.1; PID:g17131281; GSPDB:GN00179
 A:Experimental source: strain FCC 7120
 C:Genetics:
 A:Gene: a1r2190
 C:Superfamily: alpha-amylase, amy1oliquefaciens type; alpha-amylase core homology

Query Match 47.3%; Score 1345.5; DB 2; Length 492;
 Best Local Similarity 52.8%; Pred. No. 1.5e-89;
 Matches 261; Conservative 67; Mismatches 147; Indels 19; Gaps 7;

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QY 2 APPNGTMQYFEWYLPDDGTLMTKVAANEANNTSLGTLMLPYPAYKGTSSRSDVGYYDLYD 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2 AQNGTMQYFEWYLPDDGTLMTKVAANEANNTSLGTLMLPYPAYKGTSSRSDVGYYDLYD 61
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 DLYDLGEPNOKGVTFTKTKYQAYLOAIQAHAAGQYADVPFKHGAGDGTWWDAYE 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 62 DLYDLGEPNOKGVTFTKTKYQAYLOAIQAHAAGQYADVPFKHGAGDGTWWDAYE 121
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 VNPDSNOSIGTYQIAWTKFDPFGKNTYSSFKRWYHFDGVWDPE--SRKLSRIYKF 178
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 122 FPDDDLNPRGGLQDIXTYTHVFPGRQKYSNFEMHMHFPAVDYNEVNSGDRSTVLL 181
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 179 RGIGKAMDVEVDTEENGNVDYLMYADLDMDHPEVTELEKMGKMYNTNIDGFRLDAYKH 238
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 182 E--GKMFDPYVALEKSNFAYLMGCCDLPQNEWVRGVTVYWGKCCDITTKVDFRIDAIKH 239
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 239 IKFSFPPDLVSVRSQTKRPLFTVGEYMSYDINKLHNITTKDGTMSLEFADPANKFYTA 298
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 240 ISTWFPFPEWIDALERRAGDLPFVGEYMYNDINTLMYDVARGKMSYFVDYLAHNFQQA 299
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 299 SSSGGAFFDRITLMTNLMDOPTLAVTFVNDHTEPGALQSWDPWFEPKPLAYAFILTRQ 358
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 300 SSSGGINYDRILIDGTMGQORPLHAYTFVENHDSQPLQLSVSEVPEWFEPLAYAILLRQ 359
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 359 EGYPCVFYGDYVGIPI-----QYNI--PSLSKIDPELLARRDAYAGTQHDYLDHSD 407
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 360 EGYPCVFHADYGAEEYEDWGDQNRNYNIFMPSHRWIIDKLILYARKHAYAGQYNYLDHWN 419
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 408 IIGMTEEGTEKRGSLAALLTDGPGSKMYVYKQHAQKAVYDITGNRSDTYTINSQW 467
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 420 TIGMTILGDAHDF-QGMAYINSDSGEIKMEVEYKNT--KITDLTEIKKAVYTINMGW 476
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 468 GEFKVNAGSVSVV 481
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 477 GEFRCIGGSYSVWV 490
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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RESULT 9

G99160
 alpha-amylase [imported] - Streptococcus pneumoniae (strain TIGR4)
 C:Species: Streptococcus pneumoniae
 C:Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #ext_change 24-Aug-2001
 C:Accession: G99160
 R:Retelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
 son, J.D.; Umekam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapfel,
 nson, T.; Hickey, E.K.; Holt, I.E.
 Science 293, 498-506, 2001
 A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
 A.; Title: Complete Sequence of a Virulent Isolate of Streptococcus pneumoniae.
 A:Reference number: A95000; MUID:21357209; PMID:11463916
 A:Accession: G99160
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-484 <KUR>
 A:Cross-references: GB:AE005672; PIDN:AAK75480.1; PID:g14972868; GSPDB:GN00164; TIGR:SPA
 A:Experimental source: strain TIGR4
 C:Genetics:
 A:Gene: SP1382
 C:Superfamily: alpha-amylase, amy1oliquefaciens type; alpha-amylase core homology

Query Match 46.2%; Score 1315; DB 2; Length 484;

Best Local Similarity 50.7%; Pred. No. 2.3e-87;
 Matches 248; Conservative 73; Mismatches 158; Indels 10; Gaps 4;

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QY 5 NGTMQYFEWYLPDDGTLMTKVAANEANNTSLGTLMLPYPAYKGTSSRSDVGYYDLYD 64
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 3 NGTMQYFEWYLPDDGTLMTKVAANEANNTSLGTLMLPYPAYKGTSSRSDVGYYDLYD 62
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 65 LGEPNOKGVTFTKTKYQAYLOAIQAHAAGQYADVPFKHGAGDGTWWDAYE 124
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 63 LGEPNOKGVTFTKTKYQAYLOAIQAHAAGQYADVPFKHGAGDGTWWDAYE 122
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 125 DRNOEISGTYQIAWTKFDPFGKNTYSSFKRWYHFDGVWDPESRKLSRIYKFGIGKA 184
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 123 DRIVELEPPTINGWTSFTPDGRQDTYNGFHHMHFTGTDYDARKSKGILIGDNKG 182
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 185 WDME--VDTEENGYDYLMTADLDMDHPEVTELEKMGKMYNTNIDGFRLDAYKH 242
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 183 WANEELVDNENGNVDYLMYADLDPEKPEVIOHLYWADFMETTGVAQFRLDAVGHISF 242
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 243 FFPDMLSVRSQTKRPLFTVGEYMSYDINKLHNITTKDGTMSLEFADPANKFYASKG 302
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 243 FMRPFIIDMKEXYGDYFVFGSEWNPDKANLDYLEKTEHFDLVDRHLQNLFEASQAG 302
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 303 GAFFMRLTMTNLMDOPTLAVTFVNDHTEPGALQSWDPWFEPKPLAYAFILTRQGYR 362
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 303 ANYDLRGIFPDSLVLEKPKDAVTFVNDHTQRGQALSTVEWFKPAAVALILLRQDGLP 362
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 363 CVFPGDYVYGP-QYNIPLSKIDPELLIARRDAYAGTQHDYLDHSDIIGMTEEGTEKRG 421
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 363 CVFPGDYVYGSQYAOEFPFELIDRLAIRKDAYEONDYFPHANCIGWASGAENO-- 420
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 422 SGLAALITDGPSSKMYVYKQHAQKAVYDITGNRSDTYTINSQWGEFKNVAGSVSVV 481
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 421 SPLAIVLSNQGSKSFVQGEWNTQTFVLDLGNHQGYTLIDEGYGGQPPVASRYSVW- 479
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 482 PRKTYSTI 490
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 480 ---AVNTI 484
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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RESULT 10

P98026
 alpha-amylase (EC 3.2.1.1) precursor [imported] - Streptococcus pneumoniae (strain R6)
 C:Species: Streptococcus pneumoniae
 C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #ext_change 02-Nov-2001
 C:Accession: P98026
 R:Hockins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; E
 e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
 y, P.; Sun, P.M.; Winkler, M.E.
 J. Bacteriol. 183, 5709-5717, 2001
 A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
 A.; Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
 A:Reference number: A97872; MUID:21429245; PMID:11544234
 A:Accession: P98026
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-484 <KUR>
 A:Cross-references: GB:AE007317; PIDN:AA100043.1; PID:g15458876; GSPDB:GN00174
 C:Genetics:
 A:Gene: amy
 C:Superfamily: alpha-amylase, amy1oliquefaciens type; alpha-amylase core homology
 C:Keywords: glycosidase; hydrolase

Query Match 46.0%; Score 1311; DB 2; Length 484;
 Best Local Similarity 50.5%; Pred. No. 4.5e-87;
 Matches 247; Conservative 74; Mismatches 158; Indels 10; Gaps 4;

```

QY 5 NGTMQYFEWYLPDDGTLMTKVAANEANNTSLGTLMLPYPAYKGTSSRSDVGYYDLYD 64
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 3 NGTMQYFEWYLPDDGTLMTKVAANEANNTSLGTLMLPYPAYKGTSSRSDVGYYDLYD 62
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 65 LGEPNOKGVTFTKTKYQAYLOAIQAHAAGQYADVPFKHGAGDGTWWDAYE 124
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

Db 63 LGFENQKGTARTKYGKEDYLOAIQALKAGIOIPMAVDVNLNKAADHREAPQVIEVDE 122
QY 125 DRNOEISGTYOIQAMTKFDPGAGNTYSSPKRWYHFDGVMDSESKLSRIYKFRGIGKA 184
Db 123 DRTVELOEPTLNGMTSFTFDGRQDTYNGFHHMYHETGTDYDAKSKSGIYLIDQDNKG 182
QY 185 MDWE--VDTENGVNDYLMYADLMDHDEVEVTELKNNKMYVNTNTNDGPRDLAVKIKRS 242
Db 183 MANDELVDNENGNVDMYADLDPKHPVEVIGNYDMADMPETITGAFGRDLAVKIDSEF 242
QY 243 FFPDMLSVRSQTKPLFTVGEYWSYDINKLHNYITKTGDTMSLPAPLHNKFTYASKSG 302
Db 243 FMRNFIDMEKEKYGDDEYVGFGEFNSDKENLIDLEKTEHFDLVRLHQLNFEASQSG 302
QY 303 GAFPMRLMTNTLMKQDPTLAVTFVNDHTEPGQALQSWDPMFKPLAYAFILTRGEGVP 362
Db 303 ANYDLRGITFDSLVELPKAVTFVNDHDTQGOALSTVEEMFKPAAYALILRLQDGLP 362
QY 363 CVFYGDYYGIP-QYNIPSLKSIDPLLIARDYAVGTQHDYLDHSDIIGWTREGTEKGG 421
Db 363 CVFYGDYYGISGOYAQDQFKEIIDRLAIRKDLAYGQNDYFPHANCIGWVRSGAENQ-- 420
QY 422 SGLAALLTDPGSGKMYVYKQAHAKVFDLTGNRSDVTITNSDGMGEFKNGSGSVSW 481
Db 421 SPLAVLISNDQENSKSMFVGQEWNTQTFVLDLISHQGVITIDEGYQGFVSARSYSW- 479
QY 482 PRKTTVSTI 490
Db 480 ----AVNTI 484

RESULT 11
S15713
alpha-amylase (EC 3.2.1.1) - *Bacillus circulans*
C:Species: *Bacillus circulans*
C:Date: 18-Feb-1994 #sequence_rev: 10-Nov-1995 #text_change 22-Jun-1999
C:Accession: S15713
R:Marcel, T.
submitted to the EMBL Data Library, May 1991
A:Reference number: S15713
A:Accession: S15713
A:Molecule type: DNA
A:Residues: 1-493 <MAR>
A:Cross-references: EMBL:X60779; NID:G39411; PIDN:CAA43194.1; PID:G39412
C:Gene: amyE
A:Gene: amyE
C:Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Subfamily: alpha-amylase, amylioliquefaciens type; alpha-amylase core homology
C:Keywords: glycosidase; hydrolase; polysaccharide degradation
F:200-333/Domain: alpha-amylase core homology <Ami>

Query Match 44.8%; Score 1278.5; DB 2; Length 493;
Best Local Similarity 48.5%; Pred. No. 1e-84;
Matches 232; Conservative 84; Mismatches 159; Indels 3; Gaps 2;

QY 5 NGTMMQYFEMYLPPDDGLMTKVNANNTLSLIGTILMLPRAVKGRSDVGYGVDDVD 64
Db 4 NHTMMQYFEMHLLADAGHMKRLAEMAPELKAKGIDTVWVPVTKAVSAETGIVGVDDVD 63
QY 65 LGFENQKGTARTKYGKAYLOAIQAAHAGMUYADVDPDHKGAGDGTWMDAVEVNS 124
Db 64 LGFEDQKGTARTKYGKQELIEALAEQKNGIAYVDLVMNHKAGADETEVFVIEVDN 123
QY 125 DRNOEISGTYOIQAMTKFDPGAGNTYSSPKRWYHFDGVMDSESKLSRIYKFRGIGKA 184
Db 124 DRTVELOEPTLNGMTSFTFDGRQDTYNGFHHMYHETGTDYDAKSKSGIYLIDQDNKG 183
QY 185 MDWEVDTENGVNDYLMYADLMDHDEVEVTELKNNKMYVNTNTNDGPRDLAVKIKRSF 244
Db 184 MNEKVDTEFGNVDYLMYANIDYHNPVRRMIDMGKMLIDTLOCGGRDLAIGHINHEF 243

QY 245 PDMLSVRSQTKPLFTVGEYWSYDINKLHNYITKTGDTMSLPAPLHNKFTYASKSGA 304
Db 244 KEFAEMTKRKGQDPYIVGEFNSNDLACREFLTVDYQIDLPVLSLHKLHNSLNGRD 303
QY 305 FDMRLMTNTLMKQDPTLAVTFVNDHTEPGQALQSWDPMFKPLAYAFILTRGEGVP 364
Db 304 FDLKIPDPTLVQTHPFAVTFVNDHDSQPHALESWIGMFKSAVALTLRLRDGYPV 363
QY 365 FYGDYYGIP-QYNIPSLKSIDPLLIARDYAVGTQHDYLDHSDIIGWTREGTEKGG 422
Db 364 FYGDYYGIGPE-PVDGKEKELIDLLSARCKAAGEDEDFDHANTIGWVRSGEELGGS 422
QY 423 GLAALLTDPGSGKMYVYKQAHAKVFDLTGNRSDVTITNSDGMGEFKNGSGSVSW 480
Db 423 GCAYVLSGDDGKRMFGEHRAGEVWVDLTKSCDDQITTEEDGMATFHCGGGVSVM 480

RESULT 12
C86781
alpha-amylase [imported] - *Lactococcus lactis* subsp. *lactis* (strain IL1403)
C:Species: *Lactococcus lactis* subsp. *lactis*
C:Date: 23-Mar-2001 #sequence_rev: 23-Mar-2001 #text_change 03-Aug-2001
C:Accession: C86781
R:Boletun, A.; Winkler, P.; Manger, S.; Tailon, O.; Malame, K.; Weissenbach, J.; Ehrli
Genome Res. 11, 731-753, 2001
A:Title: The complete genome sequence of the lactic acid bacterium *Lactococcus lactis* ss
A:Reference number: A86625; MUID:21235186; PMID:11337471
A:Accession: C86781
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-491 <STO>
A:Cross-references: GS:AE005176; PID:G12724224; PIDN:AAK05349.1; GSPDB:GN00146
A:Experimental source: strain IL1403
C:Gene: amyL
C:Subfamily: alpha-amylase, amylioliquefaciens type; alpha-amylase core homology

Query Match 43.2%; Score 1229; DB 2; Length 491;
Best Local Similarity 47.5%; Pred. No. 3.8e-81;
Matches 231; Conservative 73; Mismatches 176; Indels 6; Gaps 5;

QY 7 TMMQYFEMYLPPDDGLMTKVNANNTLSLIGTILMLPRAVKGRSDVGYGVDDVD 65
Db 3 TILQAFEMYLPSDSQHMNNIKENIPDLCKLGFSGMLPRAKASGVEDVGYGVDDVD 62
QY 66 GEFNOKGTARTKYGKAYLOAIQAAHAGMUYADVDPDHKGAGDGTWMDAVEVNSD 125
Db 63 GEFNOKGTARTKYGKQELIEALAEQKNGIAYVDLVMNHKAGADETEVTEA-DIAED 121
QY 126 RN-QEISGTYOIQAMTKFDPGAGNTYSSPKRWYHFDGVMDSESKLSRIYKFRGIGKA 184
Db 122 NHTMMQYFEMHLLADAGHMKRLAEMAPELKAKGIDTVWVPVTKAVSAETGIVGVDDVD 179
QY 185 MDWEVDTENGVNDYLMYADLMDHDEVEVTELKNNKMYVNTNTNDGPRDLAVKIKRSF 244
Db 180 WDENDSENNPFDYLMGADLPFSVSEVLEKKGHMFSEMTKIDGPRDLAIDPKYF 239
QY 245 PDMLSVRSQTKPLFTVGEYWSYDINKLHNYITKTGDTMSLPAPLHNKFTYASKSGA 304
Db 240 DKMLQKRAKQDRLKFLYIGEYMSDDGLLEYLQSSRLDLPVLPFHNNKESSTNGE 299
QY 305 FDMRLMTNTLMKQDPTLAVTFVNDHTEPGQALQSWDPMFKPLAYAFILTRGEGVP 364
Db 300 FDMRLTFLHTLASQPELSVTFVNDHTEPGQALQSWPAMFKHAYASLILRKKEPTV 359
QY 365 FYGDYYGIP-QYNIPSLKSIDPLLIARDYAVGTQHDYLDHSDIIGWTREGTEKGG 424
Db 360 FMDGYLGPISHNVNDVGNLNTMLARKDSFLENDPDPDILIGWNTILKIDNKEGL 419
QY 425 AALLTDPGSGKMYVYKQAHAKVFDLTGNRSDVTITNSDGMGEFKNGSGSVSWPRK 484
Db 420 SCILTNKNGSKMYLIDKAYAGKYIDLFGSHIEPITLDQCGABFYVNDGSGVSWVD-K 478

Qy 485 TTVESTI 490
Db 479 EIVSKI 484

RESULT 13

B45738
alpha-amylase (EC 3.2.1.1), cytosolic - *Salmonella typhimurium*
N/Alternate names: 1,4-alpha-D-glucan glucanohydrolase
C/Species: *Salmonella typhimurium*
C/Date: 07-Apr-1994 #sequence_revision 18-Aug-1995 #text_change 18-Jun-1999
C/Accession: B45738
R/Rana, M.; Kawagishi, I.; Mueller, V.; Khara, M.; Macnab, R.M.
J/Bacteriol. 174, 6644-6652, 1992
A/Title: *Escherichia coli* produces a cytoplasmic alpha-amylase, amyA.
A/Reference number: A45738; MUID:93015717; PMID:1400215
A/Accession: B45738
A/Molecule type: DNA
A/Residues: 1-494 <PAR>
A/Cross-references: GB:L01643; NID:G154043; PIDN:AAA27110.1; PID:G154045
C/Genetics:
A/Gene: amyA
C/Function:
A/Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A/Pathway: glycoen/starch degradation
C/Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology
C/Keywords: cytosol; glycosidase; hydrolase; polysaccharide degradation
F/202-335/Domain: alpha-amylase core homology <AMY>
F/235,265,332/Active site: His, Glu, Asp #status predicted

Query Match 39.1%; Score 1112.5; DB 1; Length 494;
Best Local Similarity 44.0%; Pred. No. 1e-72;
Matches 216; Conservative 83; Mismatches 175; Indels 17; Gaps 5;

Qy 5 NGTMAQYFEMYPDDGTLMTKYANEANNLSLIGITLMLPPAYKGTSS-DVGYGVYDLX 63
Db 3 NPTLLQYFHWYYPDGGKLMSELARADGINDIGIMVWLPPACKGASGYSVGYDYLDF 62
Qy 64 DLGEFQKGTATKTKGTATQYLOAIQAHAAGQYAAVVDVPHKGAAGTEWDAVENP 123
Db 63 DLGEFQKGTATKTKGTATQYLOAIQAHAAGQYAAVVDVPHKGAAGTEWDAVENP 122
Qy 124 SDRNCEISGTQYQWTKFDPFGKNTSSFKRMWYHFDGVWDESKLSRIYFRG--I 181
Db 123 DRTQIDNNIECEGRTYTPPARAGQYSNFTWDHCHSGIDHLENPEDEGIFKIVNDYT 182
Qy 182 GKAMDEVDTEGNYDYIMYADLDMDHPEVTELEKMGKMYVNTNIDGFLDAVKIKF 241
Db 183 GQGMNDQVDEGNDYIMYADLDMDHPEVTELEKMGKMYVNTNIDGFLDAVKIKF 242
Qy 242 SFEPDWLSVRSQTKPLFTVGEYWSYDINKLHNTYITDGTMSLFDAPLNKRYTASKS 301
Db 243 WFKYEMIHVQAVARPKPLFVAVYWSHEDKQYITIDVDKTMFLDAPLNKRYTASKS 302
Qy 302 GGAFFMRTMTNTLTKDQPTLAVTFVNDHTEPGALQSWDPWPKPLAVAFILTRQGY 361
Db 303 GAEYDMRHTFTGLVEADFFAVTLVANHDTQLALAPVBPMPKPLAVAFILTRQGY 362
Qy 362 PCVFGYDYVGP-----QYNIPSLSKIDPELLIARDVAVYQTHDLSDTIG 410
Db 363 PSVFYFDLGLASVEDNGENGETCRVDMYPI-NQDLRLILARQRFHAGIQTLFFPHNPIA 421
Qy 411 WTRGGTEKPGSLALITDGPGRKMYVKGQAHGXVYFDLGNRSPTVITNSGWEF 470
Db 422 FRSRGTENP--GCYVVLNSGDDGKTLILGDNVANKTRDFLGNRSEHVITNDGEXATF 479
Qy 471 KVNAGSVSVVW 481
Db 480 PCNAGSVSVVW 490

RESULT 14
AD0751

Cytoplasmic alpha-amylase [imported] - *Salmonella enterica* subsp. *enterica* serovar Typh
C/Species: *Salmonella enterica* subsp. *enterica* serovar Typh
A/Note: this species has also been called *Salmonella typh*
C/Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C/Accession: AD0751
R/Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Main, J.; Churcher,
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Mout, S.; O'Garra, P.
Nature 413, 848-852, 2001
A/Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A/Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serovar
A/Reference number: AB0502; MUID:21534947; PMID:11677608
A/Accession: AD0751
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-494 <PAR>
A/Cross-references: GB:AL513382; PIDN:CAD05711.1; PID:G16503204; GSPDB:GN00176
C/Genetics:
A/Gene: STY2171
C/Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology

Query Match 38.7%; Score 1101.5; DB 2; Length 494;
Best Local Similarity 44.0%; Pred. No. 6.3e-72;
Matches 216; Conservative 82; Mismatches 176; Indels 17; Gaps 5;

Qy 5 NGTMAQYFEMYPDDGTLMTKYANEANNLSLIGITLMLPPAYKGTSS-DVGYGVYDLX 63
Db 3 NPTLLQYFHWYYPDGGKLMSELARADGINDIGIMVWLPPACKGASGYSVGYDYLDF 62
Qy 64 DLGEFQKGTATKTKGTATQYLOAIQAHAAGQYAAVVDVPHKGAAGTEWDAVENP 123
Db 63 DLGEFQKGTATKTKGTATQYLOAIQAHAAGQYAAVVDVPHKGAAGTEWDAVENP 122
Qy 124 SDRNCEISGTQYQWTKFDPFGKNTSSFKRMWYHFDGVWDESKLSRIYFRG--I 181
Db 123 DRTQIDNNIECEGRTYTPPARAGQYSNFTWDHCHSGIDHLENPEDEGIFKIVNDYT 182
Qy 182 GKAMDEVDTEGNYDYIMYADLDMDHPEVTELEKMGKMYVNTNIDGFLDAVKIKF 241
Db 183 GQGMNDQVDEGNDYIMYADLDMDHPEVTELEKMGKMYVNTNIDGFLDAVKIKF 242
Qy 242 SFEPDWLSVRSQTKPLFTVGEYWSYDINKLHNTYITDGTMSLFDAPLNKRYTASKS 301
Db 243 WFKYEMIHVQAVARPKPLFVAVYWSHEDKQYITIDVDKTMFLDAPLNKRYTASKS 302
Qy 302 GGAFFMRTMTNTLTKDQPTLAVTFVNDHTEPGALQSWDPWPKPLAVAFILTRQGY 361
Db 303 GAEYDMRHTFTGLVEADFFAVTLVANHDTQLALAPVBPMPKPLAVAFILTRQGY 362
Qy 362 PCVFGYDYVGP-----QYNIPSLSKIDPELLIARDVAVYQTHDLSDTIG 410
Db 363 PSVFYFDLGLASVEDNGENGETCRVDMYPI-NQDLRLILARQRFHAGIQTLFFPHNPIA 421
Qy 411 WTRGGTEKPGSLALITDGPGRKMYVKGQAHGXVYFDLGNRSPTVITNSGWEF 470
Db 422 FRSRGTENP--GCYVVLNSGDDGKTLILGDNVANKTRDFLGNRSEHVITNDGEXATF 479
Qy 471 KVNAGSVSVVW 481
Db 480 PCNAGSVSVVW 490

RESULT 15

AD0308
alpha-amylase amyA [imported] - *Agrobacterium tumefaciens* (strain C58, Dugont)
C/Species: *Agrobacterium tumefaciens*
C/Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C/Accession: AD0308
R/Mood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.
erage, G.; Gillet, W.; Grant, C.; Gentner, D.; Kutayavin, T.; Levy, R.; Li, M.; McClellan,
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A/Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Parry, M.; Gordon-Kamm, I.

ster, E.W.

A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A:Reference number: AB2577; MUID:21608550; PMID:11743193

A:Accession: AD3038

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1495 <KID>

A:Cross-references: GB:AB006889; PIDN:AAL44722.1; PID:917742354; GSPDB:GN00187

A:Experimental source: strain C58 (Duplic)

C:Genetics:

A:Gene: amya

A:Map position: linear chromosome

C:Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology

Query Match 37.9%; Score 1078.5; DB 2; Length 495;

Best Local Similarity 44.4%; Pred. No. 2.9e-70;

Matches 218; Conservative 75; Mismatches 179; Indels 19; Gaps 6;

```
QY 7 TMMQYFEWYLPDDGTLMTKVNANNNLSLIGTALMLPAAKGTSSRS-DVGYGYDYLDL 65
DB 5 TLQGFHMYPPDGLMSVAAKESLAKGITDVLPPAYKGAAGSVGVDFYDLFDL 64
QY 66 GFENQKGYRTYKGYKAQYLAIAAAGMOYADVYFDHKGADGEMWDAYEVNPSD 125
DB 65 GFEDQKGYATKYGRALAEHAGKTLKONGIRVHDVYLNHMGADKEKVRVRVNPDD 124
QY 126 RNOEISGTYQIQAMTKFDPGRGNTYSSPFKRWYHFDGVMDSEKLSRIYKF--RGIG 182
DB 125 RTDIDDEDEPALAYTRFTTPGANGKSKFTINDLKCFSGVDHTEPTEDGIFRLVNEYGDG 184
QY 183 KAMNWEVDTENGNVDIADIDMDHPEYVTELEKMGKMYVNTNIDGFRIDAVKHIFS 242
DB 185 E-WNEEVDQENGNFYLMGADVEFRRAVYEELKTYGHWLSEQYQVDGFRIDAAKHIPAW 243
QY 243 FFPDMLSYRSQTKPLFTVGEYWSYDINKLHNYITKTDGTMSLFDAPLHNFYTASKSG 302
DB 244 FPRDVGHRRETVDPDLFVVAIYHBDLALSKSYLELDVKQLMDFVALHSHFDASKOG 303
QY 303 GAFDRTLTMTNTIMKDOPTLAVTFVNDHDEPGALQSWDPEFKPLAVAFILTRQEGYP 362
DB 304 GDFDKRSIFDGLSVAVAPDHAVTLVNDHTQPLQSLAEFVEBPFKPLAVAILLREEGVP 363
QY 363 CWFYGDYVGI-----QYNIPSLKSIDPILLARRDYAYGTODHYLDHSDILGW 411
DB 364 CVFYPLFSTSTLDGNDGNEKIDIPALEC-LPKLIEKRSRFRANGPOTDIFDASCTAF 422
QY 412 TREGTEKPGSGIALIITDGPGSKMYVYKQAHGKVPYDLTGNRSDVTYINSDGWGEFK 471
DB 423 IHGRTADAP--GCVVYVMSNGEPGEKQADLGPFRAGSVWRDPLGHREHITLDESCKGTFP 480
QY 472 VNGGSYSVWVP 482
DB 481 TNGGSYSVWVP 491
```

Search completed: May 3, 2004, 20:54:07
Job time : 15.6161 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 3, 2004, 20:44:58 ; Search time 36.5403 seconds

(without alignments)
4438.289 Million cell updates/sec

Title: US-10-644-187-6

Perfect score: 2847
Sequence: 1 AAPFNGTMMQYFEMYLDDG.....TTPWTGHEFVWTEPRLVAM 514

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPREMBL 25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp Vertebrate:*
- 14: sp Unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2833	99.5	549	2	Q31193
2	2811	98.7	549	2	Q9KXV6
3	2658	93.4	521	2	P71034
4	2404	84.4	613	2	Q59222
5	1910.5	67.1	516	2	Q82839
6	1841.5	64.7	533	2	Q9A054
7	1837.5	64.5	519	2	Q9ROT8
8	1829.5	64.3	513	16	Q81A54
9	1827.5	64.2	513	16	Q81A54
10	1700	59.7	507	16	Q87HG6
11	1618	56.8	501	2	Q93148
12	1345.5	47.3	492	16	Q8YU21
13	1322.5	46.5	481	16	Q85YPI
14	1315	46.2	484	16	Q97Q49
15	1311	46.0	484	16	Q8DPC8
16	1296	45.5	488	16	Q8A0M2

17	1295	45.5	488	16	Q8E696	Q8E696 streptococc
18	1278.5	44.9	493	2	Q03E57	Q03E57 bacillus ci
19	1268	44.5	486	16	Q8DT08	Q8DT08 streptococc
20	1260	44.3	484	2	O50583	O50583 streptococc
21	1244	43.7	485	2	O53786	O53786 streptococc
22	1237	43.4	486	2	O68875	O68875 streptococc
23	1229	43.2	491	16	Q9C359	Q9C359 lactococcus
24	1101.5	38.7	494	16	Q82595	Q82595 salmonella
25	1078.5	37.9	506	16	Q8U916	Q8U916 escherichia
26	1077.5	37.8	495	16	Q8EGL8	Q8EGL8 escherichia
27	1074.5	37.7	495	16	Q8KBB6	Q8KBB6 escherichia
28	1066.5	37.5	495	16	Q7UAB0	Q7UAB0 shigella fl
29	1064.5	37.4	495	16	Q83R40	Q83R40 shigella fl
30	967	34.0	529	3	Q877B1	Q877B1 aspergillus
31	486	17.1	461	1	Q8NKR5	Q8NKR5 thermococcu
32	483.5	17.0	461	1	Q8NKR4	Q8NKR4 thermococcu
33	482	16.9	469	1	O50200	O50200 thermococcu
34	481	16.9	461	1	O33476	O33476 pyrococcus
35	475	16.7	460	1	O08452	O08452 pyrococcus
36	475	16.7	473	17	Q8U319	Q8U319 pyrococcus
37	474	16.6	460	1	Q9P9L0	Q9P9L0 pyrococcus
38	472.5	16.6	432	14	Q8JZK3	Q8JZK3 uncultured
39	469.5	16.5	457	1	Q93647	Q93647 thermococcu
40	326.5	11.5	482	2	Q60051	Q60051 thermocactin
41	317	11.1	906	10	Q8LQK4	Q8LQK4 oryza sativ
42	307.5	10.8	423	10	Q8LBS5	Q8LBS5 arabidopsis
43	307.5	10.8	423	10	Q8VZ56	Q8VZ56 arabidopsis
44	307	10.8	826	10	Q9CAR6	Q9CAR6 arabidopsis
45	307	10.8	887	10	Q94441	Q94441 arabidopsis

ALIGNMENTS

RESULT 1	Q31193	PRELIMINARY;	PRT;	549 AA.
ID	Q31193	01-JAN-1998 (TREMBLrel. 05, Created)		
AC	Q31193	01-JAN-1998 (TREMBLrel. 05, Last sequence update)		
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)			
DE	Alpha amylase.			
GN	AMI.			
OS	Bacillus stearothermophilus.			
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.			
OK	NCBI_TaxId=1422;			
RN	SEQUENCE FROM N.A.			
RP	da Silva A.C.R., Fernandes E., Pueyo M.T.;			
RC	STRAIN=ATCC 31195;			
RA	Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.			
RU	EMBL: AF032864; AAB86961.1; -			
DR	PIR: A54541; A54541.			
DR	HSSP: P06278; IVUS.			
DR	GO: GO:0004556; F:alpha-amylase activity; IEA.			
DR	GO: GO:0005975; P:carbohydrate metabolism; IEA.			
DR	InterPro: IPR006047; Alpha amyl cat.			
DR	InterPro: IPR006046; Glyco_hydro_13.			
DR	Pfam: PF00128; alpha-amylase; 1.			
DR	PRINTS: PR00110; ALPHAAMYLASE.			
DR	SMART: SM00642; Amy; 1.			
DR	SEQUENCE 549 AA; 62651 MW; 2CA689EDACC4D262 CRC64;			
QY	Query Match	99.5%; Score 2833; DB 2; Length 549;		
DB	Best Local Similarity	98.6%; Pred. No. 7.9e-186;		
	Matches 512; Conservative 1; Mismatches 1; Indels 0; Gaps 0;			
QY	1 AAPFNGTMMQYFEMYLDDGTLMTKVNANNTSSIGITALWLPAYKGTSRSDVGVY 60			
DB	35 AAPFNGTMMQYFEMYLDDGTLMTKVNANNTSSIGITALWLPAYKGTSRSDVGVY 94			
QY	61 DLYHCFRNRCKTTRTYCTKRAQYIQAIOAAHAGMNVADYVFDHKGAGDGTWVAYE 120			


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Db 95 DLYDLGFNQKGTVRKTKYGTAKQYLQAIQAHAAGQVYADVDPDHKGADGTEWDAVE 154
QY 121 VNPSPRNOEISGTQYQIQAMTKDFPPGRGNTYSSFKRMWYHFDGVDMDSEKLSRIYKFRG 180
Db 155 VNPSPRNOEISGTQYQIQAMTKDFPPGRGNTYSSFKRMWYHFDGVDMDSEKLSRIYKFRG 214
QY 181 ICKAMDWEVDTENGNYDYLYATADLMDHPEVTELBKMGKMYVNTTINDGRDLAVGHIK 240
Db 215 ICKAMDWEVDTENGNYDYLYATADLMDHPEVTELBKMGKMYVNTTINDGRDLAVGHIK 274
QY 241 FSPFPDMLSYRSQTKGLFTVGEYWSYDINKLHNYITKTGTMSLPDAPLHNFYTASK 300
Db 275 FSPFPDMLSYRSQTKGLFTVGEYWSYDINKLHNYITKTGTMSLPDAPLHNFYTASK 334
QY 301 SGGAFDMRTMTNTLMKQOPTLAVTFVNDHTEPQALQSWVDWPFKFLAYAFILTRQEG 360
Db 335 SGGAFDMRTMTNTLMKQOPTLAVTFVNDHTEPQALQSWVDWPFKFLAYAFILTRQEG 394
QY 361 YPCVFGDYGGIPOYNIPSLKSKIDPLLIARDYVGTQHDYLDHSDIIGWTRREGTEKP 420
Db 395 YPCVFGDYGGIPOYNIPSLKSKIDPLLIARDYVGTQHDYLDHSDIIGWTRREGTEKP 454
QY 421 GSGLAALITDGPFGSKMNVGKQHAGKVFYDLTGNSDPTVTINSQMGEPKNGGSVSV 480
Db 455 GSGLAALITDGPFGSKMNVGKQHAGKVFYDLTGNSDPTVTINSQMGEPKNGGSVSV 514
QY 481 VPKRTVSTIARPIITRPWTGFEVWTEPRLYAM 514
Db 515 VPKRTVSTIARPIITRPWTGFEVWTEPRLYAM 548
```

RESULT 2

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Q9KMY6 PRELIMINARY; PRT; 549 AA.
ID 09KMY6
AC 09KMY6;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Alpha-amyase (EC 3.2.1.1).
OS Bacillus stearothermophilus.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
CX NCBI_TaxId=1422;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=US100;
RA Belar S.;
RL Submitted (JUN-1998) to the EMBL/Genbank/DBJ databases.
DR EMBL; Y17557; CAB9351.7.1; -.
DR PIR; A54541; A54541.
DR HSSP; P06278; 1VUS.
DR GO; GO:0004556; F:alpha-amyase activity; IEA.
DR GO; GO:0001579; F:hydrolyase activity; acting on glycosyl bonds; IEA.
DR InterPro; IPR006047; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006589; A:alpha-amy1_cat.
DR InterPro; IPR006046; G:glyco_hydro_13.
DR Pfam; PF00128; alpha-amyase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Amy; 1.
KW Glycosylase; Hydrolase.
SQ SEQUENCE 549 AA; 62582 MM; 8DA3E6DF9120BCE CRC64;
```

Query Match 98.7%; Score 2811; DB 2; Length 549;
Best Local Similarity 99.0%; Pred. No. 2,5e-184;
Matches 509; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

```
QY 1 AAPFNGTMQYFEWYLPDDGTLMTKYANANNLSIGITALLMPPAYKGTSSDVGYGY 60
Db 35 AAPFNGTMQYFEWYLPDDGTLMTKYANANNLSIGITALLMPPAYKGTSSDVGYGY 94
QY 61 DLYDLGFNQKGTVRKTKYGTAKQYLQAIQAHAAGQVYADVDPDHKGADGTEWDAVE 120
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Db 95 DLYDLGFNQKGTVRKTKYGTAKQYLQAIQAHAAGQVYADVDPDHKGADGTEWDAVE 154
QY 121 VNPSPRNOEISGTQYQIQAMTKDFPPGRGNTYSSFKRMWYHFDGVDMDSEKLSRIYKFRG 180
Db 155 VNPSPRNOEISGTQYQIQAMTKDFPPGRGNTYSSFKRMWYHFDGVDMDSEKLSRIYKFRG 214
QY 181 ICKAMDWEVDTENGNYDYLYATADLMDHPEVTELBKMGKMYVNTTINDGRDLAVGHIK 240
Db 215 ICKAMDWEVDTENGNYDYLYATADLMDHPEVTELBKMGKMYVNTTINDGRDLAVGHIK 274
QY 241 FSPFPDMLSYRSQTKGLFTVGEYWSYDINKLHNYITKTGTMSLPDAPLHNFYTASK 300
Db 275 FSPFPDMLSYRSQTKGLFTVGEYWSYDINKLHNYITKTGTMSLPDAPLHNFYTASK 334
QY 301 SGGAFDMRTMTNTLMKQOPTLAVTFVNDHTEPQALQSWVDWPFKFLAYAFILTRQEG 360
Db 335 SGGAFDMRTMTNTLMKQOPTLAVTFVNDHTEPQALQSWVDWPFKFLAYAFILTRQEG 394
QY 361 YPCVFGDYGGIPOYNIPSLKSKIDPLLIARDYVGTQHDYLDHSDIIGWTRREGTEKP 420
Db 395 YPCVFGDYGGIPOYNIPSLKSKIDPLLIARDYVGTQHDYLDHSDIIGWTRREGTEKP 454
QY 421 GSGLAALITDGPFGSKMNVGKQHAGKVFYDLTGNSDPTVTINSQMGEPKNGGSVSV 480
Db 455 GSGLAALITDGPFGSKMNVGKQHAGKVFYDLTGNSDPTVTINSQMGEPKNGGSVSV 514
QY 481 VPKRTVSTIARPIITRPWTGFEVWTEPRLYAM 514
Db 515 VPKRTVSTIARPIITRPWTGFEVWTEPRLYAM 548
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RESULT 3

```
P71034 PRELIMINARY; PRT; 521 AA.
ID P71034
AC P71034;
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Alpha-amyase precursor.
OS Bacillus sp. MK 716.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
CX NCBI_TaxId=54116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MK 716;
RA Sidhu G.S., Chakrabarti T.;
RT Molecular cloning and expression of the gene encoding for
RT thermostable alpha-amyase of a thermophilic bacterial isolate.
RL Submitted (OCT-1996) to the EMBL/Genbank/DBJ databases.
DR EMBL; U75445; AAB18785.1; -.
DR HSSP; P06278; 1VUS.
DR GO; GO:0004556; F:alpha-amyase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amy1_cat.
DR InterPro; IPR006589; Alp_amy1_cat_sub.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; alpha-amyase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Amy; 1.
KW Signal.
FT SIGNAL 1 34
FT CHAIN 35 521 ALPHA-AMYLASE.
SQ SEQUENCE 521 AA; 59311 MM; 5612A88596D922E1 CRC64;
```

Query Match 93.4%; Score 2658; DB 2; Length 521;
Best Local Similarity 99.2%; Pred. No. 7.1e-174;
Matches 480; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```
QY 1 AAPFNGTMQYFEWYLPDDGTLMTKYANANNLSIGITALLMPPAYKGTSSDVGYGY 60
Db 35 AAPFNGTMQYFEWYLPDDGTLMTKYANANNLSIGITALLMPPAYKGTSSDVGYGY 94
QY 61 DLYDLGFNQKGTVRKTKYGTAKQYLQAIQAHAAGQVYADVDPDHKGADGTEWDAVE 120
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DB 95 DLYDGEFNQGAIVTKYGTQAQYLOALIOAHHAGMAYADVDFHKGAGDTEWDAVE 154
QY 121 VNPSPRNOEISGTQIOIQAMTKFDPPRGNTYSSFFKRWYHFDGVDMDSRLSRIYKRG 180
DB 155 VNPSPRNOEISGTQIOIQAMTKFDPPRGNTYSSFFKRWYHFDGVDMDSRLSRIYKRG 214
QY 181 ICKAMDEVDTENGVYDLYMAYADLMDHPEVYTELKNMGKMYVNTTINIDGRLDAVAKIK 240
DB 215 ICKAMDEVDTENGVYDLYMAYADLMDHPEVYTELKNMGKMYVNTTINIDGRLDAVAKIK 274
QY 241 SFPPDMLSYVSQGTGKPLFTVGEYWSYDINKLHNYITKTGMSLFDAPLHNNFYTASK 300
DB 275 SFPPDMLSYVSQGTGKPLFTVGEYWSYDINKLHNYITKTGMSLFDAPLHNNFYTASK 334
QY 301 SGAFDMRTLMTNTLMKDOPTLAVTFVNDHDEPQALQSMDPMPKPLAAYAFILTRQEG 360
DB 335 SGAFDMRTLMTNTLMKDOPTLAVTFVNDHDEPQALQSMDPMPKPLAAYAFILTRQEG 394
QY 361 YFCVFGDYGIPOYNIPLSKSKIDPLLIARDYAYGTQHDYLDHSDIIGWTRGCTEKP 420
DB 395 YFCVFGDYGIPOYNIPLSKSKIDPLLIARDYAYGTQHDYLDHSDIIGWTRGCTEKP 454
QY 421 GSGALALITDPGGSKMYVYKQKAGKVFYDLTGNRSDVTITNSDGMGEFKVNGSVSW 480
DB 455 GSGALALITDPGGSKMYVYKQKAGKVFYDLTGNRSDVTITNSDGMGEFKVNGSVSW 514
QY 481 VPRK 484
DB 515 VPRR 518

RESULT 4
Q59222 PRELIMINARY; PRT; 613 AA.
AC Q59222;
DT 01-NOV-1996 (TREMREL. 01, Created)
DT 01-NOV-1996 (TREMREL. 01, Last sequence update)
DT 01-JUN-2003 (TREMREL. 24, Last annotation update)
DE Alpha-amyase (EC 3.2.2.1).
GN AMY.
OS Bacillus sp. TS-23.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=38441;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TS-23;
RA Lin U.-L., Chu W.S., Hsu W.H.;
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
EMBL U22045; AAA63900.1; -.
HSSP; P06278; 1VUS.
DR GO:0004556; F:alpha-amyase activity; IEA.
DR GO:0016798; F:hydrolyase activity, acting on glycosyl bonds; IEA.
DR GO:0008677; F:purine nucleosidase activity; IEA.
DR GO:0005375; P:carbohydrate metabolism; IEA.
DR InterPro: IPR006047; Alpha_ami_1_cat.
DR InterPro: IPR006589; Alp_ami_1_cat.
DR InterPro: IPR006046; Glyco_hydro_13.
DR Pfam: PF00128; alpha-amyase; 1.
DR Pfam: PF00686; CBM_20; 1.
DR PRINTS; PRO0110; ALPHAMYLASE.
DR PRODOM; PD001568; CBM_4; 1.
DR SMART; SM00642; Amyy; 1.
DR GlycoSite; Hydrolase.
SQ SEQUENCE 613 AA; 69537 MW; 14684A30FC2895E8 CRC64;

Query Match 84.4%; Score 2404; DB 2; Length 613;
Best Local Similarity 84.2%; Pred. No. 2.2e-156;
Matches 43; Conservative 31; Mismatches 50; Indels 0; Gaps 0;
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DB 33 APINETMOYFEMDLNDGTLMTKVNANLSSLGITLMLPAPYKTSQSDVGYVD 92
QY 62 LYDGEFNQGAIVTKYGTQAQYLOALIOAHHAGMAYADVDFHKGAGDTEWDAVEV 121
DB 93 LYDGEFNQGAIVTKYGTQAQYLOALIOAHHAGMAYADVDFHKGAGDTEWDAVEV 152
QY 122 NPSDRNOEISGTQIOIQAMTKFDPPRGNTYSSFFKRWYHFDGVDMDSRLSRIYKRG 181
DB 153 NPSDRNOEISGTQIOIQAMTKFDPPRGNTYSSFFKRWYHFDGVDMDSRLSRIYKRG 212
QY 182 GKAMDEVDTENGVYDLYMAYADLMDHPEVYTELKNMGKMYVNTTINIDGRLDAVAKIK 241
DB 213 GKAMDEVDTENGVYDLYMAYADLMDHPEVYTELKNMGKMYVNTTINIDGRLDAVAKIK 272
QY 242 SFPPDMLSYVSQGTGKPLFTVGEYWSYDINKLHNYITKTGMSLFDAPLHNNFYTASK 301
DB 273 SFPPDMLSYVSQGTGKPLFTVGEYWSYDINKLHNYITKTGMSLFDAPLHNNFYTASK 332
QY 302 SGAFDMRTLMTNTLMKDOPTLAVTFVNDHDEPQALQSMDPMPKPLAAYAFILTRQEG 361
DB 333 SGAFDMRTLMTNTLMKDOPTLAVTFVNDHDEPQALQSMDPMPKPLAAYAFILTRQEG 392
QY 362 PCVFGDYGIPOYNIPLSKSKIDPLLIARDYAYGTQHDYLDHSDIIGWTRGCTEKP 421
DB 393 PCVFGDYGIPOYNIPLSKSKIDPLLIARDYAYGTQHDYLDHSDIIGWTRGCTEKP 452
QY 422 SGLAALITDPGGSKMYVYKQKAGKVFYDLTGNRSDVTITNSDGMGEFKVNGSVSW 481
DB 453 SGLAALITDPGGSKMYVYKQKAGKVFYDLTGNRSDVTITNSDGMGEFKVNGSVSW 512
QY 482 PKRTVSTIARPIITRPMTGEFVWTEPRIVAN 514
DB 513 AKTSNVTFTVNNATTTSGQVYVYVANIPELGNW 545

RESULT 5
Q82839 PRELIMINARY; PRT; 516 AA.
AC Q82839;
DT 01-NOV-1998 (TREMREL. 08, Created)
DT 01-NOV-1998 (TREMREL. 08, Last sequence update)
DT 01-JUN-2003 (TREMREL. 24, Last annotation update)
DE Amyase.
OS Bacillus sp.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1409;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KSM-1378;
RL MEDLINE=98342036; PubMed=9675143;
RA Igataishi K., Hatada Y., Ikawa K., Araki H., Ozawa T., Kobayashi T.,
RA Ozaki K., Ito S.;
RT "Improved thermostability of a Bacillus alpha-amyase by deletion of
RT an arginine-glycine residue is caused by enhanced calcium binding.";
RL Biochem. Biophys. Res. Commun. 248:372-377(1998).
EMBL AB008763; BA032431.1; -.
HSSP; P06278; 1VUS.
DR GO:0004556; F:alpha-amyase activity; IEA.
DR GO:0005375; P:carbohydrate metabolism; IEA.
DR InterPro: IPR006047; Alpha_ami_1_cat.
DR InterPro: IPR006589; Alp_ami_1_cat.
DR InterPro: IPR006046; Glyco_hydro_13.
DR Pfam: PF00128; alpha-amyase; 1.
DR PRINTS; PRO0110; ALPHAMYLASE.
DR SMART; SM00642; Amyy; 1.
SQ SEQUENCE 516 AA; 58841 MW; D90A8C90ECC18278 CRC64;

Query Match 67.1%; Score 1910.5; DB 2; Length 516;
Best Local Similarity 68.8%; Pred. No. 1.1e-122;
Matches 329; Conservative 69; Mismatches 79; Indels 1; Gaps 1;
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Db      37 NGTMQVPEHMLPNDGNHMRFLRDDANLKSCTTAVWIPAMGTSQNDVGYAVLYD 96
Qy      65 LGFENQKGTVRTKTKYKAQYLQAIQAARAAAGQYADVDPDKGAGDGTENVADAVEVNS 124
Db      97 LGFENQKGTVRTKTKYKTRSQLGAVTSLSKNNGIQYGVAVNMHKGAGDGTENVAVEVNS 156
Qy      125 DRNGEISGTQYQAMTKFDPGKRGNTYSSFKRMRYHFDGVNDSSRLC-SRIYFRGIGK 183
Db      157 NRNEISEEYTEATKTFDPGKRGNTYSSFKRMRYHFDGVNDSSRLC-SRIYFRGIGK 216
Qy      184 AMDVEVDIENGNDYLYMADLDMDHPEVTELKMGKMYVNTTIDGFRLLDAVGHKIFSF 243
Db      217 AMDVEVDIENGNDYLYMADLDMDHPEVTELKMGKMYVNTTIDGFRLLDAVGHKIFSF 276
Qy      244 FPDWLSYRSQGTGRFLTVGEVYMSYDINKLKNYITKDGIMSLLDAPLHKKFYTASKSG 303
Db      277 TRDWLTHVRNTTGKMEFAVAFKXNDLALIKENYLNKTSWNHSDVPLHYNLYNANSNG 336
Qy      304 AFDMKTLTNTLMKQDPTLAVTVNDHDEFGQALQSWVDPMFKPLAVAFILTRQEGYPC 363
Db      337 YFDMRNILNGSVYQKHPHATVFDVNDHSDQEGALLESFVSQFKPLAVAFILTRQEGYPC 396
Qy      364 VFYGDYIGIPQYNIPLSKSIDPELLARDAVYGTQHDYLDHSDIIGWTRREGTEKFGSG 423
Db      397 VFYGDYIGIPTHGVPSMKSIDPELLARDAVYGTQHDYLDHSDIIGWTRREGTEKFGSG 456
Qy      424 LAALITDGPQSKMYVYKQAHAGKVFYDITGNRSDYVTTINSDEGSEFKNGSVSVWV 481
Db      457 LATINSDEGSKMYVYKQAHAGKVFYDITGNRSDYVTTINSDEGSEFKNGSVSVWV 514

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RESULT 6
Q9A054 PRELIMINARY; PRT; 533 AA.
ID Q9A054;
AC Q9A054;
DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
DT 01-JUN-2003 (TREMblrel. 24, Last annotation update)
DE Alpha-amyase.
OS Bacillus megaterium.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
CX NCBI_TaxID=1404;
RN [1]
RP SEQUENCE FROM N.A.
RA Kim Y.B., Lee B.N., Son H.U., Lee J.W., Kim B.J., Kim Y.-W.,
RA Park K.-H.;
RT "Cloning of maltopentase-producing amyase from Bacillus megaterium
RT KSM B-404."
RT Submitted (JAN-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF220440; AA00598.1; -
DR HSSP; P06278; IVUS.
DR GO; GO:0004556; F:alpha-amyase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_ami_cat.
DR InterPro; IPR006589; Alp_ami1_cat_sub.
DR Pfam; PF00128; alpha-amyase; 1.
DR SMART; SM00642; Aamy; 1.
SQ SEQUENCE 533 AA, 60557 MW, 7890CECD6A19C7DDE CRC64;

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Query Match 64.7%; Score 1841.5; DB 2; Length 533;
 Best Local Similarity 65.8%; Pred. No. 6.2e-118;
 Matches 317; Conservative 70; Mismatches 92; Indels 3; Gaps 1;

```

Qy      5 NGTMQVPEHMLPNDGNHMRFLRDDANLKSCTTAVWIPAMGTSQNDVGYAVLYD 64
Db      52 NGTMQVPEHMLPNDGNHMRFLRDDANLKSCTTAVWIPAMGTSQNDVGYAVLYD 111
Qy      65 LGFENQKGTVRTKTKYKAQYLQAIQAARAAAGQYADVDPDKGAGDGTENVADAVEVNS 124
Db      112 LGFENQKGTVRTKTKYKTRSQLGAVTSLSKNNGIQYGVAVNMHKGAGDGTENVAVEVNS 171
Qy      125 DRNGEISGTQYQAMTKFDPGKRGNTYSSFKRMRYHFDGVNDSSRLC-SRIYFRGIGK 184

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Db      172 NRNEVSGDYELSAWTGNFPGKRGNTYSSFKRMRYHFDGVNDSSRLC-SRIYFRGIGK 231
Qy      185 KMEVVDIENGNDYLYMADLDMDHPEVTELKMGKMYVNTTIDGFRLLDAVGHKIFSF 244
Db      232 KMEVVDIENGNDYLYMADLDMDHPEVTELKMGKMYVNTTIDGFRLLDAVGHKIFSF 291
Qy      245 PDWLSYRSQGTGRFLTVGEVYMSYDINKLKNYITKDGIMSLLDAPLHKKFYTASKSG 304
Db      292 PDWLSYRSQGTGRFLTVGEVYMSYDINKLKNYITKDGIMSLLDAPLHKKFYTASKSG 351
Qy      305 FDMKTLTNTLMKQDPTLAVTVNDHDEFGQALQSWVDPMFKPLAVAFILTRQEGYPC 364
Db      352 FDMKTLTNTLMKQDPTLAVTVNDHDEFGQALQSWVDPMFKPLAVAFILTRQEGYPC 411
Qy      365 FPGDYIGIPQYNIPLSKSIDPELLARDAVYGTQHDYLDHSDIIGWTRREGTEKFG 421
Db      412 FPGDYIGIPQYNIPLSKSIDPELLARDAVYGTQHDYLDHSDIIGWTRREGTEKFG 471
Qy      422 SGALITDGPQSKMYVYKQAHAGKVFYDITGNRSDYVTTINSDEGSEFKNGSVSVWV 481
Db      472 SGALITDGPQSKMYVYKQAHAGKVFYDITGNRSDYVTTINSDEGSEFKNGSVSVWV 531
Qy      482 PR 483
Db      532 QR 533

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RESULT 7
Q9RQ78 PRELIMINARY; PRT; 519 AA.
ID Q9RQ78;
AC Q9RQ78;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMblrel. 24, Last annotation update)
DE Raw starch digesting amyase precursor.
OS Cytophaga sp.
OC Bacteria; Bacteroidetes; Sphingobacteriales;
OC Flexibacteraceae; Cytophaga.
CX NCBI_TaxID=29535;
RN [1]
RP SEQUENCE FROM N.A.
RA Jeang C.L., Chen L.S., Chen M.Y.;
RT Submitted (MAY-1998) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF067653; AAP00567.1; -
DR HSSP; P06278; IVUS.
DR GO; GO:0004556; F:alpha-amyase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_ami_cat.
DR InterPro; IPR006589; Alp_ami1_cat_sub.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; alpha-amyase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Aamy; 1.
FT SIGNAL 1 57
FT CHAIN 58 519
SQ SEQUENCE 519 AA, 58337 MW, 36688A4D98B163 CRC64;

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Query Match 64.5%; Score 1837.5; DB 2; Length 519;
 Best Local Similarity 67.4%; Pred. No. 1.1e-117;
 Matches 326; Conservative 57; Mismatches 98; Indels 3; Gaps 1;

```

Qy      1 AAPNGTMQVPEHMLPNDGNHMRFLRDDANLKSCTTAVWIPAMGTSQNDVGYAVLYD 60
Db      34 AAPNGTMQVPEHMLPNDGNHMRFLRDDANLKSCTTAVWIPAMGTSQNDVGYAVLYD 93
Qy      61 DLYDLGFEHQKGTVRTKTKYKAQYLQAIQAARAAAGQYADVDPDKGAGDGTENVADAVEVNS 120
Db      94 DLYDLGFEHQKGTVRTKTKYKTRSQLGAVTSLSKNNGIQYGVAVNMHKGAGDGTENVAVEVNS 153
Qy      121 VNSDRNGEISGTQYQAMTKFDPGKRGNTYSSFKRMRYHFDGVNDSSRLC-SRIYFRGIGK 180
Db      154 VNSDRNGEISGTQYQAMTKFDPGKRGNTYSSFKRMRYHFDGVNDSSRLC-SRIYFRGIGK 213

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Db 124 LGFENQKGTATRTKTKYQOLKSAIEALHKONI DVGVDVNMHKGADVTETVTAVEVDN 151
QY 125 DRNOEISGTYQIQAATKTFDPGRGNTYSSFFKRWYHFDGVDMDSRKLRIYKFRGIGKA 184
Db 152 NNNVSVSGDYIEISAWTGKFNFGKGNYSNFKWKWHPDGTDMDEGRKLNRIYKFRGIGKA 211
QY 155 WMEVDTEGNNDYLYMADLMDHDEPVYTELKNWCKWYNTNTNIDGFDLAVKIKTSFF 244
Db 212 WMEVTSSENGNDYLYMADLMDHDEPVYTELKNWCKWYNTNTNIDGFDLAVKIKTSFF 271
QY 245 PDWLSVYASQTKPLFTVGEYWSYDINKLHNYITKTGMSLFPAPLNKFEYASKSQGA 304
Db 272 RDMVNHVHQQTGKEMFTVAEYQNDIQTLNNYLAKVYNQGVFADPLHNFYHVASKSGN 331
QY 305 FDMRLMTNTLMKQOPTLAFTVNDHDEPGALQSWDPMFKPLAFAFILTREGYPCV 364
Db 332 YNNRNILNLTQVQNPALAVTLVENHDSQPGSLSVSVSPMKPLAFAFILTREGYPCV 391
QY 365 FYGDIYGGI---PQYNIPLSKSIDPULIARDYAYGTQHDYLDHSDIIGWREGGTEPG 421
Db 392 FYGDIYGGTSGNSSEIPLKXIDPILNARKNFAYGTQHDYLDHSDIIGWREGGTEPG 451
QY 422 SGLAALLIDGPGGSKMRYVKGQKAGKRVFDLTGNSDPTVTINSQGWGFEKXNGSGSVYV 481
Db 452 SGLAALLIDGPGGSKMRYVKGQKAGKRVFDLTGNSDPTVTINSQGWGFEKXNGSGSVYV 511

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RESULT 10

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ID 087H6 PRELIMINARY: PRT: 507 AA.
AC 087H6;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Alpha-amylase.
GN VPA0999.
OS Vibrio parahaemolyticus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrrio.
OX NCBI_TaxID=670;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RIMD 2210633 / Serotype O3:K6;
RX MEDLINE=22508454; PubMed=12620739;
RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
RA Iijima Y., Naito M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
RA Yasunaga T., Honda T., Shingawa H., Hatford M., Iida T.;
RT "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
RT distinct from that of V. cholerae.";
RL Lancet 361:743-749 (2003).
DR EMBL: AP005087; BAC62342.1;
DR GO: GO:0004556; F:alpha-amylase activity; IEA.
DR GO: GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro: IPR006047; Alpha_ami_cat.
DR Pfam: PF00128; alpha-amylase; 1.
KW Complete proteome.
SQ SEQUENCE 507 AA; 58428 MW; 91B549E2BE0700BD CRC64;

```

Query Match 59.7%; Score 1700; DB 16; Length 507;

Best Local Similarity 63.1%; Pred. No. 2.8e-108; Indels 10; Gaps 6;

Matches 305; Conservative 66; Mismatches 102; Indels 10; Gaps 6;

5 NGTMQYFEWYLPDDGTLMTKVANEANNLSLGITLMLPFAVYKGTSSRS-DVGVGVYLY 63

26 NGTMQYFEWYLPDDGTLMTKVANEANNLSLGITLMLPFAVYKGTSSRS-DVGVGVYLY 85

64 DLGEFNQKGTATRTKTKYQOLKSAIEALHKONI DVGVDVNMHKGADVTETVTAVEVDN 123

86 DLGEFNQKGTATRTKTKYQOLKSAIEALHKONI DVGVDVNMHKGADVTETVTAVEVDN 145

124 SPNNOEISGTYQIQAATKTFDPGRGNTYSSFFKRWYHFDGVDMDSRKLRIYKFRGIGK 183

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Db 146 DNENIEL-GDKWIEAMVEFNFGKNDKYSNFWHTWYHFDGVDMDSRKLRIYKFRGIGK 204
QY 184 WMEVDTEGNNDYLYMADLMDHDEPVYTELKNWCKWYNTNTNIDGFDLAVKIKTSFF 243
Db 205 WMEVTSSENGNDYLYMADLMDHDEPVYTELKNWCKWYNTNTNIDGFDLAVKIKTSFF 264
QY 244 PDWLSVYASQTKPLFTVGEYWSYDINKLHNYITKTGMSLFPAPLNKFEYASKSQGA 303
Db 265 LQEMIDHLMKTKGKELFTVGEYWSYDINKLHNYITKTGMSLFPAPLNKFEYASKSQGA 324
QY 304 APMRLMTNTLMKQOPTLAFTVNDHDEPGALQSWDPMFKPLAFAFILTREGYPCV 363
Db 325 NYDMRQINNGTLMKQNPVAVTLVENHDSQPGSLSVSVSPMKPLAFAFILTREGYPCV 384
QY 364 FYGDIYGGI---PQYNIPLSKSIDPULIARDYAYGTQHDYLDHSDIIGWREGGTE 418
Db 385 FYGDIYGGTSGNSSEIPLKXIDPILNARKNFAYGTQHDYLDHSDIIGWREGGTE 444
QY 419 KPGSGLAALLIDGPGGSKMRYVKGQKAGKRVFDLTGNSDPTVTINSQGWGFEKXNGSGSV 478
Db 445 HPRS-NAVIMSDGPGGTSMYTGKESTR--YVDKLGIRTEYMTDANGMAEPVNGSGSV 501
QY 479 VWV 481
Db 502 VWV 504

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RESULT 11

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ID 093I48 PRELIMINARY: PRT: 501 AA.
AC 093I48;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Amylase.
GN AMYK38.
OS Bacillus sp. KSM-K38.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=129736;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KSM-K38;
RA Hayaishi Y.;
RT "Isolation of a new Bacillus alpha-amylase.";
RL Submitted (NCV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB051102; BAB71820.1;
DR GO: GO:0004556; F:alpha-amylase activity; IEA.
DR GO: GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro: IPR006047; Alpha_ami_cat.
DR Pfam: PF00128; alpha-amylase; 1.
SQ SEQUENCE 501 AA; 57485 MW; 1240F46739A5CC11 CRC64;

```

Query Match 56.8%; Score 1618; DB 2; Length 501;

Best Local Similarity 59.3%; Pred. No. 1.2e-102; Indels 2; Gaps 1;

Matches 283; Conservative 80; Mismatches 112; Indels 2; Gaps 1;

5 NGTMQYFEWYLPDDGTLMTKVANEANNLSLGITLMLPFAVYKGTSSRS-DVGVGVYLY 64

25 NGTMQYFEWYLPDDGTLMTKVANEANNLSLGITLMLPFAVYKGTSSRS-DVGVGVYLY 84

65 LGFENQKGTATRTKTKYQOLKSAIEALHKONI DVGVDVNMHKGADVTETVTAVEVDN 124

85 LGFENQKGTATRTKTKYQOLKSAIEALHKONI DVGVDVNMHKGADVTETVTAVEVDN 144

125 DRNOEISGTYQIQAATKTFDPGRGNTYSSFFKRWYHFDGVDMDSRKLRIYKFRGIGKA 184

145 NRMQDISGATIDAMTGDFSGANNAYSDPKRWYHFDGVDMDSRKLRIYKFRGIGKA 202

185 WMEVDTEGNNDYLYMADLMDHDEPVYTELKNWCKWYNTNTNIDGFDLAVKIKTSFF 244

203 WNRVVEENENYLYLGSNIDFSEHPEVQDELKDWGWFDELDLDSYRDLAKHIFWYT 262

245 PDWLSVYASQTKPLFTVGEYWSYDINKLHNYITKTGMSLFPAPLNKFEYASKSQGA 304

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Db 263 SWVRHQRNEADODLEFVGEYWKDVGALEFYLIDENNMESLFDVPLVNFYRASQGGG 322
Qy 305 FDMRTLMTNTLTKDQFTLAVTFVDNHDTEPGALQSWVDPMFKPLAYAFILTROGYP 364
Db 323 YMRNRLRSLVBAHMHMAVTFVDNHDTEPGSLSWADNFKPLAYAFILTRGGYENV 382
Qy 365 FPGDYIGIPQVNIPLSKSIDPELLARBYAGTQHDYDHDHDIIGMTREGTEKPSGL 424
Db 383 FPGDYIGIPNDNISAKKMIIDELARQVAYGTQHDYFDHWDVVGWTRBSSSRPNSGL 442
Qy 425 AALITPGSGSKMAYVKGKAGVFDLTGNRSPTYINSQMGSEFKXNGSVSYVW 481
Db 443 ATIMSGPGSGKMAYVGRNAGQGTWDTLGNNGASTTNGDGMGEFFNGSVSYVY 499

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RESULT 12

```

Q8YU21 PRELIMINARY; PRT; 492 AA.
AC Q8YU21;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Alpha-amy1ase.
GN ALR2190.
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=103690;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21595285; PubMed=11759840;
RA Kaneo T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
RA Matanabe A., Iiguchi M., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakazaki N., Shimo S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
RT cyanobacterium Anabaena sp. strain PCC 7120."
RL DNA Res. 8:205-213(2001).
DR EMBL/ AP003588; BAB73889.1; -.
DR PIR; AH2079; AH2079.
DR GO; GO:0004556; F:alpha-amy1ase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amy1_cat.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; alpha-amy1ase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
KM Complete proteome.
SQ SEQUENCE 492 AA; 57063 MW; 11B5D6EGF2P18288 CRC64;

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Query Match 47.3%; Score 1345.5; DB 16; Length 492;

Best Local Similarity 52.8%; Pred. No. 5,2e-84;

Matches 261; Conservative 67; Mismatches 147; Indels 19; Gaps 7;

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Qy 2 APRNGTMMQYFEMYLPPDDGTLMTKVNANNNLSLITLALMPAYKGSRS-DVGYGY 60
Db 2 AQANGTMMQYFHHYIPDGNLMSKEASAPELADAGFTLMLPRAKGFAGSFDGYGY 61
Qy 61 DLYDLGFNQKGVTRTKYGTGAQYLOAIQAHAAGQVYADVFDHKGAGDGTWDAVE 120
Db 62 DLEDFLGFQKGSVTRTYGTROQYLDVKSILQTHGQVYADAVLNHKGAGDVEFTKATP 121
Qy 121 VNSDRQGLISGYIOAMTKFDPFGKNTYSFFKRWYHFDGVNDE--SRKLSRYKF 178
Db 122 PPDDRLNPKGLODITTYTHNFPGRQKYSNFEHMHAFDAVDVNEKSGRSTVYLL 181
Qy 179 RGIQKAWDEVDTENGNYDYLMYADLMDHPEVYTELKMGKRYVNTINIDGFRIDAVE 238
Db 182 E--GKNDDYVALLEKGFAYLMGCDLDFQNEWRGEVYWGKVCIDTTKVDGFRIDAKH 239
Qy 239 IKSFPEDMLSYRSQGRKLFYVGEYWSYDINKLNYITKIDGMSLDAPLHNKYTA 298
Db 240 ISTWFFPEWIDALERRAGKDLFVGEYWNIDITLLMYDAVGRKMSFVDPVLIHFQA 299

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Qy 299 SKSGAFDMRTLMTNTLTKDQFTLAVTFVDNHDTEPGALQSWVDPMFKPLAYAFILTRO 358
Db 300 SKSGGNDMRTLIDGTMMQGRPTHAVTFVKNHDSQPLQLESVEPMFKPLAYAFILTRO 359
Qy 359 EGYPCVFGDYGIP-----QYNI--PSLSKSIDPELLARBYAGTQHDYDHDSD 407
Db 360 EGYPCVHFADYGAKEVDEWCKDGNRYNIEMPSHRMIIDKLYARKGAYAGPQNYLDHNM 419
Qy 408 IIGMTREGTEKPSGLAALITPGSGSKMAYVKGKAGVFDLTGNRSPTYINSQMG 467
Db 420 TIGTRFGDGDHP--QGAIVATMSDGSSEGIKWEVEKGENT--KFLDTEHIEAVYTNEMGW 476
Qy 468 GEFKNGSVSYVW 481
Db 477 GEFRCIGSVSYVW 490

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RESULT 13

```

Q89YPI PRELIMINARY; PRT; 481 AA.
AC Q89YPI;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Alpha-amy1ase precursor.
GN B74690.
OS Bacteroides thetaiotaomicron.
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=818;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=VPI-5482 / ATCC 29148;
RX MEDLINE=22550858; PubMed=12663928;
RA Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,
RA Chiang H.C., Hooper L.V., Gordon J.I.;
RT "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis."
RL Science 299:2074-2076(2003).
DR EMBL/ AB016946; AA079795.1; -.
DR GO; GO:0004556; F:alpha-amy1ase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amy1_cat.
DR InterPro; IPR006589; Alp_amy1_cat_sub.
DR Pfam; PF00128; alpha-amy1ase; 1.
DR SMART; SM00642; Amyy; 1.
KM Complete proteome.
SQ SEQUENCE 481 AA; 55343 MW; B6BF237011F5EE1A CRC64;

```

Query Match 46.5%; Score 1322.5; DB 16; Length 481;

Best Local Similarity 49.3%; Pred. No. 1.9e-87;

Matches 236; Conservative 89; Mismatches 153; Indels 1; Gaps 1;

```

Qy 5 NGTMMQYFEMYLPPDDGTLMTKVNANNNLSLITLALMPAYKGSRS-DVGYGY 64
Db 3 NGVMQYFEMHLPDGLMTKQIKEDALHLIDIGTAVWIPRAYKADQDEGATYDLYD 62
Qy 65 LGEFNQKGVTRTKYGTGAQYLOAIQAHAAGQVYADVFDHKGAGDGTWDAVEYNPS 124
Db 63 LGEFDQKGTTRTKYGTDELKRMIDELKHYHIAVYLDVNLNKAAGDFTKFMVVEVDPK 122
Qy 125 DRNQGISTGYIOAMTKFDPFGKNTYSFFKRWYHFDGVNDESRKLSRYKRGIGKA 184
Db 123 ERTALBEPFELQWGTYSFHRKDKSDPKFMHYNHSGFGDDAQRSGVFOIGEGKA 182
Qy 185 WDMVEVDENGNVYDLYMADLMDHPEVYTELKMGKRYVNTINIDGFRIDAVEIKRSFF 244
Db 183 WSEGVDSNGYVDLCLNDIDLDHPEVASELNKRGKVSSELDNDRDLAIKMKQGFV 242
Qy 245 PDMLSYRSQGRKLFYVGEYWSYDINKLNYITKIDGMSLDAPLHNKYTA 304
Db 243 AQFLDAYRSEKGNDFVAVGEYWNIDLEALAYIEAVGHKNLFDVPLHYMFGASQSGKD 302

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QY      303  EDRBLTAMTNTMDQCLTAVTFVDNNDTEBPGLASWDPMWPKPLAYAFILTROEGYPCV 364
      303  YDRLDIKDLTVVHHPLDLAVTVINDNIDTROGSLSEBNEDMKPLAYCLILMEKGGPCL 364
Db
QY      365  FYGDDYIGPQYNIPLSKSIDPLLIARDAVYGTGHDYLDHSDILGMRREGATEKPGSGL 422
      363  FYGDDYIYIKKEKSPHRI-IDILLDRKKYANGDQIETFDHSTGTGFRTOGDEHNSGL 422
Db
QY      425  AALITDPGGSXMMYVYVKQHAQKIFYDLTGNSDTYVINDSGWGEFKYNGSVSVWVPR 483
      422  VFLMSNDPAGSKMSLCEKFKGVMHEITGSISEBITDDEBNQSGFVSFESNNLAVWYXK 480
Db

```

RESULT 14	
Q97Q49	
ID Q97Q49	PRELIMINARY; PRT; 484 AA

DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, last annotation update)
DE Alpha-amyase.
GN SP1382.
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae
OC Streptococcus.
OC NCBI_TaxID=1313;

RP SEQUENCE FROM N.A. / TIGR4:
RC STRAIN=ATCC BAA-334 /
RX MEDLINE=21357209; PubMed=11439316;
RA Tetteijn H., Nelsson K.E., Paulsen I.T., Eisen J.A., Read T.D.,
RA Petersen S., Hedelberg J., DeBoy R.T., Haft D.H., Dodson R.J.,
RA Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,
RA Umayam I.A., White O., Salzberg S.L., Lewis M.R., Raudne D.,
RA Holtzapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L.,
RA McDonald L.A., Feldbush T.V., Angiolini S., Dickinson T., Hickey E.K.,
RA Holt I.E., Loftus B.J., Yang F., Smith H.C., Venter J.C.,
RA Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.,
RT "Complete genome sequence of a virulent isolate of *Streptococcus*

RL	Science	293	:498-506(2001).
DR	EMBL,	A6007435:	AAK75480.1; --
DR	PIR,	G9S160;	G9S160.
DR	TIGR,	SPL382;	--
DR	GO;	GO:0004555;	F.alpha.-amy1ase activity; IEA.
DR	GO;	GO:0005975;	F.cabobohydrate metabolism; IEA.
DR	InterPro;	IIPR06047;	Calpha_ami_cat.
DR	InterPro;	IIPR06589;	Alp_ami1_cat sub.
DR	InterPro;	IIPR06046;	Glyco_hydro_I3.
DR	Pfam;	PF00128;	alpha-amy1ase; 1.
DR	PRINTS;	PR00110;	ALPHAAMYLASE.
DR	SMART;	SM00642;	Amy1; 1.
DR	Complete	Protome.	
SW	SEQUENCE	484 AA;	55918 MW; 4B30DA50A30E7B8C CRC64

Query Match 46.2%; Score 1315; DB 16; Length 484;

Matches 248; Conservative 73; Mismatches 158; Indels 10

QY 5 NGTMMQYFEWYL PDDGTLWTKVANEANNLSSLGITALLWLPAYKGTSRSDVC

3 NQTLMOYFEWYLPBGQHWTRLAENAPHLAHGISHVMPPAFKATNEKDV

65 LGFENQKGTVRTKYGTKAQYLQAIQAHAAGMOVYADVDFDHKGADGTEW

Db 63 LGFENQKGTVRTKYGEKEDYLQAIQALKAQGIQPMADVVLNHKAAADHREAF

QY 125 DRNQEISGTYQIQAWTKFDFPGRGNTYSSFKWRWYHFDGVDWDESRKLSRIY

Db 123 DRVVEIGEPFTINGWTSFTFDGRQDTYNGFHHWHYHFTGTDYDAKRSKSGIY

185 WDWE--VDTENGNYDLMYADLDMDHPVTELEKNWGWVNTTNIDGFRLL

[illegible]

Db	18	MANBELVDMENQNYLYWYADLDFGHPREVIQNIYDMADMWETTGAVGFRIIDAVKHIISF	242
Qy	243	FEDDMLSYRSQGTQKPELFTVGEYMSYDINLKHNHYTKTDGMSLFDPAPLHNKFTATKSG	302
Db	243	FNMNFRDMKEXKAGDGFYVGEFNMNPKRANMIDYLEKTEBEHFDLVYRLHQNLEFSAQAG	302
Qy	303	GADNMTLMTNMLMDQPLTAAVTFPNNDHDPBGAOLQSVNDPWRKPLAVALILRLQSGYR	366
Db	303	ANYDLGIGTTSIVELKRPKAVTFVNDNDTQGGALBSVTEWNRKPAAYALILRLQGLP	366
Qy	363	CVFEGYGYGIP-QYNIPSLKSKIDPELLARRDAYGTQHDYLDHSITIGWTREGTEKFG	422
Db	363	CVFEGYGYGYSQGYAOGDEKILDLDLILRLDLAAGEQNDVFDANCIQWVRSAGENO--	420

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Qy      422  SGLAALITDGPGGSKMMIVYKQKHAGVFYFLITGNPSDVTITNSDGWGEFKNAGGSVSIVW 481
      | : | | : | | | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      421  SPIAVLISNDQENSKSMFVQGEENTNQTFLVLLGNHGGVTTIDEEGYQFPVSARSVSIVW- 479

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Qy	482	PKRTVSTI	490
Db	480	----AVNTI	484

RESULT 15
Q8DPC8
ID Q8DPC8 PRELIMINARY:
PRT: 484 AA

AC	Q8DPC8;	01-MAR-2003 (TREMBLrel_23, Created)
DT	01-MAR-2003 (TREMBLrel_23, Last sequence update)	
DT	01-JUN-2003 (TREMBLrel_24, Last annotation update)	
DT	01-JUN-2003 (TREMBLrel_23, Last annotation update)	
DE	Alpha-amylase (EC 3.2.1.1).	
GN	AMY OR SPRI339.	
OS	Streptococcus pneumoniae (strain ATCC BAA-255 / R6).	
OC	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae	
OC	Streptococcus	
CC		
NCBI	_taxid=171101;	
NCBI	[1]	
RD	SEQUENCE FROM N.A.	
RX	MEDLINE=21429245; PubMed=11544234; Med 7	

RA Dehoff B.S., Extrem S.T., Fritz L., Fu D.-J., Fuller W., Geringer C.
RA Gilmour B.S., Glass J.S., Khoja H., Kraft A.R., Lacase R.E.,
RA Leblanc D.J., Lee L.N., Leffkowitz E.J., Lu J., Matsushina P.,
RA McInnes S.M., McHenry M., Mclester K., Mundy C.W., Nicot T.I.,
RA Norris F.H., O'Gara M., Peery R.B., Robertson G.T., Rokey P.,
RA Sun P.-W., Winkler M.E., Yang Y., Young-Bellido M., Zhao C.,
RA Zook C.A., Baltz R.H., Uekusa S.R., Kosteck P.R., Skerfving P.L.,
RA Glass J.I.,
RT "Genome of the bacterium *Streptococcus pneumoniae* strain R6",
RL J. Bacteriol. 183:5709-5717 (2001).
DR EMBL; AF008485; AL00043.1; -.
DR PIR; P98026; P98026.
DR GO; GO:0004556; P:alpha-amylase activity; IEA.
DR GO; GO:0016798; P:hydrolase activity, acting on glycosyl bonds; IEA.

DR	InterPro	IPR006047	Alpha_amyl_cat.
InterPro	IPR006047	Alpha_amyl_cat.	
InterPro	IPR006047	Alpha_amyl_cat.	

DR InterPro; IPR006046; Glyco_hydro_13.
Dfam: DF00138; Alpha-amylase_1

DR PRINTS; PRO0110; ALPHAMYLAASE.
CMTBT: SM00642; NAME: 1

KW Glycosidase; Hydrolase; Complete proteome.
Accession Number: P01196918710ECC CYP6C4.
EC Number: 3.2.1.17

CONFIDENTIAL
NOV 1967

100-108881-1000

DB 1C
TOP SECRET

Best Local Similarity 50.5%; Pred. No. 1.2e-81;
 Matched 347, Mismatched 159, Tied 10

1. NAME OF THE PARTY _____

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Tue May 4 14:34:50 2004

us-10-644-187-6.rspc

Page 9

```
Db 63 LGFBNKGIYRTKYGKEDYLQALQALKAQGIQPMADVVLNHNKAAADHREAFQVIEVDPV 122
QY 125 DRNOEISGTYQIQAMTKFDFPGRGNTYSSFKRKHWHFDGVNDWDESKLSRIYKFRGIGKA 184
Db 123 DRTVELGEPTFTINGWTSFTPDGRQDYYNGFHHMHFTGTIDYDAKRSKSGIYLIQDNKG 182
QY 185 WDMW--VDTENGVYDYLMYADLMDHPEVYTELXNNGKXVYVNTNIDGFRLDVAVKHIFS 242
Db 183 WANEELVDNENGNIDYLMYADLMDHPEVYTELXNNGKXVYVNTNIDGFRLDVAVKHIDSF 242
QY 243 FPDWLSYVRSQTKPLFTVGEYWSYDINKLANYITKDGWMSLFDAPLHNKPYTASKSG 302
Db 243 FMEHFIRDMKEKYGDDEYVGEFWMNSDKKANLDYLEKTEHFDLVDRHLHONLFEASQAG 302
QY 303 GAFDMRTLMNTIMKQOPTLAVTFVNDHDEPGQALQSWYDPWFKPLAVAFILITRQEGYP 362
Db 303 ANYDLRGITFDSLVELKPKAVTFVNDHDTQRGQALSTVEEMFKPAAYALILLRQDGLP 362
QY 363 CVFYGDYVYGP-QYNIPLSKSIDPULIARADYAGTQHDYLDHSDIIGMTRGGTEKPG 421
Db 363 CVFYGDYVYGSQYAOQDFKEILLRLAIRKDLAYGEONDYFDHANCIGWVRSQAMNQ-- 420
QY 422 SGLAALITDGPBGSKMYVYKQAHAKVFDLTGNRSDTYTINSDGWGEFKNGSGYSYVW 481
Db 421 SPIAVLISNDQENSKMVFQJQEWNTQTFVDLGSHQGVITIDEGYGFVSARSYSVW- 479
QY 482 PRKTVSTI 490
Db 480 ----AVNTI 484
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Search completed: May 3, 2004, 20:53:14
Job time : 37.5403 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 3, 2004, 20:45:43 ; Search time 13.6493 Seconds
(without alignments)
3382.735 Million cell updates/sec

Title: US-10-644-187-4

Perfect score: 2624

Sequence: 1 VNGTLMQYFEWYTPNDQHW.....KIGSDGMEFHVNDGSIV 480

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:
2: p1r2:
3: p1r3:
4: p1r4:

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2624	100.0	514	1	ALBSN
2	2173	82.8	512	1	ALBSL
3	1826	69.6	518	1	A27705
4	1768.5	67.4	549	1	A54541
5	1758.5	67.0	549	1	A24436
6	1754.5	66.9	548	1	A24549
7	1695	64.6	549	1	ALBSF
8	1253	47.8	493	2	S15713
9	1217	46.4	484	2	G95160
10	1212	46.2	484	2	F98026
11	1197	45.6	492	2	AH2079
12	1187	42.9	491	2	C86781
13	1050	40.0	495	2	AD3038
14	1050	40.0	506	2	G98247
15	1035	38.7	494	1	B45738
16	1006	38.3	494	2	AD0751
17	999	38.1	495	2	B90962
18	998	38.0	495	1	A45738
19	980	37.3	495	2	B85810
20	620	23.6	217	2	A19506
21	351.5	13.4	826	2	E96720
22	3346	13.2	440	2	S14558
23	3334	12.7	441	2	S10514
24	324	12.3	431	2	S14956
25	323	12.3	1196	2	A29130
26	319	12.2	438	2	S14957
27	318	12.1	435	2	S12625
28	317	12.1	435	2	JC7337
29	315.5	12.0	437	2	UT0946

30	315.5	12.0	437	2	JC7138	alpha-amyase (EC
31	315	12.0	413	1	ALMT3	alpha-amyase (EC
32	310	11.8	504	2	A55861	alpha-amyase (EC
33	307.5	11.7	423	2	T09942	alpha-amyase (EC
34	307.5	11.7	438	1	ALBS	alpha-amyase (EC
35	305	11.6	439	2	T02956	alpha-amyase (EC
36	289	11.0	429	1	JR0406	alpha-amyase (EC
37	287	10.9	428	2	T05521	alpha-amyase (EC
38	285.5	10.9	713	2	S09196	cyclomalitodextrin
39	284.5	10.8	443	2	J01527	alpha-amyase (EC
40	284.5	10.8	445	2	S19990	alpha-amyase (EC
41	283	10.8	427	1	ALBSB	alpha-amyase (EC
42	282.5	10.8	437	2	S07040	alpha-amyase (EC
43	279.5	10.7	482	2	S31478	alpha-amyase (EC
44	277.5	10.6	713	2	A58800	cyclomalitodextrin
45	272	10.4	713	1	ALBSG7	cyclomalitodextrin

ALIGNMENTS

RESULT 1

ALBSN
alpha-amyase (EC 3.2.1.1) precursor - Bacillus amyloliquefaciens
N/Alternate names: 1,4-alpha-D-glucan glucanohydrolase
C/Species: Bacillus amyloliquefaciens
C/Date: 30-Nov-1980 #sequence_revision 30-Jun-1987 #ext_change 18-Jun-1999
C/Accession: A92389; A90307; I39756; I39763; A00843
R/Takkinen, K.; Petersson, R.F.; Kalkkinen, N.; Palva, I.; Soderlund, H.; Kaariainen, L.
J. Biol. Chem. 258, 1007-1013, 1983
A/Title: Amino acid sequence of alpha-amyase from Bacillus amyloliquefaciens deduced fr
A/Reference number: A92389; PMID:83108808; PMID:6185474
A/Content: PubMed
A/Accession: A92389
A/Molecule type: DNA
A/Residues: 1-514 <TRX>
A/Cross-references: GB:J01542; GB:J01543; GB:M12033; GB:M12034; NID:G142428; PIDN:AAA221
R/Chung, H.S.; Friedberg, F.
Biochem. U. 185, 387-395, 1980
A/Title: Sequence of the N-terminal half of Bacillus amyloliquefaciens alpha-amyase.
A/Reference number: A90307; PMID:80241725; PMID:6156671
A/Accession: A90307
A/Molecule type: Protein
A/Residues: 32-53; I, 55-63, 'L', 65-78, 'D', 80-83, 'S', 85-222 <CH>
R/Palva, I.; Petersson, R.F.; Kalkkinen, N.; Lehtovaara, P.; Sarvas, M.; Soderlund, H.;
Gene 15, 43-51, 1981
A/Title: Nucleotide sequence of the promoter and NH2-terminal signal peptide region of t
A/Reference number: I39756; PMID:82051296; PMID:6170339
A/Accession: I39756
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-96 <RES>
R/Ruohonen, L.; Hackman, P.; Lehtovaara, P.; Knowles, J.K.C.; Karanen, S.
Gene 59, 161-170, 1987
A/Title: Efficient secretion of Bacillus amyloliquefaciens alpha-amyase cells by its ow
A/Reference number: I39763; PMID:88137952; PMID:2830166
A/Accession: I39763
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-59 <RES>
A/Cross-references: GB:M18424; NID:G142430; PIDN:AAA22192.1; PID:G142431
C/Function:
A/Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A/Pathway: glycogen/starch degradation
C/Superfamily: alpha-amyase, amyloliquefaciens type; alpha-amyase core homology
C/Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation
R/1-31/Domain: signal sequence #status predicted <SIG>
R/32-514/Product: alpha-amyase #status predicted <MP>
F/229-362/Domain: alpha-amyase core homology <AMY>
F/133,231,266/Binding site: calcium (Asn, Asp, His) #status predicted
F/262,299,359/Active site: Asp, Glu, Asp #status predicted

Query Match 100.0%; Score 2624; DB 1; Length 514;
 Best Local Similarity 100.0%; Pred. No. 1.5e-178;
 Matches 480; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 VNGTLMQYFEWYVNDGQHWKRLONDAEHLSDIGITAWIPPAKYGLSGSDNGYGYDLY 60
DB 32 VNGTLMQYFEWYVNDGQHWKRLONDAEHLSDIGITAWIPPAKYGLSGSDNGYGYDLY 91
QY 61 DLGEFOQKGVTRTKYKTKSELODAIGSHSRNVOYGVADVILNHKAGADATEDVTAVERN 120
DB 92 DLGEFOQKGVTRTKYKTKSELODAIGSHSRNVOYGVADVILNHKAGADATEDVTAVERN 151
QY 121 ANRNOETSEEVQIAWMDPFRPPRGNTYSDPKMHWYFDGADNDESKIRIKFRGECK 180
DB 152 ANRNOETSEEVQIAWMDPFRPPRGNTYSDPKMHWYFDGADNDESKIRIKFRGECK 211
QY 181 AMDMEVSENGNYDYLWYADVDYDHPVVAETKMGWYANETSLDGFRIIDAAKHIFSF 240
DB 212 AMDMEVSENGNYDYLWYADVDYDHPVVAETKMGWYANETSLDGFRIIDAAKHIFSF 271
QY 241 LRDWQAVRQATGKEMFTVAEYWMONNAKLENYLNTKTSFNOSVDFVPLHFNLOAASQGG 300
DB 272 LRDWQAVRQATGKEMFTVAEYWMONNAKLENYLNTKTSFNOSVDFVPLHFNLOAASQGG 331
QY 301 GYDMRRLIDGTWVSRHPKAVTFPENHDPTOPGSLSTVOTWFPKPLAYAFILTEESGYPC 360
DB 332 GYDMRRLIDGTWVSRHPKAVTFPENHDPTOPGSLSTVOTWFPKPLAYAFILTEESGYPC 391
QY 361 VFYGMVYTKGTSPKEIPSLKDNIEPIKAKEXVAYGQPHDYIDHPVIGWTEGDSAA 420
DB 392 VFYGMVYTKGTSPKEIPSLKDNIEPIKAKEXVAYGQPHDYIDHPVIGWTEGDSAA 451
QY 421 KSGLAALITDGPQSGKRWYAGLKNAGETWYDITGNRSPTVYIGSDGGEFHNNGSYSIY 480
DB 452 KSGLAALITDGPQSGKRWYAGLKNAGETWYDITGNRSPTVYIGSDGGEFHNNGSYSIY 511

```

RESULT 2

ALBISL

alpha-amyLase (EC 3.2.1.1) precursor [validated] - Bacillus licheniformis
 N/Aternate names: 1,4-alpha-D-glucan glucanohydrolase

C/Species: Bacillus licheniformis
 C/Date: 30-Jun-1987 #sequence revision 24-Apr-1998 #text change 15-Sep-2000

C/Accession: A91997; B24549; A91796; A21663; I39774; I39772; A26151; S53788; A00844
 R/Yuuki, T.; Nomura, T.; Tezuka, H.; Tsuboi, A.; Yamaguchi, N.; Ueda, S.

J. Biochem. 98, 1147-1156, 1985
 A/Title: Complete nucleotide sequence of a gene coding for heat- and pH-stable alpha-amy-

ases deduced from the DNA sequences
 A/Reference number: A91997; MUID:86111694; PMID:2418011

A/Accession: A91997
 A/Molecule type: DNA

A/Residues: 1-162, 'R', 164-512 <YU>
 A/Cross-references: GB:X03236; NID:G39551; PIDN:CAA26981.1; PID:G39552

A/Experimental source: ATCC 27811
 R/Gray, C.L.; Weiner, S.R.; Rey, M.W.; Lamsa, M.H.; Kindie, K.L.; Carmona, C.; Regardt,

U. Bacteriol. 166, 635-643, 1986
 A/Title: Structural genes encoding the thermophilic alpha-amyLases of Bacillus stearother-

A/Reference number: A91817; MUID:86195857; PMID:3009417
 A/Accession: B24549

A/Molecule type: DNA
 A/Residues: 1-338, 'G', 340-348, 'S', 350-512 <GRA>

A/Cross-references: GB:M13256; NID:9142510; PIDN:AAA22240.1; PID:9142511
 A/Experimental source: NCIB 8061 Ollington, J.F.; McConnell, D.J.

R/Stephens, M.A.; Ortlepp, S.A. J. Bacteriol. 158, 369-372, 1984
 A/Title: Nucleotide sequence of the 5' region of the Bacillus licheniformis alpha-amyLase

A/Reference number: A91796; MUID:84185455; PMID:6609154
 A/Accession: A91796

A/Molecule type: DNA
 A/Residues: 1-104 <STE>

A/Cross-references: GB:K01984; NID:9142432; PIDN:AAA22193.1; PID:9142433
 R/Sidakov, M.; Palva, I.

Eur. J. Biochem. 145, 567-572, 1984

A/Title: Isolation and the 5'-end nucleotide sequence of Bacillus licheniformis alpha-amylase
 A/Reference number: A21663; MUID:85076654; PMID:6334606
 A/Accession: A21663

A/Molecule type: DNA
 A/Residues: 1-3, 'H', 5-12, 'P', 14-47, 'R', 49-61, 'V', 63, 'D', 65-67, 'VA', 70-71, 'S', 73-80, 'D', 8;

A/Note: the authors translated the codon CGT for residue 48 as Gly and GAC for residue 6
 R/naide, B.W.; Chambliss, G.H.; McConnell, D.J.

J. Bacteriol. 171, 2435-2442, 1989
 A/Title: Bacillus licheniformis alpha-amyLase gene, amyL, is subject to promoter-independent

A/Reference number: I39773; MUID:89213924; PMID:2540150
 A/Accession: I39774

A/Status: translated from GB/EMBL/DBJ
 A/Molecule type: DNA

A/Residues: 1-29 <LMO>
 A/Cross-references: GB:M26412; NID:G341477; PIDN:AAA22337.1; PID:9516550

R/Jorgensen, P.L.; Hansen, C.K.; Poulsen, G.B.; Didrichsen, B.
 Gene 96, 37-41, 1990

A/Title: In vivo genetic engineering: homologous recombination as a tool for plasmid com-
 A/Reference number: I39772; MUID:91092499; PMID:2265757

A/Accession: I39772
 A/Status: translated from GB/EMBL/DBJ

A/Residues: 1-32, 'I' <JOR>
 A/Molecule type: DNA

A/Cross-references: GB:M2637; NID:G142498; PIDN:AAA22332.1; PID:G142499
 R/Kuhn, H.; Fietzek, P.P.; Lampen, J.O.

J. Bacteriol. 149, 372-373, 1982
 A/Title: N-terminal amino acid sequence of Bacillus licheniformis alpha-amyLase: compari-

A/Reference number: A26151; MUID:82098050; PMID:6172418
 A/Accession: A26151

A/Molecule type: protein
 A/Residues: 30-37, 'E', 39-41, 'X', 43-47 <KUH>

R/Machius, M.; Wiegand, G.; Huber, R.
 J. Mol. Biol. 246, 545-559, 1995

A/Title: Crystal structure of calcium-depleted Bacillus licheniformis alpha-amyLase at 2.
 A/Reference number: S53788; MUID:95182462; PMID:7877175

A/Accession: S53788
 A/Molecule type: protein

A/Residues: 'D', 220-227 <MAC>
 A/Note: sequence represents amino end of an internal fragment created by a single enzymat-

R/Machius, M.; Wiegand, G.; Huber, R.
 submitted to the Brookhaven Protein Data Bank, July 1995

A/Reference number: A63206; PDB:1BPL
 A/Contents: annotation. X-ray crystallography, 2.2 angstroms, residues 32-210/222-511

A/Note: these structural studies suggest 163 is less rather than Arg
 R/Song, H.K.; Hwang, K.Y.; Chang, C.; Suh, S.W.

submitted to the Brookhaven Protein Data Bank, October 1996
 A/Reference number: A66860; PDB:1VUS

A/Contents: annotation; X-ray crystallography, 1.7 angstroms, residues 32-210/222-511
 C/Genetics:

A/Gene: amyL
 A/Function:

A/Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
 A/Pathway: glycogen/starch degradation

C/Superfamily: alpha-amyLase, amyLoligofaciens type; alpha-amyLase core homology
 C/Keywords: extracellular protein; glycosylase; heat-stable protein; hydrolase; polysacchi-

F.1.29/Domains: signal sequence #status predicted <SIG>
 F.1.30-512/Product: alpha-amyLase #status experimental <MNT>

F.1.32/Domain: alpha-amyLase core homology <AMY>
 F.1.33-229, 264/Binding site: calcium (Asn, Asp, His) #status experimental

F.1.34-290, 357/Active site: Asp, Glu, Asp #status experimental
 F.260, 290, 357/Active site: Asp, Glu, Asp #status experimental

Query Match 82.8%; Score 2173; DB 1; Length 512;
 Best Local Similarity 80.6%; Pred. No. 1.6e-146;

Matches 387; Conservative 41; Mismatches 50; Indels 2; Gaps 1;

```

QY 1 VNGTLMQYFEWYVNDGQHWKRLONDAEHLSDIGITAWIPPAKYGLSGSDNGYGYDLY 60
DB 32 VNGTLMQYFEWYVNDGQHWKRLONDAEHLSDIGITAWIPPAKYGLSGSDNGYGYDLY 91
QY 61 DLGEFOQKGVTRTKYKTKSELODAIGSHSRNVOYGVADVILNHKAGADATEDVTAVERN 120
DB 92 DLGEFOQKGVTRTKYKTKSELODAIGSHSRNVOYGVADVILNHKAGADATEDVTAVERN 151

```

```
QY 121 ANNOETSEYQIAWMDPFRPGSGNTYSPFKMWHYFDGADNDESKISIRIFKREGCK 180
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 152 ADRNRVLSGEHLIKAMTHFHPGRGSTYSPFKMWHYFDGADNDESKIRIYKF--QK 209
QY 181 AMDWEVSENGNYIYIYADVDYDHPDVVAETKMGKIYANELSLDGFRIIDAAHIKFSF 240
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 210 AMDWEVSENGNYIYIYADVDYDHPDVVAETKMGKIYANELSLDGFRIIDAAHIKFSF 269
QY 241 LRDWVAQRAQTGKEMFTVAEYWMONNAKLENYLNTKTSFNOSVDFPLAFHNLQAASSQGG 300
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 270 LRDWVAQRAQTGKEMFTVAEYWMONNAKLENYLNTKTSFNOSVDFPLAFHNLQAASSQGG 329
QY 301 GYDMRLLDGTVYSHRPEKATVFNENHDTPGOSLESTVQWTFKPLAYAFILTRREGSYPQ 360
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 330 GYDMRLLDGTVYSHRPEKATVFNENHDTPGOSLESTVQWTFKPLAYAFILTRREGSYPQ 389
QY 361 VFYGDWYGTGKSPKELPSLKDNIPEILAKREYAGPQHDYIDHPDVIQWTRBGSSAA 420
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 390 VFYGDWYGTGKSPKELPSLKDNIPEILAKREYAGPQHDYIDHPDVIQWTRBGSSAA 449
QY 421 KSGLAALITDGPQSGKMYAGLKNAGETWYDITGNRSDTVKIGSDGCEHFHYNDGSYSY 480
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 450 NSGLAALITDGPQSGKMYAGLKNAGETWYDITGNRSDTVKIGSDGCEHFHYNDGSYSY 509
```

RESULT 3

```
A27705
alpha-amylase (EC 3.2.1.1) precursor - Bacillus sp.
N:Alternate names: 1,4-alpha-D-glucan glucanohydrolase; G6-amylase
C:Species: Bacillus sp.
C>Date: 31-Mar-1989 #sequence_revision 18-Aug-1995 #text_change 18-Jun-1999
C:Accession: A27705
R:Tsukamoto, A.; Kimura, K.; Ishii, Y.; Takano, T.; Yamane, K.
Biochem. Biophys. Res. Commun. 151, 25-31, 1988
A:Title: Nucleotide sequence of the maltotetraose-producing amylase gene from an alkalophi
A:Reference number: A27705; WUID:86162814; PMID:3258152
A:Accession: A27705
A:Molecule type: DNA
A:Residues: 1-518 <TSU>
A:Cross-references: GB:M18862; NID:G142496; PIDN:AAA2231.1; PID:G142497
A:Experimental source: chromosomal DNA of strain 707
A>Note: amino end of mature protein also determined
C:Comment: This is the smallest of five starch-hydrolyzing enzymes from this organism.
C:Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: alpha-amylase, amy101quefaciens type; alpha-amylase core homology
C:Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation
F:1-33/Domain: signal sequence #status predicted <SIG>
F:34-518/Product: alpha-amylase #status experimental <NAT>
F:236-369/Domain: alpha-amylase core homology <AMY>
F:139,237/Binding site: calcium (Asp, Asp, His) #status predicted
F:269,299,366/Active site: Asp, Glu, Asp #status predicted
```

```
Query Match 69.6%; Score 1826; DB 1; Length 518;
Best Local Similarity 66.6%; Pred. No. 6,8e-122;
Matches 31; Conservative 63; Mismatches 90; Indels 8; Gaps 3;
```

```
QY 2 NGTLMQFEWYTPNDGQWKRLLQNDABHLSDIGITAVWIPPAYKGLSQSDNGYGPYDLYD 61
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 39 NGTLMQFEWYTPNDGQWKRLLQNDABHLSDIGITAVWIPPAYKGLSQSDNGYGPYDLYD 98
QY 62 LGFQKQGVTRTKYKXKSLQDAIGSLHSNNVQYGVVILNHKAGADATEDVTAVEVNP 121
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 99 LGFQKQGVTRTKYKXKSLQDAIGSLHSNNVQYGVVILNHKAGADATEDVTAVEVNP 158
QY 122 NRNOETSEBYQIAWMDPFRPGSGNTYSPFKMWHYFDGADNDESKIRISIFKREGCK 180
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 159 NRNOETSEBYQIAWMDPFRPGSGNTYSPFKMWHYFDGADNDESKIRISIFKREGCK 218
QY 181 AMDWEVSENGNYIYIYADVDYDHPDVVAETKMGKIYANELSLDGFRIIDAAHIKFSF 240
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

```
Db 219 AMDWEVDTENGNYDIYIYADVDYDHPDVVAETKMGKIYANELSLDGFRIIDAAHIKFSF 278
QY 241 LRDWVAQRAQTGKEMFTVAEYWMONNAKLENYLNTKTSFNOSVDFPLAFHNLQAASSQGG 300
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 279 LRDWVAQRAQTGKEMFTVAEYWMONNAKLENYLNTKTSFNOSVDFPLAFHNLQAASSQGG 338
QY 301 GYDMRLLDGTVYSHRPEKATVFNENHDTPGOSLESTVQWTFKPLAYAFILTRREGSYPQ 360
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 339 GYDMRLLDGTVYSHRPEKATVFNENHDTPGOSLESTVQWTFKPLAYAFILTRREGSYPQ 398
QY 361 VFYGDWYGTGKSPKELPSLKDNIPEILAKREYAGPQHDYIDHPDVIQWTRBGSSAA 418
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 399 VFYGDWYGTGKSPKELPSLKDNIPEILAKREYAGPQHDYIDHPDVIQWTRBGSSAA 453
QY 419 AAKSGLAALITDGPQSGKMYAGLKNAGETWYDITGNRSDTVKIGSDGCEHFHYNDGSYS 478
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 454 AAKSGLAALITDGPQSGKMYAGLKNAGETWYDITGNRSDTVKIGSDGCEHFHYNDGSYS 513
QY 479 IY 480
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 514 IY 515
```

RESULT 4

```
A54541
alpha-amylase (EC 3.2.1.1) precursor - Bacillus stearothermophilus (strain DN1792)
N:Alternate names: 1,4-alpha-D-glucan glucanohydrolase
C:Species: Bacillus stearothermophilus
C>Date: 28-Oct-1994 #sequence_revision 18-Aug-1995 #text_change 13-Jun-1997
C:Accession: A54541
R:Jorgensen, P.L.; Poulsen, G.B.; Diderichsen, B.
FEBS Microbiol. Lett. 77, 271-276, 1991
A:Title: Cloning of a chromosomal alpha-amylase gene from Bacillus stearothermophilus.
A:Reference number: A54541
A:Accession: A54541
A:Molecule type: DNA
A:Residues: 1-549 <JOR>
A:Cross-references: GB:X59476
A:Experimental source: chromosomal DNA of strain DN1792
A:Comment: Alpha-amylase genes have been found on plasmids and in multiple copies on the
C:Genetics:
A:Start codon: GTG
C:Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: alpha-amylase, amy101quefaciens type; alpha-amylase core homology
C:Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; polysac
F:1-34/Domain: signal sequence #status predicted <SIG>
F:35-549/Product: alpha-amylase #status predicted <NAT>
F:235-368/Domain: alpha-amylase core homology <AMY>
F:139,237,272/Binding site: calcium (Asp, Asp, His) #status predicted
F:268,298,365/Active site: Asp, Glu, Asp #status predicted
```

```
Query Match 67.4%; Score 1768.5; DB 1; Length 549;
Best Local Similarity 65.6%; Pred. No. 8,9e-118;
Matches 31; Conservative 56; Mismatches 104; Indels 5; Gaps 2;
```

```
QY 2 NGTLMQFEWYTPNDGQWKRLLQNDABHLSDIGITAVWIPPAYKGLSQSDNGYGPYDLYD 61
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 39 NGTLMQFEWYTPNDGQWKRLLQNDABHLSDIGITAVWIPPAYKGLSQSDNGYGPYDLYD 98
QY 62 LGFQKQGVTRTKYKXKSLQDAIGSLHSNNVQYGVVILNHKAGADATEDVTAVEVNP 121
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 99 LGFQKQGVTRTKYKXKSLQDAIGSLHSNNVQYGVVILNHKAGADATEDVTAVEVNP 158
QY 122 NRNOETSEBYQIAWMDPFRPGSGNTYSPFKMWHYFDGADNDESKIRISIFKREGCK 181
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 159 NRNOETSEBYQIAWMDPFRPGSGNTYSPFKMWHYFDGADNDESKIRISIFKREGCK 218
QY 182 WDWEVSENGNYDIYIYADVDYDHPDVVAETKMGKIYANELSLDGFRIIDAAHIKFSF 241
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 219 WDWEVSENGNYDIYIYADVDYDHPDVVAETKMGKIYANELSLDGFRIIDAAHIKFSF 278
```

QY 24 RDWQVARRAQTGKEMFTVAEYQNNAGKLENTLSTNSGVSFVPLPHLNGAASSGGG 301

Db 279 PDMISVYRSGTGPPLTFTVEBWSYDINKLHNITTDGTMSLFAPLHNKPYTLASKGGA 338

QY 302 YDMERLLDGVVSRHPEKAVTEVENHDTPQGSLSESTVQWFKPLAFAFILTRSGYPOV 361

Db 339 FDMRLTMTNLMMDQGTAVTFVDNHDHDPGALQSWDPPFKPLAFAFILTRSGYPCV 398

QY 362 FYGDMTGTGKTSFK-EIPSLKDNIEPILKARREYVGHQHDYIDHPVYIGWTRGSSAA 420

Db 399 FYGDPYGI----PQYVNPISLKSRIPELILARDDVYVGHQHDYLDHSDIIGWTRGSTEKP 454

QY 421 KSGLAALLIDGPGGSKRMVAGLKNAGETMYDITGRSTVYKIGSDMGGEFVANDGSISY 480

Db 455 GSGLAALLIDGPGGSKRMVVGQGHAKGFYDITGRSTVYKINDMGEEFVANGGSVSW 514

RESULT 5

alpha-amy-lase EC 3.2.1.1) precursor - *Bacillus stearothermophilus* plasmid pAT5
N:Alternate names: 1,4-alpha-D-glucan glucanohydrolase
C:Species: *Bacillus stearothermophilus*
C:Date: 05-Jun-1987 #sequence_revision 18-Aug-1995 #text_change 18-Jun-1999
C:Accession: A24436; I39777
R:Nakajima, R.; Imanaka, T.; Alba, S.
J. Bacteriol. 163, 401-406, 1985
A:Reference number: A24436; PMID:85234394; PMID:3924897
A:Accession: A24436
A:Molecule type: DNA
A:Residues: 1-549 <NA>
A:Cross-references: GB:M11450
A:Experimental source: plasmid pAT5
A>Note: amino end of the mature protein also determined
R:Jorgensen, P.L.; Hansen, C.K.; Poulsen, G.B.; Dietrichsen, B.
Gene 96, 37-41, 1990
A:Title: In vivo genetic engineering: homologous recombination as a tool for plasmid con-
A:Reference number: I39772; PMID:91092499; PMID:1265757
A:Accession: I39777
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-45 <RES>
A:Cross-references: GB:M2638; NID:G142514; PIDN:AAA22242.1; PID:G142515
C:Comment: Alpha-amy-lase genes have been found on plasmids and in multiple copies on the
C:Genetics:
A:Gene: amyS
A:Genome: Plasmid
A:Start codon: GTG
C:Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: alpha-amy-lase, amyloglucosylase type; alpha-amy-lase core homology
C:Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; polysaccharide
F:1-94/Domain: signal sequence #status predicted <SIG>
F:35-549/Product: alpha-amy-lase #status experimental <AMT>
E:235-356/Domain: alpha-amy-lase core homology <AMT>
E:113,237,272/Binding site: calcium (Asp, Asp, His) #status predicted
E:126,298,365/Active site: Asp, Glu, Asp #status predicted

Query Match	67.0%	Score 1758.5;	DB 1;	Length 549;
Best Local Similarity	65.4%	Pred. NO. 4.6e-117;		
Matches 314; Conservative	57;	Mismatches 104;	Indels 5;	Gaps 2;

2 NGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAYKGLSQSDNGYGPYDLYD 61

Db 39 NGTMQYFEWYL PDDGTLWTKVANEANLSSLGITALWLPAYKGTSRSDVGVDLYD 98

QY 62 LGEFQQKGTVRTKYGTKELODAIGSLHSRNVQYGDVVLNHKAGADATEDVTAVEVNP 12

Db 99 LGEFNQKGAVRTKYGTKAQYLQAIQAAHAAGM¹⁰⁰YADVFDHKGGADGTEWDAVEVNP¹⁵⁰S

QY 122 NRNQETSEEYQIKAWTDFRFPGRGNTYSDFKWHYHFDGADWDESKRISRIKFRGEGKA 18

Db 159 DRNQEISGTYQIQAWTKDFPGRGNTYSSFKRWRYHFDGVDWDESRKLSRIYKFRGIGKA 21

Qy	182	MDMEVSESNENYNYLWYAADVDYDHPDVAETKKGWYANEJSLQFRIIDAKHKKFSEFL	241
Db	219	MDMEVPTENENYNYLWYAADLDMDDHPEVVELKSKMGKMYNTNTINDQFRIDAVYHKKFSFP	278
Qy	242	RDWYQVAVRQATGEMETVAEYWGNNAGKXEJENLANKTSEFNGSFEVDYBIHNTLQAASSQGGG	301
Db	279	EDMLSDYRSGTQGFELTVGGEYWSYDINKLHMYIMKTNGTMSLFDAPLHKKFATAKSGGT	338
Qy	302	YDMRLLDGVYVSRHEKCAPTEYNDHDPOGGSLESTYQWTKPCLAYAAIILREGGYPQY	361
Db	339	FDHRTLMNTLMDDQPLAVIEVDNHDHIEGQALQGSWDPMFKPLAYAFILRQGGYFVY	398
Qy	362	FYGDHMTKQTSK-EIPLSKDNIEPLKARREYAYGPHDITDHPDVTGWRREGDSSAA	420
Db	399	FYGGYGI-----QYNYIPSKSKYIDPLTARRDYALGTQHDHLDSDIILGWRBGEVTEKP	454
Qy	421	KSGIALIITDGPGRKMTAGLKNAGEYWDYITGRSDYTKIGSDQWGEFHHVNDGSVSY	480
Db	455	GSGIALIITDGPGRSKMYTVGKQHAQKAYEYDITGRSDYVITNSDQWGEFKYNGGSYSVW	514

RESULT 6

N.alpha-amyLase EC 3.2.1.1) pDiscusor - *Bacillus stearothermophilus* (strain NZ-3)

C:Alternate names: 1,4-alpha-D-glucan glucanohydrolase

C:Species: *Bacillus stearothermophilus*

C:Date: 30-Jun-1988 #sequence_revision 18-Aug-1995 #text_change 18-Jun-1999

C:Accession: A24549; I39501; I39770

C:Gray, G.L.; Manzner, S.E.; Rey, M.W.; Lamsa, M.H.; Kindler, K.L.; Carmona, C.; Regnadt, J. *Bacteriol.* 166, 635-643, 1986

A:Title: Structural genes encoding the thermophilic alpha-amyLases of *Bacillus stearothermophilus*

A:Reference number: A91817; WCID:86195857; PMID:3009417

A:Accession: A24549

A:Molecule type: DNA

A:Residues: 1549 <GRA>

A:Cross-references: GB:I39555; NID:G142512; PIDDN:AAA22241.1; PID:G142513

A:Experimental source: genomic DNA of strain NZ-3

J:Satoh, H.; Nishida, H.; Isono, K.

J: *Bacteriol.* 170, 1034-1040, 1988

A:Title: Evidence for movement of the alpha-amyLase gene into two phylogenetically distant

A:Reference number: I39501; WCID:88139156; PMID:3257753

A:Accession: I39501

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 536-549 <RBS>

A:Cross-references: GB:I429577; NID:G142476; PIDDN:AAA22225.1; PID:G142478

A:Experimental source: strain DY-5

A:Accession: I39770

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 536-549 <R2>

A:Cross-references: GB:M29578; NID:G142484; PIDDN:AAA22228.1; PID:G142486

A:Experimental source: strain 799

C:Comment: Alpha-amyLase genes have been found on plasmids and in multiple copies on the

C:Genetics:

A:Start codon: GTG

A:Function:

A>Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
 A_Pathway: glycogen/starch degradation

Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase;

F;35-549/Product: alpha-amylase #status predicted <MAT>

F:139,237,272/Binding site: calcium (Asp, Asp, His) #status predicted

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Best Local Similarity 65.2%; Pred. No. 8.7e-117;

[illegible]

QY 2 NGTLMQYFEWYTPNDGQHMKRLQNDAEHLSDIGITAWIIPRAYKGLSQSDNGYGPYDLYD 61

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Db      39 NGTMMQYFEMWLPDDGTLMTKVAENANNLSLIGITLALMLPPAYKGTSSDVGYGYDLYD 98
        62 LGEPQOKGTVRTKTKYKSELDQALIGSLHSRNVOYGVYVNLNKAQADATEDVTAVERNPA 121
        99 LGEPNOKGTVRTKTKYKSELDQALIGSLHSRNVOYGVYVNLNKAQADATEDVTAVERNPA 158
        122 NNNQETSEBYOIKAMTDFRPPGRGNTYSDPKMWHYHFDGADWDESKISRIKFEKGEKKA 181
        159 DNNQETISGTYQIQAWTKFDPGRGNTYSEFKRMWHYHFDGADWDESKISRIKFEKGEKKA 218
        182 WMEVSSSENGNTDYLMTADVDYDHPDYVAETKKMGITWANEISLDGFRIDAKHKEFPL 241
        219 WMEVDTENGNTDYLMTADVDYDHPDYVAETKKMGITWANEISLDGFRIDAKHKEFPL 278
        242 RDMVOAVRQATGKEMFTVAEYWNQNAKLENTLNTSFNOSYEDVPLHFNLOAASQSGG 301
        279 PDMLSYRSQTKGKPLFTVGEYWSYDINKLHNITKTNGTMSLFDAPLHKKFYASKSGGA 338
        302 YDMRLLDGTIVSRHPEKAVTFVENHDTPQGSLSTVQTMFKPLAFAFILTRREGYPOV 361
        339 FDMSTLMMNTLMDQOPLTAVFDNHDTEPQALQSWDPMEKPLAFAFILTRREGYPCV 398
        362 FYGDMVGTGKTSRK-EIPLSKXNIEPILKARKEVYAGPOHDYDHPDYVGMTREGSSAA 420
        399 FYGDIYGI---PQYNIPLSKXIDPLLARRDYAGTQHDYLDHSDIIGWTRREGYTEKP 454
        421 KSGLAALITDGPQSGSKMYAGLKNAGETWYDITGNRSDTVKIGSDGSGEFHYNDGSVSIY 480
        455 GSGLAALITDGPQSGSKMYAGLKNAGETWYDITGNRSDTVKIGSDGSGEFHYNDGSVSIY 514

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RESULT 7

ALBSF

alpha-amyase (EC 3.2.1.1) precursor - *Bacillus stearothermophilus* (strain DY-5) plasmid

N/Alternate names: 1,4-alpha-D-glucan glucanohydrolase

C/Species: *Bacillus stearothermophilus*

C/Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 16-Feb-1997

C/Accession: A91999; B91999; A91804; A00845

R/Author: H. Sasaki, T.; Tsuboi, A.; Yamagata, H.; Tsukagoshi, N.; Uda, S.

J. Biochem. 98, 95-103, 1985

A/Title: Complete nucleotide sequence of a thermophilic alpha-amyase gene: homology bet

A/Reference number: A91999; NCID:86008166; PMID:3876333

A/Accession: A91999

A/Molecule type: DNA

A/Residues: 1-548 <TH1>

A/Cross-references: GB:X02769

A/Experimental source: plasmid PH1300 from strain DY-5

A/Accession: B91999

A/Molecule type: protein

A/Residues: 35-48 <TH2>

A/Experimental source: strain DY-5

R/Author: H. Sasaki, T.; Takemura, T.; Ihara, H.; Idota, Y.; Yamagata,

J. Biochem. 164, 1182-1187, 1985

A/Title: Efficient synthesis and secretion of a thermophilic alpha-amyase by protein-pr

A/Reference number: A91804; NCID:86059211; PMID:2999073

A/Accession: A91804

A/Molecule type: DNA

A/Residues: 1-29, 'Q', 31-75, 'W', 77-122 <TSU>

C/Comment: Alpha-amyase genes have been found on plasmids and in multiple copies on the

C/Genetics:

A/Genome: plasmid

A/Start codon: GTG

C/Function:

A/Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds

C/Pathway: glycogen/starch degradation

C/Suprafamily: alpha-amyase, amyloliquefaciens type; alpha-amyase core homology

C/Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; polysac

F/35-548/Product: alpha-amyase #status experimental <MAT>

F/335-368/Domain: alpha-amyase core homology <AMT>

F/268,298,365/Active site: Asp, Glu, Asp #status predicted

Query Match 64.6%; Score 1695; DB 1; Length 548;

Best Local Similarity 64.0%; Pred. No. 1,5e-112;

Matches 307; Conservative 56; Mismatches 111; Indels 6; Gaps 3;

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        2 NGTMMQYFEMWLPDDGTLMTKVAENANNLSLIGITLALMLPPAYKGTSSDVGYGYDLYD 61
        39 NGTMMQYFEMWLPDDGTLMTKVAENANNLSLIGITLALMLPPAYKGTSSDVGYGYDLYD 98
        62 LGEPQOKGTVRTKTKYKSELDQALIGSLHSRNVOYGVYVNLNKAQADATEDVTAVERNPA 121
        99 LGEPNOKGTVRTKTKYKSELDQALIGSLHSRNVOYGVYVNLNKAQADATEDVTAVERNPA 158
        122 NNNQETSEBYOIKAMTDFRPPGRGNTYSDPKMWHYHFDGADWDESKISRIKFEKGEKKA 181
        159 DNNQETISGTYQIQAWTKFDPGRGNTYSEFKRMWHYHFDGADWDESKISRIKFEKGEKKA 218
        182 WMEVSSSENGNTDYLMTADVDYDHPDYVAETKKMGITWANEISLDGFRIDAKHKEFPL 241
        219 WMEVDTENGNTDYLMTADVDYDHPDYVAETKKMGITWANEISLDGFRIDAKHKEFPL 278
        242 RDMVOAVRQATGKEMFTVAEYWNQNAKLENTLNTSFNOSYEDVPLHFNLOAASQSGG 301
        279 PDMLSYRSQTKGKPLFTVGEYWSYDINKLHNITKTNGTMSLFDAPLHKKFYASKSGGA 338
        302 YDMRLLDGTIVSRHPEKAVTFVENHDTPQGSLSTVQTMFKPLAFAFILTRREGYPOV 361
        339 FDMSTLMMNTLMDQOPLTAVFDNHDTEPQALQSWDPMEKPLAFAFILTRREGYPCV 397
        362 FYGDMVGTGKTSRK-EIPLSKXNIEPILKARKEVYAGPOHDYDHPDYVGMTREGSSAA 420
        398 FYGDIYGI---PQYNIPLSKXIDPLLARRDYAGTQHDYLDHSDIIGWTRREGYTEKP 453
        421 KSGLAALITDGPQSGSKMYAGLKNAGETWYDITGNRSDTVKIGSDGSGEFHYNDGSVSIY 480
        454 GSGLAALITDGPQSGSKMYAGLKNAGETWYDITGNRSDTVKIGSDGSGEFHYNDGSVSIY 513

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RESULT 8

alpha-amyase (EC 3.2.1.1) - *Bacillus circulans*

C/Species: *Bacillus circulans*

C/Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 22-Jun-1999

C/Accession: S15713

R/Author: T. Marcel

submitted to the EMBL Data Library, May 1991

A/Reference number: S15713

A/Accession: S15713

A/Molecule type: DNA

A/Residues: 1-493 <MAR>

A/Cross-references: EMBL:X60779; NID:939411; PIDN:CAA43194.1; PID:939412

C/Genetics:

A/Genes: amyE

C/Function: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds

A/Pathway: glycogen/starch degradation

C/Suprafamily: alpha-amyase, amyloliquefaciens type; alpha-amyase core homology

C/Keywords: glycosidase; hydrolase; polysaccharide degradation

F/200-333/Domain: alpha-amyase core homology <AMT>

Query Match 47.8%; Score 1253; DB 2; Length 493;

Best Local Similarity 47.2%; Pred. No. 3e-81;

Matches 226; Conservative 74; Mismatches 177; Indels 2; Gaps 1;

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        2 NGTMMQYFEMWLPDDGTLMTKVAENANNLSLIGITLALMLPPAYKGTSSDVGYGYDLYD 61
        4 NHTMMQYFEMWLPDDGTLMTKVAENANNLSLIGITLALMLPPAYKGTSSDVGYGYDLYD 63
        62 LGEPQOKGTVRTKTKYKSELDQALIGSLHSRNVOYGVYVNLNKAQADATEDVTAVERNPA 121
        99 LGEPNOKGTVRTKTKYKSELDQALIGSLHSRNVOYGVYVNLNKAQADATEDVTAVERNPA 158
        122 NNNQETSEBYOIKAMTDFRPPGRGNTYSDPKMWHYHFDGADWDESKISRIKFEKGEKKA 181
        159 DNNQETISGTYQIQAWTKFDPGRGNTYSEFKRMWHYHFDGADWDESKISRIKFEKGEKKA 218
        182 WMEVSSSENGNTDYLMTADVDYDHPDYVAETKKMGITWANEISLDGFRIDAKHKEFPL 241
        219 WMEVDTENGNTDYLMTADVDYDHPDYVAETKKMGITWANEISLDGFRIDAKHKEFPL 278
        242 RDMVOAVRQATGKEMFTVAEYWNQNAKLENTLNTSFNOSYEDVPLHFNLOAASQSGG 301
        279 PDMLSYRSQTKGKPLFTVGEYWSYDINKLHNITKTNGTMSLFDAPLHKKFYASKSGGA 338
        302 YDMRLLDGTIVSRHPEKAVTFVENHDTPQGSLSTVQTMFKPLAFAFILTRREGYPOV 361
        339 FDMSTLMMNTLMDQOPLTAVFDNHDTEPQALQSWDPMEKPLAFAFILTRREGYPCV 397
        362 FYGDMVGTGKTSRK-EIPLSKXNIEPILKARKEVYAGPOHDYDHPDYVGMTREGSSAA 420
        398 FYGDIYGI---PQYNIPLSKXIDPLLARRDYAGTQHDYLDHSDIIGWTRREGYTEKP 453
        421 KSGLAALITDGPQSGSKMYAGLKNAGETWYDITGNRSDTVKIGSDGSGEFHYNDGSVSIY 480
        454 GSGLAALITDGPQSGSKMYAGLKNAGETWYDITGNRSDTVKIGSDGSGEFHYNDGSVSIY 513

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QY 122 NRNETSEEVOKAWTDFRFRGRNTYSDPKMHWHEFDGADMDSRKISRIKFRGEGKA 181
DB 124 DRTREISEPFEIEGWTFTFEGRGDQYSSFRKNSSEHNGDIDFDRREERTVLAGENKK 183
QY 182 WDWESSENGNYDYLMYADVDYDHPDYVAETKMGWYANELSLDGRIDAAKHIFESFL 241
DB 184 WNEVNDPEFGNYDLMFANIDYDHPDYREMIWDMGKMLIDTLQCGFRLDAIKHINEFI 243
QY 242 RDWYQARQATGKEMFTYAEYQNNAGLENYLAKTSEFNSVFPVPHFNLQAASSQGG 301
DB 244 KEFAEMIRKRGQGFYIYIGEFWNSLDA CREFLDTVDYQIDLPVSLHYKHEHSLGRD 303
QY 302 YDMERLLDGTVSRHPEKAVTFVENHDTQPGQSLSTVQTFKFLAYAFILITRESGYQV 361
DB 304 FDLKSIFFDITVQHTPHAVTFVNDHDSQPHALESWIGDMFKPSAVALTLLRSDYFPV 363
QY 362 FYGDMYGTGTSPEKIEPSLKNIEPILKARKEYAGPOHDIYDHPDIYIGWTREDSGA 421
DB 364 FYGDIYGGIG--PEPYDCKEILDLILSLARCNKAYGEQEDYFDHANTIGWRRGVEIEG 421
QY 422 SGLAALITDGPQGSKRWYAGLKNAGETWYDITGNRSPTVKIGSDGMBEFHVDGVSIX 480
DB 422 SGCAVINSNGDDEKEMTIGHRAGEVWVDLTKSCDDQITTEEDGMATFHVCGGVSIVW 480
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RESULT 9

```
alpha-amy1ase (imported) - Streptococcus pneumoniae (strain TIGR4)
C/Species: Streptococcus pneumoniae
C/Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 24-Aug-2001
C/Accession: G95160
R/RefSeq: H. J. Nelson, K. E. Paulsen, I. T. Eisen, J. A. Read, T. D. Peterson, S. J. Heide-
on, J. D. Unal, L. A. White, O. J. Salzbach, S. L. Lewis, M. R. Radune, D. J. Holtapple,
son, T. J. Hickey, E. K. Holt, I. E.
Science 293, 498-506, 2001
A/Authors: Loftus, B. J.; Yang, F.; Smith, H. O.; Venter, J. C.; Dougherty, B. A.; Morrison,
A.; Reference number: A95000; MUID: 21357209; PMID: 11463916
A/Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A/Accession: G95160
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-484 <KUR>
A/Cross-references: GB:AE005672; PIDN:AAK75480.1; PID:G14972868; GSPDB:GN00164; TIGR:SP4
A/Experimental source: strain TIGR4
C/Genetics:
A/Gene: SP1382
C/Superfamily: alpha-amy1ase, amy1oliquefaciens type; alpha-amy1ase core homology
```

Query Match 46.4%; Score 1217; DB 2; Length 484;

Best Local Similarity 47.0%; Pred. No. 1e-76;

Matches 226; Conservative 81; Mismatches 168; Indels 6; Gaps 3;

```
QY 2 NGLTMQYFMYTPNDGQWKRLLQNDAEHLSDIGITAWIIPRAYKLSQSDNGGYDYLD 61
DB 3 NGLTMQYFMYTPNDGQWKRLLQNDAEHLSDIGITAWIIPRAYKLSQSDNGGYDYLD 62
QY 62 LGFPOQKGVTRTKYGTGKSLQDAISLSRNVQYGVVNLNKAADATDEVTAVEVNA 121
DB 63 LGFPOQKGVTRTKYGTGKSLQDAISLSRNVQYGVVNLNKAADATDEVTAVEVNA 122
QY 122 NRNETSEEVOKAWTDFRFRGRNTYSDPKMHWHEFDGADMDSRKISRIKFRGEGKA 181
DB 124 DRTREISEPFEIEGWTFTFEGRGDQYSSFRKNSSEHNGDIDFDRREERTVLAGENKK 183
QY 182 WDWESSENGNYDYLMYADVDYDHPDYVAETKMGWYANELSLDGRIDAAKHIFESFL 241
DB 184 WNEVNDPEFGNYDLMFANIDYDHPDYREMIWDMGKMLIDTLQCGFRLDAIKHINEFI 243
QY 242 RDWYQARQATGKEMFTYAEYQNNAGLENYLAKTSEFNSVFPVPHFNLQAASSQGG 301
DB 244 KEFAEMIRKRGQGFYIYIGEFWNSLDA CREFLDTVDYQIDLPVSLHYKHEHSLGRD 303
QY 302 YDMERLLDGTVSRHPEKAVTFVENHDTQPGQSLSTVQTFKFLAYAFILITRESGYQV 361
DB 304 FDLKSIFFDITVQHTPHAVTFVNDHDSQPHALESWIGDMFKPSAVALTLLRSDYFPV 363
QY 362 FYGDMYGTGTSPEKIEPSLKNIEPILKARKEYAGPOHDIYDHPDIYIGWTREDSGA 421
DB 364 FYGDIYGGIG--PEPYDCKEILDLILSLARCNKAYGEQEDYFDHANTIGWRRGVEIEG 421
QY 422 SGLAALITDGPQGSKRWYAGLKNAGETWYDITGNRSPTVKIGSDGMBEFHVDGVSIX 480
DB 422 SGCAVINSNGDDEKEMTIGHRAGEVWVDLTKSCDDQITTEEDGMATFHVCGGVSIVW 480
```

```
DB 303 ANYDLRGIFTDLSVLEKPKDAVTFVNDHDTQPGQSLSTVEEMFKPAAYALLILRQDGLP 362
QY 360 QVYFGDMYGTGTSPEKIEPSLKNIEPILKARKEYAGPOHDIYDHPDIYIGWTREDSGA 419
DB 363 CVFYGDYGGISQYAOE--DFKEILDLRLAIRKDLAIGQNDYFDHANCIGWRSAGEN- 419
QY 420 AKSGLAALITDGPQGSKRWYAGLKNAGETWYDITGNRSPTVKIGSDGMBEFHVDGVSIX 479
DB 420 QSPIAVINSNGQENSKMFPVGOEWNTQTFVLLGNHQQGYTIDEGYGFVARSVSV 478
QY 480 Y 480
DB 479 W 479
```

RESULT 10

```
alpha-amy1ase (EC 3.2.1.1) precursor (imported) - Streptococcus pneumoniae (strain R6)
C/Species: Streptococcus pneumoniae
C/Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 02-Nov-2001
C/Accession: F98026
R/RefSeq: J. K. Alborn Jr., W. J. Arnold, J. J. Blaszcak, L. J. Burgett, S. J. DeHoff, B. S. J. Mc-
e, R. J. Leblanc, D. J. Lee, L. N. J. Letkowitz, E. J. Lu, J. J. Matsushima, P. J. McAhren, S. J. Mc-
e, R. J. Sun, P. M. Winkler, M. E.
J. Bacteriol. 183, 5709-5717, 2001
A/Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R. H.; Jaskunas, S. R.;
A/Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A/Reference number: A97872; MUID: 21429245; PMID: 11544234
A/Accession: F98026
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-484 <KUR>
A/Cross-references: GB:AE007317; PIDN:AAU0043.1; PID:G15458876; GSPDB:GN00174
C/Genetics:
A/Gene: amy
C/Superfamily: alpha-amy1ase, amy1oliquefaciens type; alpha-amy1ase core homology
C/Keywords: glycosidase; hydrolase
```

Query Match 46.2%; Score 1212; DB 2; Length 484;

Best Local Similarity 46.6%; Pred. No. 2.4e-78;

Matches 224; Conservative 84; Mismatches 167; Indels 6; Gaps 3;

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QY 2 NGLTMQYFMYTPNDGQWKRLLQNDAEHLSDIGITAWIIPRAYKLSQSDNGGYDYLD 61
DB 3 NGLTMQYFMYTPNDGQWKRLLQNDAEHLSDIGITAWIIPRAYKLSQSDNGGYDYLD 62
QY 62 LGFPOQKGVTRTKYGTGKSLQDAISLSRNVQYGVVNLNKAADATDEVTAVEVNA 121
DB 63 LGFPOQKGVTRTKYGTGKSLQDAISLSRNVQYGVVNLNKAADATDEVTAVEVNA 122
QY 122 NRNETSEEVOKAWTDFRFRGRNTYSDPKMHWHEFDGADMDSRKISRIKFRGEGKA 181
DB 124 DRTREISEPFEIEGWTFTFEGRGDQYSSFRKNSSEHNGDIDFDRREERTVLAGENKK 183
QY 182 WDWESSENGNYDYLMYADVDYDHPDYVAETKMGWYANELSLDGRIDAAKHIFESFL 241
DB 184 WNEVNDPEFGNYDLMFANIDYDHPDYREMIWDMGKMLIDTLQCGFRLDAIKHINEFI 243
QY 242 RDWYQARQATGKEMFTYAEYQNNAGLENYLAKTSEFNSVFPVPHFNLQAASSQGG 301
DB 244 KEFAEMIRKRGQGFYIYIGEFWNSLDA CREFLDTVDYQIDLPVSLHYKHEHSLGRD 303
QY 302 YDMERLLDGTVSRHPEKAVTFVENHDTQPGQSLSTVQTFKFLAYAFILITRESGYQV 361
DB 304 FDLKSIFFDITVQHTPHAVTFVNDHDSQPHALESWIGDMFKPSAVALTLLRSDYFPV 363
QY 362 FYGDMYGTGTSPEKIEPSLKNIEPILKARKEYAGPOHDIYDHPDIYIGWTREDSGA 421
DB 364 FYGDIYGGIG--PEPYDCKEILDLILSLARCNKAYGEQEDYFDHANTIGWRRGVEIEG 421
QY 422 SGLAALITDGPQGSKRWYAGLKNAGETWYDITGNRSPTVKIGSDGMBEFHVDGVSIX 480
DB 422 SGCAVINSNGDDEKEMTIGHRAGEVWVDLTKSCDDQITTEEDGMATFHVCGGVSIVW 480
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Db 420 -OSPIALISNDQENSKMNFVQEWNTQTFVDLLGSHQGVITIDEGYQGFVSARSYSV 478
QY 480 Y 480
Db 479 W 479

RESULT 11

AH2079
Alpha-amylase [imported] - Nostoc sp. (strain PCC 7120)
C/Species: Nostoc sp. PCC 7120
A/Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C/Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C/Accession: AH2079
R/Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kurlitz, T.; Sasamoto, S.; Watanabe, A.; Iriyuchi, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A/Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena
A/Reference number: AB1807; MUID:2155285; PMID:1175840
A/Accession: AH2079
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-492 <KUR>
A/Cross-references: GB:BA000019; PIDN:BAW7389.1; PID:gl7131281; GSPDB:GN00179
A/Experimental source: strain PCC 7120
C/Genetics:
A/Gene: alr2190
C/Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology

Query Match 45.6%; Score 1197; DB 2; Length 492;
Best Local Similarity 47.3%; Pred. No. 2.8e-77;
Matches 233; Conservative 74; Mismatches 163; Indels 24; Gaps 7;

QY 1 VNGTLQYFEMWYPPNDGQHWKRLQNDAEHLSDIGITAWIIPYKGLSOS-DNGYPPYL 59
Db 4 MNGTMMQYFEMWYPPNDGQHWKRLQNDAEHLSDIGITAWIIPYKGLSOS-DNGYPPYL 63
QY 60 YDGEPOKGTFRKYGKTSKSELQDAIGLSHRVQYGVVNLHKKAGADATDVTA--- 116
Db 64 FDLGEFQKGSVTKYKTRQYLDYVKSQTHGLQYADAVLNHKKAGADATDVTA--- 123
QY 117 ---EVNPNANQETSEBYQIKAWTDFRPPGRGNTYSDFKMWHYFDGADWDSRKISRIE 173
Db 124 QDRLNPKGLQD-----IKTYHYNFPGRQGYKSNFEMHMHFPAVDVNEYSNGDRST 177
QY 174 KFRGEGKAMWSEYSENGNVDYLMYADVDYDHPVVAETKKGIWYANELSLDGFRIIDA 233
Db 178 VYLLGKMFDDYVLEKGNFVYLMGCDLPQNEKWRGEVTVYWGKCLDTTKVDGFRIDAI 237
QY 234 KHIFSLRDMVQAVRQATGKEMFTVAEYQNNAGKLENTLNTSFQSVFDPVPLHFNQ 293
Db 238 KHISTWFFPEWIDALSHAGKDLFMVGEWYNDINTLLWYDAVRGMSYFDPVPLHFNH 297
QY 294 AASSQGGGYDMRRLDGTYSRHEKAVTVENHDPQGSLSSTVQTMFKPLAYAFIL 353
Db 298 QASKSGNVDYMRRLDGTYSRHEKAVTVENHDPQGSLSSTVQTMFKPLAYAFIL 357
QY 354 RESGYPOVYGDWYGT---GTSPEK---IPSLKNIEPIIKAKKAYAVGPHDYID 405
Db 358 RQEGYPCVFNADYGALEYDWMGKGNRYNIFMPSHRMIDKLAYARKGYAVGQYVYLDH 417
QY 406 PDVYGMTRREGDSSAAKGLALITDGPQSKMAYAGKAGETWYDITGRSDTVKIGSD 465
Db 418 WNTIGWRLGDADHPQ-GMAVYMSDGSBGIKMVEKENT--KFDLTHIKKAVYTNEM 474
QY 466 GMGEFHYNDGSVSIV 480
Db 475 GMGFRICGSGSVSW 489

RESULT 12
C66781
alpha-amylase [imported] - Lactococcus lactis subsp. lactis (strain IL1403)

C/Species: Lactococcus lactis subsp. lactis
C/Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
C/Accession: C66781
R/Bolotin, A.; Mincker, P.; Manger, S.; Jallou, O.; Malarme, K.; Weissenbach, J.; Ehrlich, G.
Genome Res. 11, 731-753, 2001
A/Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ss
A/Reference number: A86625; MUID:21235186; PMID:11337471
A/Accession: C66781
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-491 <STO>
A/Cross-references: GB:AE005176; PID:gl2724224; PIDN:AAK05349.1; GSPDB:GN00146
A/Experimental source: strain IL1403
C/Genetics:
A/Gene: amyL
C/Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology

Query Match 42.9%; Score 1127; DB 2; Length 491;
Best Local Similarity 43.1%; Pred. No. 2.6e-72;
Matches 208; Conservative 85; Mismatches 174; Indels 16; Gaps 4;

QY 4 TIMQYFEMWYPPNDGQHWKRLQNDAEHLSDIGITAWIIPYKGLS-OSDNGYPPYLD 62
Db 3 TILQAFEMWYPPNDGQHWKRLQNDAEHLSDIGITAWIIPYKGLS-OSDNGYPPYLD 62
QY 63 GEFOKGTFRKYGKTSKSELQDAIGLSHRVQYGVVNLHKKAGADATDVTA--- 122
Db 63 GEFOKGTFRKYGKTSKSELQDAIGLSHRVQYGVVNLHKKAGADATDVTA--- 122
QY 123 RQETSEBYQIKAWTDFRPPGRGNTYSDFKMWHYFDGADWDSRKISRIEFGREGKAW 182
Db 123 HAHNENKQVAVWTKFPPGRQGYKSNFEMHMHFPAVDVNEYSNGDRST 180
QY 183 DWEYSENGNVDYLMYADVDYDHPVVAETKKGIWYANELSLDGFRIIDAKIKFSLR 242
Db 181 DENVDSENNNDYLMGADLPDSVSEVLEKQKWHMSSEMTKIDGFFLDALIKIDFCTFD 240
QY 243 DWQAVRQATGKEMFTVAEYQNNAGKLENTLNTSFQSVFDPVPLHFNQ 302
Db 241 KMLEGRARQKRLPIVEYVSDLGKLELYLEQSSRIOLFVPLHFNHKEASSTNGEF 300
QY 303 DMRRLDGTYSRHEKAVTVENHDPQGSLSSTVQTMFKPLAYAFILTRBSGYQVF 362
Db 301 DMRFLDHTLTAQSELSVTFVDHNDPQGSLSSTVQTMFKPLAYAFILTRBSGYQVF 360
QY 363 YGDWYGTGTSPEKIPS-----LKNIEPIIKAKKAYAVGPHDYIDHPVYIGWTRSGDS 417
Db 361 WDDLYG-----IPSHNVPVGDNLRTMLARKDSFLENDYFDPHDIIGWNTILKI 412
QY 418 SAAKGLALITDGPQSKMAYAGKAGETWYDITGRSDTVKIGSDGMEFHYNDGSV 477
Db 413 DKREYGLSCILITNKKGSKYVIDXAVAKYIDLFGHREPIITLDQNGAEFYNDGSV 472
QY 478 STY 480
Db 473 SWW 475

RESULT 13

AD3038
alpha-amylase amyA [imported] - Agrobacterium tumefaciens (strain C58, Dugont)
C/Species: Agrobacterium tumefaciens
C/Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
R/Wood, D.W.; Setudal, U.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A/Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Ferry, M.; Gordon-Kamm, J.E.
A/Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A/Reference number: AB2577; MUID:21608550; PMID:11743193
A/Accession: AD3038

A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-495 <KUR>
 A:Cross-references: GB:AE008689; PIDN:AA44722.1; PID:G17742354; GSPDB:GN00187
 A:Experimental source: strain C58 (Dupont)
 C:Genetics:
 A:Gene: amyA
 A:Map position: linear chromosome
 C:Superfamily: alpha-amyLase, amyLoliquefaciens type; alpha-amyLase core homology

Query Match 40.0%; Score 1050; DB 2; Length 495;

Best Local Similarity 43.6%; Pred. No. 7,66-67;
 Matches 213; Conservative 77; Mismatches 183; Indels 16; Gaps 6;

```

QY 4 TLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVMTTPAYKGLSOSDN-GYGPYDLYDL 62
DB 5 TLQGFHMYYPDGGKLMSEVAEKASLAKMGITVWMLPPAYKGAAGSVGYDYYDLYDL 64
QY 63 GEPQCKGTATKTKYKSELQDAIGSLHSRNQYGVVYLNKAGADATEDVTAVENPAN 122
DB 65 GEPDCKGTATKTKYGRALBHAAGTKLKNGRVYIHDVYLNKMGADDEKRYRVRVPPD 124
QY 123 KNOETSEBYQIKAWTDFEFPGRGNTYSDFKMWHYFDGADWDESKISRTFKF---RGE 179
DB 125 RTDIDEDFPALAYTRFTFPGRNKGSKFIDWLCFSGVDHIEEPTEDGIFRLVNEYGDG 184
QY 180 KAMDWESENGNRYLYMAYADVDPVVAETKMGWYANELSLDGFRIIDAKHIFKS 239
DB 185 E-WNEEVDQENGFYLMGADVEFRNRAVYELKMGKMLSEQYQVDFRLDAKHIPAW 243
QY 240 FLRDWQAVRQATGKEMFTVAEYMONNAGKLENTLNTKTSFQSVFVPLPHNLQAASSQG 299
DB 244 FFRDWGHRBETVPDPLFVAEYWHFPLEALKSYLELVKQMLFDVALHHSFHDASKOG 303
QY 300 GGYDMRRLDGTVGRHBEKAVTFVENHDTPQGSLSTVQTWPKPLAYAFILTRSGYP 359
DB 304 GDFMRSIFDGLSVSAVVDHATLVNDHDTLPQSLSEAPVFPWPKPLAYAILILRESGVP 363
QY 360 QVFYDMYGTGKTSRK-----EIPSLKDNIEPILAKREYVAGPOHYDIDHPDVI 411
DB 364 CVFYFDLPSTSTYDTPGNDGNEKXIDIPAI-ECLPLIARSRFANGPQTDIFDDASCI 422
QY 412 TREBSSAAKSGIALITDGPCKSRMYAGLKNAGETTYDITGNRSOTVKIGSGMGEFH 471
DB 423 IRHGTA--PGCVVMSNGEPGEKQADLGERASVWRDLGHRHEHITLDESCKGTFP 480
QY 472 VNDGSYSY 480
DB 481 TNGGSYSVM 489

```

RESULT 14

G98247
 Cytoplasmic alpha-amyLase (1,4-alpha-D-glucan glucanohydrolase) [imported] - Agrobacteri
 C:Species: Agrobacterium tumefaciens
 C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 18-Nov-2002
 C:Accession: G98247
 A:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
 A.; Liu, F.; Woliam, C.; Allinger, M.; Doughty, D.; Scott, C.; Jappas, C.; Markelz, B.;
 Science 294, 2333-2338, 2001
 A>Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
 A:Reference number: A97359; MUID:21608551; PMID:11743194
 A:Accession: G98247
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-506 <KUR>
 A:Cross-references: GB:AE007870; PIDN:AAK89505.1; PID:G15159379; GSPDB:GN00170
 C:Genetics:
 A:Gene: AGR_L1863
 A:Map position: linear chromosome
 C:Superfamily: alpha-amyLase, amyLoliquefaciens type; alpha-amyLase core homology

Query Match 40.0%; Score 1050; DB 2; Length 506;

Best Local Similarity 43.6%; Pred. No. 7,96-67;
 Matches 213; Conservative 77; Mismatches 183; Indels 16; Gaps 6;

```

QY 4 TLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVMTTPAYKGLSOSDN-GYGPYDLYDL 62
DB 16 TLQGFHMYYPDGGKLMSEVAEKASLAKMGITVWMLPPAYKGAAGSVGYDYYDLYDL 75
QY 63 GEPQCKGTATKTKYKSELQDAIGSLHSRNQYGVVYLNKAGADATEDVTAVENPAN 122
DB 76 GEPDCKGTATKTKYGRALBHAAGTKLKNGRVYIHDVYLNKMGADDEKRYRVRVPPD 135
QY 123 KNOETSEBYQIKAWTDFEFPGRGNTYSDFKMWHYFDGADWDESKISRTFKF---RGE 179
DB 136 RTDIDEDFPALAYTRFTFPGRNKGSKFIDWLCFSGVDHIEEPTEDGIFRLVNEYGDG 195
QY 180 KAMDWESENGNRYLYMAYADVDPVVAETKMGWYANELSLDGFRIIDAKHIFKS 239
DB 196 E-WNEEVDQENGFYLMGADVEFRNRAVYELKMGKMLSEQYQVDFRLDAKHIPAW 254
QY 240 FLRDWQAVRQATGKEMFTVAEYMONNAGKLENTLNTKTSFQSVFVPLPHNLQAASSQG 299
DB 255 FFRDWGHRBETVPDPLFVAEYWHFPLEALKSYLELVKQMLFDVALHHSFHDASKOG 314
QY 300 GGYDMRRLDGTVGRHBEKAVTFVENHDTPQGSLSTVQTWPKPLAYAFILTRSGYP 359
DB 315 GDFMRSIFDGLSVSAVVDHATLVNDHDTLPQSLSEAPVFPWPKPLAYAILILRESGVP 374
QY 360 QVFYDMYGTGKTSRK-----EIPSLKDNIEPILAKREYVAGPOHYDIDHPDVI 411
DB 375 CVFYFDLPSTSTYDTPGNDGNEKXIDIPAI-ECLPLIARSRFANGPQTDIFDDASCI 433
QY 412 TREBSSAAKSGIALITDGPCKSRMYAGLKNAGETTYDITGNRSOTVKIGSGMGEFH 471
DB 434 IRHGTA--PGCVVMSNGEPGEKQADLGERASVWRDLGHRHEHITLDESCKGTFP 491
QY 472 VNDGSYSY 480
DB 492 TNGGSYSVM 500

```

RESULT 15

B45738
 alpha-amyLase (EC 3.2.1.1), cytosolic - Salmonella typhimurium
 N:Alternate names: 1,4-alpha-D-glucan glucanohydrolase
 C:Species: Salmonella typhimurium
 C>Date: 07-Apr-1994 #sequence_revision 18-Aug-1995 #text_change 18-Jun-1999
 C:Accession: B45738
 R:Raha, M.; Kawagishi, I.; Mueller, V.; Khara, M.; Macnab, R.M.
 J. Bacteriol. 174, 6644-6652, 1992
 A>Title: Escherichia coli produces a cytoplasmic alpha-amyLase, amyA.
 A:Reference number: A45738; MUID:93015717; PMID:1400215
 A:Accession: B45738
 A:Molecule type: DNA
 A:Residues: 1-494 <DAH>
 A:Cross-references: GB:L01643; NID:G154043; PIDN:AAA27110.1; PID:G154045
 C:Genetics:
 A:Gene: amyA
 A:Function:
 A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
 A:Pathway: glycogen/starch degradation
 C:Superfamily: alpha-amyLase, amyLoliquefaciens type; alpha-amyLase core homology
 C:Keywords: cytosol; glycosidase; hydrolase; polysaccharide degradation
 F:202-335/Domain: alpha-amyLase core homology <AMY>
 F:239,265,332/Active site: His, Glu, Asp #status predicted

Query Match 38.7%; Score 1015; DB 1; Length 494;
 Best Local Similarity 41.2%; Pred. No. 2,36-64;
 Matches 202; Conservative 77; Mismatches 197; Indels 14; Gaps 5;

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QY 2 NGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVMTTPAYKGLSOSDN-GYGPYDLY 60
DB 3 NPTLMQYFEWYTPDGGKLMSELAERADGLINDIGINWMLPPAYKGAAGSVGYDYYDLYDL 62

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Tue May 4 14:34:47 2004

us-10-644-187-4.rpr

QY 61 DLGEFOOKGIVRTYKYSKSELODAIGSLHSHNNVOYGVVJLNHKGADATEDVTAVEVNP 120
63 DLGEFDQKGTATATKYGKQQLTALDALKKNIAVLLDVVYNNHMGADBEKERIRVQRVNQ 122
QY 121 ANRQETSEEYQIATMDFRFPGRGNTYSDFKMTWYHFDGADNDESKRISIRFKRGE-- 178
Db 123 DDKTQIDNNIECGWTRTYTPPARAGQVSNFIMDYHCFSGIDHLENPDEGIFKIVNDYT 182
QY 179 GKAWDWEYSENGVNDYLMYADVDDYDHPDVVAETKKGIMYANELSLDGFRIIDAKHIF 238
Db 183 GDGNNDQVDDMGNDYLMGENIDFRNNAVTEELKWAARWMEQTHCDGFRLLDAVKHIPA 242
QY 239 SFLRDWQAVQATGKEMFTVAETWQNNAGKLENTYLNKTSFNQSVFDPVPLHFNLOASSQ 298
Db 243 WFKYKWIETHVQAVAPKPLFIVAETWWSHEDKLTQYIDQVDGKTMLFDAPLOMKPHEASRQ 302
QY 299 GGGYDMRRLDGTIVVSRHPEKAVTFVENHDTQPGOSLES TVQTWFKPLAVAFILTRRESGY 358
Db 303 GAETDMRHIFTGTLVEADPPHATVILVANHDTOPLOALEAPYEPWFKPLAYALLILRENGV 362
QY 359 PQVYGDWYGTK-----GTSPEKIPSLKONIEPIIKARKEYAYGPQHDYIDHPVIG 410
Db 363 PSVFYDLYGASYEDSGENGETCRVDMWEVI-NQLDRLLIARQRFAGHGIQTLFFDHFNCA 421
QY 411 WTRBGDSAAKSGLAALITDGPBGSKRMVAGLKNAGETWYDITGNRSOTVYKISDGMGEF 470
Db 422 FSRSG--TEENPGCVVVLNSGDDGKTLILLGDNITANKTWDPFGNRDEYVVTNDQGEATF 479
QY 471 HUNDGSVSIY 480
Db 480 FCNAGSVSVW 489

Search completed: May 3, 2004, 20:54:06
Job time : 15.6493 secs

Tue May 4 14:34:47 2004

us-10-644-187-4.rsp

Page 1

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OM protein - protein search, using sw model

Run on: May 3, 2004, 20:36:03 ; Search time 10.3995 Seconds

(without alignments)
2403.363 Million cell updates/sec

Title: US-10-644-187-4

Perfect score: 2624

Sequence: 1 VNGTLMQYFEMWTFPNDQHM.....KISDQWGFHVNDGSVSIY 480

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2624	100.0	514	1	AMY_BACAM
2	2176	82.9	512	1	AMY_BACLI
3	1826	69.6	518	1	AMY6_BACST
4	1758.5	67.0	549	1	AMY_BACST
5	1013	38.6	494	1	AMY2_SALTY
6	998	38.0	495	1	AMY2_ECOLI
7	346	13.2	440	1	AMY3_ORYSA
8	333.5	12.7	421	1	AMYA_VIGMU
9	324	12.3	437	1	AMY3_ORYSA
10	323	12.3	1196	1	AMYB_PABPO
11	319	12.2	438	1	AMYB_ORYSA
12	318	12.1	435	1	AMY3_ORYSA
13	315.5	12.0	437	1	AMY3_ORYSA
14	315	12.0	413	1	AMY3_WHEAT
15	307.5	11.7	438	1	AMY1_HORVU
16	289	11.0	429	1	AMY6_HORVU
17	285.5	10.9	713	1	CDGT_BACSS
18	284.5	10.8	443	1	AMY2_ORYSA
19	284.5	10.8	445	1	AMC2_ORYSA
20	283	10.8	427	1	AMY2_HORVU
21	282	10.7	368	1	AMY3_HORVU
22	277.5	10.6	713	1	CDGT_BACCI
23	272	10.4	713	1	CDGT_BACSP
24	270	10.3	428	1	AMY1_ORYSA
25	267.5	10.2	919	1	AMY_STRLI
26	255	9.7	712	1	CDGT_BACCI
27	253	9.6	718	1	CDGT_BACCI
28	253	9.6	718	1	CDGT_BACSS
29	251	9.6	713	1	CDGT_BACSO
30	246	9.4	581	1	AMY1_SCHPO
31	245	9.3	719	1	AMYM_BACST
32	244.5	9.3	478	1	YQ29_SCHPO
33	244.5	9.3	528	1	AMY_BACCI

34	242.5	9.2	718	1	CDGT_BACLI	P14014 bacillus li
35	241	9.2	564	1	AMY4_SCHPO	Q97789 schizosacch
36	240.5	9.2	710	1	CDGT_THETU	P26827 thermoaer
37	240	9.1	494	1	AMY1_SACFI	P21567 saccharomyc
38	234.5	8.9	711	1	CDGT_BACST	P31797 bacillus st
39	232	8.8	498	1	AMY3_DICIT	P14885 dictyoglomu
40	229	8.7	441	1	MGTA_THEMA	P80099 thermotoga
41	228.5	8.7	499	1	AMYA_ASFOR	P10529 aspergillus
42	228	8.7	676	1	AMY1_ECOLI	P25718 escherichia
43	225.5	8.6	442	1	MGTA_THENE	O86956 thermotoga
44	225.5	8.6	499	1	AMY_ASPEH	P30292 aspergillus
45	222.5	8.5	498	1	AMYA_ASFAM	Q02905 aspergillus

ALIGNMENTS

RESULT 1
AMY_BACAM STANDARD; PRT; 514 AA.
ID AMY_BACAM
AC P00692;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Alpha-amylase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
DE glucanohydrolase).
OS Bacillus amyloliquefaciens.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxId=1390;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IH.
RX MEDLINE=8310808; PubMed=6185474.
RA Takkinen K., Petersson R.F., Kalkkinen N., Palva I., Seoderlund H.,
RA Kaeserlaeinen L.;
RT "Amino acid sequence of alpha-amylase from Bacillus amyloliquefaciens
RT deduced from the nucleotide sequence of the cloned gene.";
RL J. Biol. Chem. 258:1007-1013(1983).
RN [2]
RP SEQUENCE OF 32-222.
RX MEDLINE=80241725; PubMed=6156671;
RA Chung H.S., Friedberg F.;
RT "Sequence of the N-terminal half of Bacillus amyloliquefaciens alpha-
RT amylase.";
RL Biochem. J. 185:387-395(1980).
RN [3]
RP SEQUENCE OF 1-96 FROM N.A.
RX MEDLINE=82051296; PubMed=6170539;
RA Palva I., Petersson R.F., Kalkkinen N., Lehtoavaara P., Sarvas M.,
RA Soederlund H., Takkinen K., Kaeserlaeinen L.;
RT "Nucleotide sequence of the promoter and N2-terminal signal peptide
RT region of the alpha-amylase gene from Bacillus amyloliquefaciens.";
RL Gene 15:43-51(1981).
RN [4]
RP SEQUENCE OF 1-39 FROM N.A.
RX MEDLINE=88137952; PubMed=2830166;
RA Ruohonen L., Hackman P., Lehtoavaara P., Knowles J.K.C., Karanen S.;
RT "Efficient secretion of Bacillus amyloliquefaciens alpha-amylase by
RT its own signal peptide from Saccharomyces cerevisiae host cells.";
RL Gene 59:161-170(1987).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 32-331.
RX MEDLINE=20384196; PubMed=10924103;
RA Brzezowski A.M., Lawson D.M., Turkenburg J.P., Biegaard-Frantzen H.,
RA Svendsen A., Borchert T.V., Dauter Z., Wilson K.S., Davies G.J.;
RT "Structural analysis of a chimeric bacterial alpha-amylase.
RT High-resolution analysis of native and ligand complexes.";
RL Biochemistry 39:9099-9107(2000)
CC -I- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -I- COFACTOR: Binds 3 calcium ions and 1 sodium ion per subunit.
CC -I- SUBUNIT: Monomer.
CC -I- SUBCELLULAR LOCATION: Secreted.

RP MAPING OF SUBSTRATE-BINDING SITE.
[7]
RP MEDLINE=1992788; PubMed=11997021;
RA Kendra L., Geyman G., Remyer J., Hovanszki G., Liprak A.;
RT "Action pattern and substrate mapping of Bacillus licheniformis
alpha-amylase (BLA) with modified maltotriosecarbohydrate substrates.";
RL FEBS Lett. 518:79-82(2002).
RN [8]
RP MUTAGENESIS OF HIS-64, HIS-162, HIS-276; HIS-322; HIS-435 AND HIS-479
RC STRAIN=ATCC 6598;
RX MEDLINE=90368748; PubMed=2394736;
RA Declerck N., Joyet P., Gallardin C., Maeson J.M.;
RT "Use of amber suppressors to investigate the thermostability of
Bacillus licheniformis alpha-amylase. Amino acid replacements at 6
RT histidine residues reveal a critical position at His-133.";
RL J. Biol. Chem. 265:15481-15488(1990).
RN [9]
RP MUTAGENESIS OF ALA-238.
RC STRAIN=ATCC 6598;
RX MEDLINE=96367070; PubMed=8721184;
RA Declerck N., Joyet P., Troiset J.Y., Garnier J., Gallardin C.;
RT "Hyperthermostable mutants of Bacillus licheniformis alpha-amylase:
RT multiple amino acid replacements and molecular modelling.";
RL Protein Eng. 8:1029-1037(1995).
RN [10]
RP MUTAGENESIS OF ASP-150; ASN-155; ARG-175; ASP-193; ASN-201; GLN-207;
RP ASN-217; ASN-219; ASN-221, ASP-229; ASP-233; ALA-288; GLU-300; GLN-355
RP AND GLU-365.
RN [11]
RC STRAIN=ATCC 6598;
RX MEDLINE=20425100; PubMed=10968804;
RA Declerck N., Machius M., Wiegand G., Huber R., Gallardin C.;
RT "Probing structural determinants specifying high thermostability in
RT Bacillus licheniformis alpha-amylase.";
RL J. Mol. Biol. 301:1041-1057(2000).
RN [12]
RP MUTAGENESIS OF GLN-293 AND ASN-294.
RC STRAIN=ATCC 6598;
RX MEDLINE=22622182; PubMed=12736372;
RA Declerck N., Machius M., Joyet P., Wiegand G., Huber R.,
RA Gallardin C.;
RT "Hyperthermostabilization of Bacillus licheniformis alpha-amylase and
RT modulation of its stability over a 50 degrees C temperature range.";
RL Protein Eng. 16:287-293(2003).
RN [13]
RP MUTAGENESIS OF TRP-292 AND VAL-315.
RC STRAIN=ATCC 27811;
RX MEDLINE=22797417; PubMed=12915728;
RA Rivera M.H., Lopez-Munguia A., Soberton X., Saab-Rincon G.;
RT "Alpha-amylase from Bacillus licheniformis mutants near to the
RT catalytic site: effects on hydrolytic and transglycosylation
RT activity";
RL Protein Eng. 16:505-514(2003).
RN [14]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RC STRAIN=ATCC 27811;
RX MEDLINE=95182462; PubMed=7877175;
RA Machius M., Wiegand G., Huber R.;
RT "Crystal structure of calcium-depleted Bacillus licheniformis alpha-
RT amylase at 2.2-A resolution.";
RL J. Mol. Biol. 246:545-559(1995).
RN [15]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 330-512.
RX MEDLINE=20384196; PubMed=10294103;
RA Swadzowski A.M., Lawson D.M., Tuckenburg J.P., Bisgaard-Frantzen H.,
RA Svendsen A., Borchert T.V., Dauter Z., Wilson K.S., Davies G.J.;

Query Match	Best Local Similarity	Score 2176; DB 1; Length 512; Pred. No. 8.8e-147;
FT CHAIN	30	512
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FT ACT_SITE	264	264
FT ACT_SITE	357	357
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FT METAL	190	190
FT METAL	210	210
FT METAL	212	212
FT METAL	223	223
FT METAL	229	229
FT METAL	231	231
FT METAL	233	233
FT SIGNAL	1	29
FT CHAIN	30	512
FT ACT_SITE	260	260
FT ACT_SITE	264	264
FT ACT_SITE	357	357
FT METAL	133	133
FT METAL	190	190
FT METAL	210	210
FT METAL	212	212
FT METAL	223	223
FT METAL	229	229
FT METAL	231	231
FT METAL	233	233

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Matches 387; Conservative 42; Mismatches 49; Indels 2; Gaps 1
OY 1 VNGTLMGVFEVYTRNDQGHWRQLONDAEHLSDIGTAVWIPPAKGLSGSDNGCGPYDLY 60
Db 32 LNTGLTMQFEFMYMRNDGGHWRRLONDSVYLAHEGITLAWIPPAKGTSGQADVGAIDLY 91
OY 61 DLGEFOCKGTARTKXGTSGSELQDAIGSLHSRNVVYGPVLMNRYAGADATEDVAVENV 120
Db 92 DLGEFHQGTARTKXGTSGELQSAIKSLHSRINWYGDVVLNHHGADATEDVAVENV 151
OY 121 ANRNGTSEEEVQIKAMDPRFPGGNTYSDPKMTMYHEDGADMPESKRISIFERESEK 180
Db 152 ADRNRVVISGERIKRAMTFHFPPRGSTYSDPKMMWYHFDGIDWBSKRNRIYF--QCK 209
OY 181 AMDWEVSSENGNYDLYMADYVDYDPDVAETKMGKIWYANESLSDGRIDAAKHIFSF 240
Db 210 AMDWEVSSENGNYDLYMADYDIDYDPVAALIKEMGTYANELDLDGRILDVAGHIFSF 269
OY 241 LRDWVQAQRKATGKEMFTVAAYWOMNNAKLENTYNTKISFNQSVDPVLPHEFLQAASQGG 300
Db 270 LRDWVNHREKTEGEMFTVAAYWQDLCALENTYNTKINFSVDPVLPHYFHAASQGG 329
OY 301 GYDMRRLLDGTGVSSHPEKAVTFVENHDTQGGSLSTVQTWTFKPLVAFILITRESGYPQ 360
Db 330 GYDMRRKLINSTVSGHPLKAVTFVNDHTQGGSLSTVQTWTFKPLVAFILITRESGYPQ 389
OY 361 VFYGMVGTGKSPPEIRSLKDNTEPLIKARKEVAYGGQHYIHPDIDVIGTRGDSAA 420
Db 390 VFYGMVGTGKDSQELPALKKKEPLIKARKQIYAYGGQHYIPPHIDVIGTRGDSVA 449
OY 421 KSGIALALITDGPQGSKMYAGIKVAGETWYDITGNRSDTVKISGDGWEHFVNDGSVY 480
Db 450 NSGLAALITDGGGAKRMVYGRNGRGTWMDITGNRSEPVINSEGMGEHFVNGGSVY 509

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[illegible]

DT 01-FEB-1996 (Rel. 33, last sequence update)
DT 15-MAR-2004 (Rel. 43, last annotation update)
DE Alpha-amylase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
DE glucanoyldiolase).
GN AMYS.
OS Bacillus stearothermophilus.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.
OX NCBI_TaxID=1422;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 35-39.
RX MEDLINE=85234394; PubMed=3924897;
RA Nakajima R., Imanaka T., Alba S.;
RT "Nucleotide sequence of the Bacillus stearothermophilus alpha-amylase
RT gene.";
RL J. Bacteriol. 163:401-406 (1985).
RN [2]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX STRAIN=D15/PH1307;
MEDLINE=86008166; PubMed=3876333;
RA Ihara H., Sasaki T., Tsuboi A., Yamagata H., Tsukagoshi N., Udaoka S.;
RT "Complete nucleotide sequence of a thermophilic alpha-amylase gene:
RT homology between prokaryotic and eukaryotic alpha-amylases at the
RT active sites.";
RL J. Biochem. 98:195-103 (1985).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=NZ-3;
MEDLINE=86195857; PubMed=3009417;
RA Gray G.L., Mainzer S.E., Rey M.W., Lamsa M.H., Kindle K.L.,
RA Carmona C., Reguad C.;
RT "Structural genes encoding the thermophilic alpha-amylases of
RT Bacillus stearothermophilus and Bacillus licheniformis.";
RL J. Bacteriol. 166:635-643 (1986).
RN [4]
RP SEQUENCE FROM N.A.
RA Suominen I., Karp M., Lautamo J., Knowles J., Mantsaala P.;
RT "Thermotable alpha amylase of Bacillus stearothermophilus: cloning,
RT expression, and secretion by Escherichia coli.";
RL (In: Chaloupka J., Krumpal V. (eds.);
RL Extracellular enzymes of microorganisms, pp.129-137, Plenum Press,
RL New York (1987).
RN [5]
RP SEQUENCE OF 1-122 FROM N.A., AND SEQUENCE OF 35-48.
RX STRAIN=DY-5;
MEDLINE=86059211; PubMed=2999073;
RA Tsukagoshi N., Iritani S., Sasaki T., Takemura T., Ihara H.,
RA Idota Y., Yamagata H., Udaoka S.;
RT "Efficient synthesis and secretion of a thermophilic alpha-amylase by
RT protein-producing Bacillus brevis 47 carrying the Bacillus
RT stearothermophilus amylase gene.";
RL J. Bacteriol. 164:1182-1187 (1985).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=21125602; PubMed=11226887;
RA Suwa D., Fujimoto Z., Takase K., Matsumura M., Mizuno H.;
RT "Crystal structure of Bacillus stearothermophilus alpha-amylase:
RT possible factors determining the thermostability.";
RL J. Biochem. 129:461-468 (2001).
RN [7]
RP CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
RN linkages in oligosaccharides and polysaccharides.
CC -1- COPROCTOR: Binds 3 calcium ions and 1 sodium ion per subunit.
CC -1- SUBUNIT: Monomer.
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
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CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
DR FMRI M11450 AAA22235 2

DR EMBL; X02769; CAA26547.1; -;
DR EMBL; M57457; AAA22227.1; -;
DR EMBL; M13255; AAA22241.1; -;
DR PIR; A24436; A24436.
DR PIR; A91999; ALBSF.
DR PDB; 1HVX; 05-AUG-03.
DR InterPro; IPR006589; Alp_aml_cat_sub.
DR InterPro; IPR006047; Alpha_aml_cat.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Amy; 1.
KW Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
KW Signal; 3D-structure.
FT SIGNAL 1 34
FT CHAIN 35 549
FT ACT_SITE 268 268
FT ACT_SITE 272 272
FT ACT_SITE 365 365
FT METAL 139 139
FT METAL 196 196
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SQ SEQUENCE 549 AA; 62670 MM; 3A2DD93A955E79D3 CRC64;
Query Match 67.0%; Score 1758.5; DB 1; Length 549;
Best Local Similarity 65.4%; Pred. No. 3.6e-117;
Matches 314; Conservative 57; Mismatches 104; Indels 5; Gaps 2;
QY 2 NGTMOYFEPYTPPDQGMKRLNDDEHSDITVWIPPAKGSQSNDNGGPPDIYD 61
DB 39 NGTMOYFEPYTPPDQGMKRLNDDEHSDITVWIPPAKGSQSNDNGGPPDIYD 98
QY 62 LGSEFOQKGTATKTKYKSELDALIGSLASHNNVOYGVVTLNHRGADATEDVAVEVNP 121
DB 99 LGSEFOQKGTATKTKYKSELDALIGSLASHNNVOYGVVTLNHRGADATEDVAVEVNP 158
QY 122 NKNQETSEEEQIKAMPDFPRPGKNTYSDPKMTWYHPDADMDPSKISLIFFRGEGKA 181
DB 159 DRNQEISGTQIOAWKTFDPGKNTYSSFKMTWYHPDADMDPSKISLIFFRGEGKA 218
QY 182 WDMVESSENGNYVILMADVDYDHPVAVETKKGKIYANESLIDGFRIDPAAGIKFSFL 241
DB 219 WDMVEVDYFENQNYDILMADVDYDHPVAVETKKGKIYANESLIDGFRIDPAAGIKFSFL 278

AMY2_ECOLI STANDARD; PRT; 495 AA.
ID AMY2_ECOLI STANDARD; PRT; 495 AA.
AC P26612; P78072;
DT 01-NOV-1992 (Rel. 23, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cytoplasmic alpha-amylase (EC 3.2.1.1) (1,4-alpha-D-glucan
glycanhydrolase).
GN AMYA OR B1927.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=J11;
RX MEDLINE=93015717; PubMed=1400215;
RA Raha M., Kawagishi I., Mueller V., Kihara M., Macnab R.M.;
RT "Escherichia coli produces a cytoplasmic alpha-amylase, AmyA";
RL J. Bacteriol. 174:6644-6652(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12";
RL Science 277:1453-1474(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97251358; PubMed=9097040;
RA Itoh T., Alba H., Baba T., Fujita K., Hayashi K., Inada T.,
RA Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M.,
RA Makino K., Maki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T.,
RA Saito N., Sampei G., Seki Y., Sivasubraman S., Tagami H.,
RA Takeda J., Takekoshi K., Wada C., Yamamoto Y., Horikuchi T.;
RT "A 460-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 40.1-50.0 min region on the linkage map";
RL DNA Res. 3:379-392(1996).
RN [4]
RP SEQUENCE OF 1-5 FROM N.A.
RC STRAIN=J11;
RX MEDLINE=92407478; PubMed=1527488;
RA Kawagishi I., Mueller V., Williams A.W., Irikura V.M., Macnab R.M.;
RT "Subdivision of flagellar region III of the Escherichia coli and
RT Salmonella typhimurium chromosomes and identification of two
RT additional flagellar genes";
RL J. Gen. Microbiol. 138:1051-1065(1992).
RN [5]
RP SEQUENCE OF 475-495 FROM N.A.
RC STRAIN=J11;
RX MEDLINE=93381452; PubMed=8371104;
RA Raha M., Kihara M., Kawagishi I., Macnab R.M.;
RT "Organization of the Escherichia coli and Salmonella typhimurium
RT chromosomes between flagellar regions Iria and IriB, including a
RT large non-coding region";
RL J. Gen. Microbiol. 139:1401-1407(1993).
RN [6]
RP CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
RN linkages in oligosaccharides and polysaccharides.
CC -1- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
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CC use by non-profit institutions as long as its content is in no way
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CC -----
DR EMBL; L01642; AAA23810.1; -
DR EMBL; AE000285; AAC74994.1; -
DR EMBL; D50833; BAA15755.1; -
DR EMBL; M85240; -; NOT ANNOTATED CDS.
DR EMBL; L13279; AAA82575.1; -
DR PIR; D64956; A45738.
DR HSSP; P06278; IVS.
DR BioGene; EG11387; AMYA.
DR InterPro; IPR006589; Alp_amy1_cat_sub.
DR InterPro; IPR006047; Alpha_amy1_cat.
DR Pfam; PF00128; alpha-amylase; 1.
DR SMART; SM00642; AmyA; 1.
KW Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
KW Complete proteome.
FT ACT_SITE 235 235 BY SIMILARITY.
FT ACT_SITE 265 265 BY SIMILARITY.
FT ACT_SITE 332 332 BY SIMILARITY.
FT METAL 104 104 CALCIUM (BY SIMILARITY).
FT METAL 239 239 CALCIUM (VIA CARBOXYL OXYGEN) (BY
FT SIMILARITY).
FT CONFLICT 19 20 KL -> SS (IN REF. 1).
FT CONFLICT 109 109 A -> V (IN REF. 1).
FT CONFLICT 149 149 Q -> E (IN REF. 1).
FT CONFLICT 234 234 L -> I (IN REF. 1).
SQ SEQUENCE 495 AA; 56639 MW; 26AF6797DDA54D6 CRC64;
Query Match 38.0%; Score 998; DB 1; Length 495;
Best Local Similarity 40.7%; Pred. No. 2,3e-63;
Matches 200; Conservative 79; Mismatches 195; Indels 18; Gaps 6;
QY 2 NGTLMQFPMYTPNDGQHKRLQNDASHSDIGITAWTPPKYKLSQSDN-GYGPDYLY 60
DB 3 NPTLLCCFFMYPPPEGKMPLEAERADGNDIGINWVLPYKASGGYSGYSTDF 62
QY 61 DLGEPOQKTVTRKYTKSELQDAIGSLSRNVQYGVVNLNKGADATEDVAVENP 120
DB 63 DLGEPOQKSIPIKRYDRAQLAIDLAKNDIAVLDDVNVHKGADKEKIRQRYVA 122
QY 121 ANNQETSEBYQIKANTDFRPFQKNTYSDFKWHYHPDQADWDSKRSIFK----FR 176
DB 123 DERTQIDBEIIECEGTRTYTPPARAQYQSFIMDFCEFGIHIINPDEDGIFKIVNDT 182
QY 177 GEGKAWDEVSSENGYDYLMAVDYDHPDVAETKKGIVYANBLSLDFGRIDAKHI 236
DB 183 GEG-KWDQVDELDGPNFLMGENDIFRHAATBEIKYARVMQTCQDGRLDVAKHI 240
QY 237 KFSPLDWMYQAVQATGKMFVAEYVQNNACKLENYLNKTSFNQSVFDPVPHNLQAAS 296
DB 241 PAMFYKEMIEHVQEVAPKPLFIVAERYSHVVKLQYVIDQVSGKTMLPAPLQMKHEHS 300
QY 297 SOGGYDMMRLDGTIVSSHPEKAVTFVENHDTOPQOSLESTVQTFKFLAVAFITRES 356
DB 301 RMGRDDYMQITFTGLTLEADPFRAVTLVANHDTQPLQLEAVEPEFKLALAILIREN 360
QY 357 GYPOVYGDWYGTK-----GTSPEKELPSLKDNIETPLKARKEVAYPQHDYIDHPV 408
DB 361 GYPSVFYPLDYGHYHDVGADGQTYIDWPII-EQLDEILARQSFHAGVQTLFPDHPNC 419
QY 409 IGTFTREGDSAAAGLAILITGPGSKRMVYGLKAGETWYDITGNBSDTYKISDDGNG 468
DB 420 IAFSGSGTDEF--PGCVVWNSGDDSEKTIHSENYGKTKMDFLGNRGERVYTDENGSA 477
QY 469 EFTVNDGSVSIY 480
DB 478 TFFCNGSGSVSW 489
RESULT 7
AM3A_ORYSA STANDARD; PRT; 440 AA.

AC P27932; (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Alpha-amylase isozyme 3A precursor (EC 3.2.1.1) (1,4-alpha-D-glucan glucanohydrolase).
 GN AMY.2 OR AMY3A.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Magnoliophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Euphorbiaceae; Oryzae; Oryza.
 NCBI_TaxID=4530;
 RX MEDLINE=91329692; PubMed=1714318;
 RA Suttcliffe T.D., Huang N., Lites J.C., Rodriguez R.L.;
 RL Plant Mol. Biol. 16:579-591(1991).
 CC - FUNCTION: Important for breakdown of endosperm starch during germination.
 CC - CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic linkages in oligosaccharides and polysaccharides.
 CC - COFACTOR: Binds 3 calcium ions per subunit (By similarity).
 CC - SUBUNIT: Monomer.
 CC - TISSUE SPECIFICITY: Most abundant in embryo-derived callus tissue.
 CC - DEVELOPMENTAL STAGE: Expressed at a high level during germination in the aleurone cells under the control of the plant hormone gibberellic acid and in the developing grains at a low level.
 CC - SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
 CC -----
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 CC -----
 CC EMBL, X56356; CAA39776.1; -
 DR PIR; S14958; S14958.
 DR HSP; P04063; IAVA.
 DR InterPro; P27932; -
 DR InterPro; IPR006589; Alp_amy1_cat_sub.
 DR InterPro; IPR006047; Alpha_amy1_cat.
 DR InterPro; IPR006046; Glyco_hydro_13.
 DR Pfam; PF00128; alpha-amylase; 1.
 DR PRINTS; PR00110; ALPHAAMYLASE.
 DR SMART; SM00642; Amy; 1.
 KW Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding; Signal; Multigene family.
 FT SIGNAL; Multigene family.
 FT CHAIN 1 26
 FT ACT_SITE 27 440
 FT ACT_SITE 207 207
 FT ACT_SITE 315 315
 FT METAL 119 119
 FT METAL 145 145
 FT METAL 155 155
 FT METAL 166 166
 FT METAL 169 169
 FT METAL 170 170
 FT METAL 171 171
 FT METAL 174 174
 FT METAL 176 176
 FT SEQUENCE 440 AA; 46872 MW; 5E9B78C29A91C2B CRC64;
 Query Match 13.2%; Score 346; DB 1; Length 440;
 Best Local Similarity 25.0%; Pred. No. 2.9e-17;
 Matches 128; Conservative 63; Mismatches 151; Indels 170; Gaps 21;

QY 5 LMQVFEWTPNDGQMKR-----LQNDAEHLSDIGITAVWIPPAKGLSQSDNGXGPGY 57
 DB 31 LQGFNNW-----DSMKQGGGWNNLKDQVGDIAAGVTHWLPFFTH--SVSPGQVWPG 82
 QY 58 DLYDGEFOQKGTVRKTKYKSELQDAIGLSHRNVQYGVVNLHKAGADATEDVTAVE 117
 DB 83 RLYDNLN-----ASKYGTKAELKSLIAAFPAKGIKCAVDIVWHRC----- 122
 QY 118 VNPANNGTSEHYQIKAWTDFRFGKNTYSDFKMWHYFEGADWDSRKISRIFKFRG 177
 DB 123 -----ADDKRGKGYCIFKGG 139
 QY 178 EGRKMDW-----EVSSNGN-----YDLYMTADVDYDHPDVAETKWKGIYANEL 223
 DB 140 PRGCLDWGSPMKCCDDTQYSDGTGHRDGTGADPFAAPADIDHNLFLVQRELSDMLRWLRDV 199
 QY 224 SLDFGRIDAKKHIKESFLRDWQAVRQATGKMEFTVAEYWG-----NNAG--- 268
 DB 200 GFDGWRDLDAKGYSAVARTTYQNAKPS-----FVAELWNSLSDGSGKPAANDGGRQ 254
 QY 269 KLENYLNTKTSFNQSVFDEVLHFNLTQAASQGGYDMRRLDGT---VSRHPEKAVTVE 325
 DB 255 ELVNWVQVQGPATAFDFTKGLQSA--VQGLWEMRD--KQKAPGMIGWYBEKAVTFVD 312
 QY 326 NHDTPRGQSLSTVQTFWEK-----LAVAFILTRSGYQVGYGMYGTKGTSFKEIFSL 380
 DB 313 NHDTP-----GSTQKRWPFPSDKVILGVAVILT--HPGVCFIYDQVFDW-----NL 356
 QY 381 KDNIEPILAKREYAVGPOHDYIDHPDVIGWTRBDSNAKSGLAALITDGGGSKEMYA 440
 DB 357 KQKINLAATRK-----RNGINAGSKRLVLAASD-----WVY 389
 QY 441 GLKNAGETWYDITGRSPVTKIGSDMGGRHY 472
 DB 390 AM--VDERVITKIGPR--IEVGNIIIPSDFI 416
 RESULT 8
 AMYA_VIGMU
 ID AMYA_VIGMU STANDARD, PRT; 421 AA.
 AC P17859;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Alpha-amylase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan glucanohydrolase).
 GN AMY1.1.
 OS Vigna mungo (Black gram).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Magnoliophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC Euphorbiaceae; Fabaceae; Papilionaceae; Phaseoleae; Vigna.
 NCBI_TaxID=3915;
 RN [1]
 RP SEQUENCE FROM N.A.
 RP TISSUE=Cotyledon;
 RX MEDLINE=90332425; PubMed=2377468;
 RA Yamauchi D., Minamikawa T.;
 RT "Nucleotide sequence of cDNA for alpha-amylase from cotyledons of germinating Vigna mungo seeds";
 RL Nucleic Acids Res. 18:4250-4250(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94120017; PubMed=8290640;
 RA Takenuchi H., Yamauchi D., Wada S., Minamikawa T.;
 RT "Nucleotide sequence of the alpha-amylase gene from Vigna mungo";
 RL Plant Physiol. 103:1459-1459(1993).
 CC - CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic linkages in oligosaccharides and polysaccharides.
 CC - COFACTOR: Binds 3 calcium ions per subunit (By similarity).
 CC - SUBUNIT: Monomer (By similarity).
 CC - SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
 CC -----
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 CC or send an email to license@isb-sib.ch).

DR EMBL; X53049; CAA37217.1; -
 DR EMBL; X73301; CAA51734.1; -
 DR PIR; S10514; S10514.
 DR HSSP; P04063; IAVA.
 DR InterPro; IPR006589; Alp_amy1_cat_sub.
 DR InterPro; IPR006047; Alpha_amy1_cat.
 DR Pfam; PF00128; alpha-amy1ase; 1.
 DR PRINTS; PR00110; ALPHAAMYLAZE.
 DR SMART; SM00642; Amy; 1.

KM Carbohydrate metabolism; Hydrolyase; Glycosidase; Calcium-binding;
 KM Signal.

FT SIGNAL 1 23 PROBABLE
 FT CHAIN 24 421 ALPHA-AMYLAZE.
 FT ACT SITE 201 201 BY SIMILARITY.
 FT ACT SITE 309 309 BY SIMILARITY.
 FT METAL 113 113 CALCIUM 1 (BY SIMILARITY).
 FT METAL 130 130 CALCIUM 2 (BY SIMILARITY).
 FT METAL 133 133 CALCIUM 2 (BY SIMILARITY).
 FT METAL 135 135 CALCIUM 2 (BY SIMILARITY).
 FT METAL 139 139 CALCIUM 2 (BY SIMILARITY).
 FT METAL 149 149 CALCIUM 3 (BY SIMILARITY).
 FT METAL 160 160 CALCIUM 3 (BY SIMILARITY).
 FT METAL 166 166 CALCIUM 3 (VIA CARBONYL OXYGEN) (BY
 SIMILARITY).

FT METAL 170 170 CALCIUM 1 AND 3 (BY SIMILARITY).
 SQ SEQUENCE 421 AA; 46898 MM; 15CA0DBADDB4656 CRC64;

Query Match 12.7%; Score 333.5; DB 1; Length 421;
 Best Local Similarity 26.5%; Pred. No. 2.1e-16;
 Matches 121; Conservative 55; Mismatches 166; Indels 115; Gaps 17;

QY 5 LQVFFWYTPNDGQHKRLQNDLHSDIGTRVWPPRAYKGLSGSDNGYGYDYLDGE 64
 DB 26 LFGGFWESSKKGWNSLKNISIPDLNAGITHWLPPSQSVSPBGLGRLLDLD- 82
 QY 65 FQCKGTVRTYKGTSELDQALGSLHSRNVQVGVVLANHAGADATEDTAVEVNPANRN 124
 DB 83 -----ASKYSGKNEKSLIAFHKKIKCLADIVINR----- 115
 QY 125 QETSEYQIKAMTDFEPFGKNTYSDPKMWHYFDGADMDSEKIKIRIKFGGKAMW 164
 DB 116 --TAE-----KRDGRG-----IYCFEGTDPDRDQWSPSTICD-----DT 150
 QY 185 EVSEKNGNDV-----YMTADVDPVAVETKQWIMYANELSLDGFIDAKHIFSF 240
 DB 151 AYSDGNGNDSGEGYDAAPDIDHNPQVRELSMMWMLKTEIGFGWAFDPYKGYAPSI 210
 QY 241 LRDVQAVROATKEMFTVAEYV-----ONNAGKLENLYNKSFSNOSVD 285
 DB 211 SKTYMEQT-----KPPFAVGEKWDISLYGQDGKPNYNOSHREALVWVESAGATTAD 265
 QY 286 VPLHFNQAASSGGGVDMRLDGT-----VSRHPEKVFTEVNHDTOPGSLSTVQ 340
 DB 266 FTTKGIQQA-VQG--ELMRLIDPCKPCKMIGVPEKNAVITIDHDT-----GSTGR 315
 QY 341 TWFRP-----LAVAFILITRESGYPOVYGMGTGTSPELPSLKNIDPEPIKAKEXYA 395
 DB 316 LMFPPSDKWKQGYAVIIT-HPGTFSIYDHFDFW-----GLXEQIAKLSISRL--- 362
 QY 396 YGPHQYIDHPDVTIGWTRGSDSAKSGALALITDP 432
 DB 363 ---RNGINEXSYKYNASEGDLVYAKIDNKIMVKGIP 396

RESULT 9

AM3C_ORYSA
 ID AM3C_ORYSA STANDARD; PRT; 437 AA.
 AC P27939;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Alpha-amy1ase isozyme 3C precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
 DE glucanohydrolase).
 GN AMY1.7 OR AMY3B.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzae; Oryza.
 OX NCBI_TaxID=4530;
 (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Japonica M202; TISSUE=Etiolated leaf;
 RX MEDLINE=91329692; PubMed=1714318;
 RA Sutcliffe T.D., Huang N., Lites J.C., Rodriguez R.L.;
 FT "Characterization of an alpha-amy1ase multigene cluster in rice";
 RL Plant Mol. Biol. 15:579-591(1991).
 CC -1- FUNCTION: Important for breakdown of endosperm starch during
 CC germination.
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
 CC linkages in oligosaccharides and polysaccharides.
 CC -1- COFACTOR: Binds 3 calcium ions per subunit (By similarity).
 CC -1- SUBUNIT: Monomer.
 CC -1- TISSUE SPECIFICITY: Germinating seeds.
 CC -1- DEVELOPMENTAL STAGE: Expressed at a high level during germination
 CC in the aleurone cells under the control of the plant hormone
 CC gibberellic acid and in the developing grains at a low level.
 CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
 CC
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 CC or send an email to license@isb-sib.ch).

DR EMBL; X56338; CAA39778.1; -
 DR PIR; S14956; S14956.
 DR HSSP; P04063; IAVA.
 DR Gramene; P27939; -
 DR InterPro; IPR006589; Alp_amy1_cat_sub.
 DR InterPro; IPR006047; Alpha_amy1_cat.
 DR InterPro; IPR006046; Glyco_hydro_13.
 DR Pfam; PF00128; alpha-amy1ase; 1.
 DR PRINTS; PR00110; ALPHAAMYLAZE.
 DR SMART; SM00642; Amy; 1.
 KW Carbohydrate metabolism; Hydrolyase; Glycosidase; Calcium-binding;
 KW Signal; Multigene family.
 FT SIGNAL 1 26
 FT CHAIN 27 437
 FT ACT SITE 205 205
 FT ACT SITE 313 313
 FT METAL 117 117
 FT METAL 134 134
 FT METAL 137 137
 FT METAL 139 139
 FT METAL 143 143
 FT METAL 153 153
 FT METAL 164 164
 FT METAL 167 167
 FT METAL 168 168
 FT METAL 169 169
 FT METAL 172 172
 FT METAL 174 174
 SQ SEQUENCE 437 AA; 48637 MM; BD04250E40C7AB8 CRC64;

Query Match 12.3%; Score 324; DB 1; Length 437;
 Best Local Similarity 24.9%; Pred. No. 1.1e-15;
 Matches 108; Conservative 56; Mismatches 140; Indels 130; Gaps 15;

QY 5 LMOYFMYWPNDOGHKR-LQNDAEHLSDIGTAWWIPAYVGLSGSDGYPDYLDIG 63
 DB 29 LFGGFWESNKKCGGMVNFHSHVDIATGVHMLP--PSHSAVPGGVPGSLYDD 86
 QY 64 EFOQGTWRTKYGKSELQDAISLSRVQYGVVLNKKAGADATEDVTAVEVNPANR 123
 DB 87 -----ASKYGTGALRELLIAFHSKSIKVAIVINRRC----- 120
 QY 124 NQETSEBYQIKAMTDRFPKRGTYGDFKMMWHPGADWDESKRSIRIFKRGSGKMD 183
 DB 121 -----ADYKSRGTYICIFEGGTPDSRLD 143
 QY 184 W--EVSSENGNY-----DYLMADVDYDHPDYVAETKMGIVYANELSIDGR 229
 DB 144 WGDPMICSDDTQYNSNGRHRTGADPGAPADIDHNTVQTELSDWLMLKSDVGFQWR 203
 QY 230 IDAAKHKEFLDMVQAVQAKGKMFYAEYWN-----NAGKLENYL 274
 DB 204 LDFPKYGSATVATYVYDNTDPS-----FVVAELTSMNRYDNGEPMNODGDEQLVNA 258
 QY 275 NKTSFNOSVDPVPLHFNILQASSQGGGYDVRRLDGT-----VSRHPEKAVTFENHDT 329
 DB 259 QAVGGRASAFDFTTKGELQA--VQ---ELMRKDKGKAPKMGIMLPEKAVTFIDNHD 314
 QY 330 QPGGSLSTVQYTFKP-----LAVAFILRESGYPOVFYDMVGTGTSKELPSKXNI 384
 DB 315 -----GSTONSWPFPEDKVMQRYAYILT-HPGVCIFYHDVDM-----NIKOEI 358
 QY 385 EPIKARKEYAYGP 398
 DB 359 STLAAVSRNGIHP 372

RT "Sequence of an active fragment of B. polymyxa beta amylase";
 RL Nucleic Acids Res. 15:3934-3934(1987).
 RN (4) DISULFIDE BOND, AND KOTTAGENESIS OF CYSTEINE RESIDUES.
 RP MEDLINE=91215008; PubMed=1827035;
 RA Uozumi N., Matsuda T., Tsukagoshi N., Uda S.;
 RT "Structural and functional roles of cysteine residues of Bacillus
 RT polymyxa beta-amylase";
 RT Biochemistry 30:4594-4599(1991).
 CC -1- FUNCTION: THE PRECURSOR PROTEIN IS PROTEOLYTICALLY CLEAVED TO
 CC PRODUCE MULTIFORM BETA-AMYLASES AND A 48 kDa ALPHA-AMYLASE AFTER
 CC SECRETION.
 CC -1- CATALYTIC ACTIVITY: Hydrolysis of 1,4-alpha-glucosidic linkages in
 CC polysaccharides so as to remove successive maltose units from the
 CC non-reducing ends of the chains.
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
 CC linkages in oligosaccharides and polysaccharides.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: In the N-terminal section; belongs to family 14 of
 CC glycosyl hydrolases.
 CC -1- SIMILARITY: In the C-terminal section; belongs to family 13 of
 CC glycosyl hydrolases.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: M15817; AA85446.1; -;
 CC EMBL: Y00150; CA68344.1; -;
 CC PIR: A29130; A29130.
 CC HSP: P36924; I892.
 CC InterPro: IPR006589; Alp_amy1_cat_sub.
 CC InterPro: IPR006048; Alpha_amy1_C.
 CC InterPro: IPR006047; Alpha_amy1_cat.
 CC InterPro: IPR005085; Cbm_25.
 CC InterPro: IPR006046; Glyco_hydro_13.
 CC InterPro: IPR001554; Glyco_hydro_14.
 CC Pfam: PF00128; alpha-amyase; 1.
 CC Pfam: PF02806; alpha-amyase_C; 1.
 CC Pfam: PF03423; Cbm_25; 2.
 CC Pfam: PF01373; Glyco_hydro_14; 1.
 CC PRINTS: PR00110; ALPHAMYLASE.
 CC PRINTS: PR00750; BETRAYLASE.
 CC SMART: SM00642; Amy; 1.
 CC SMART: SM00632; Amy_C; 1.
 CC PROSITE: PS00506; BETA_AMYLASE_1; 1.
 CC PROSITE: PS00679; BETA_AMYLASE_2; 1.
 CC K1 Multifunctional enzyme; Hydrolase; Glycosidase; signal;
 CC K1 Polysaccharide degradation; Repeat.
 CC STGNL 1 35
 CC CHAIN 36 1196
 CC DOMAIN 36 454
 CC REPEAT 455 558
 CC REPEAT 565 668
 CC DOMAIN 669 1196
 CC DISULFID 118 126
 CC ACT_SITE 198 198
 CC ACT_SITE 394 394
 CC NUTAGEN 118 118
 CC NUTAGEN 126 126
 CC NUTAGEN 358 358
 CC CONFLICT 1 67
 CC CONFLICT 100 100
 CC CONFLICT 154 154
 CC CONFLICT 177 177
 CC CONFLICT 227 228
 CC CONFLICT 330 330
 CC CONFLICT 425 425
 CC
 CC BETA/ALPHA-AMYLASE.
 CC BETA-AMYLASE.
 CC
 CC ALPHA-AMYLASE.
 CC BY SIMILARITY.
 CC C->S: 5-FOLD DECREASE IN ACTIVITY.
 CC C->V: 20-FOLD DECREASE IN ACTIVITY.
 CC C->S: 60-FOLD DECREASE IN ACTIVITY.
 CC M->S (IN REF. 3).
 CC N->S (IN REF. 3).
 CC S->D (IN REF. 3).
 CC S->N (IN REF. 3).
 CC E->Q (IN REF. 3).
 CC NA->KS (IN REF. 3).
 CC G->S (IN REF. 3).
 CC N->S (IN REF. 3).

```
FT CONFLICT 493 493 D -> A (IN REF. 3)
FT CONFLICT 532 532 S -> L (IN REF. 3)
FT CONFLICT 559 559 A -> T (IN REF. 3)
FT CONFLICT 665 665 A -> T (IN REF. 3)
FT CONFLICT 681 681 D -> N (IN REF. 3)
FT CONFLICT 686 686 T -> A (IN REF. 3)
FT CONFLICT 725 728 AFTS -> VESP (IN REF. 3)
FT CONFLICT 736 736 N -> K (IN REF. 3)
FT CONFLICT 741 741 N -> S (IN REF. 3)
FT CONFLICT 758 758 S -> N (IN REF. 3)
SQ SEQUENCE 1196 AA, 130893 MM, A41EA6B70F257064 CRC64;

Query Match 12.3%; Score 323; DB 1; Length 1196;
Best Local Similarity 21.5%; Pred. No. 4,4e-15;
Matches 112; Conservative 82; Mismatches 162; Indels 164; Gaps 24;

QY 10 EMTYNDQHWKRLQNDAEHLSDIGITAVWIIPRAYKGLSQSDNGYGPYDLUDGEFGQK 68
DB 779 KWH---GADFOGINKLDYIKMGFTAWITPTMOKSEYAYHGYHTTDFY----- 826
QY 69 GTVRIKYGTSKSELQDAIGSLHSRVQYGVYDLVNLHKKAGADATEDVTAVEVNPANRQETS 128
DB 827 -AVDCHLGTMDKLOGLVARKADKNIAVWVYVNNHTG----- 862
QY 129 EBYQKANTDRFRPGKNTYSDF-KMHYHFDG---ADMDESKRISRIKFRGEGKAMD 183
DB 863 -----DFO-PENGFAKAPFDADYVHNGDITDGDVSNNO----- 897
QY 184 WEVSENGNYDYLMADYDHPVVAETKKGWYANELSLDFRIDAAGIKFSELRD 243
DB 898 WKI---ENG--DVAAGDLDHNNPANTANLKNWIKMLNETGIDGLRDLDTGVHVKGFLLD 953
QY 244 WVQAVRQATGKEMFTVAEYWMONNAGKLENYLNKTSFNOSVDVPLHNLCAASSQGGCYD 303
DB 954 FDOAA-----NFTMGELIFHGDPAYVGDY--TRYDLAALDFMYIYIKVNF--GHDQS 1002
QY 304 MRRLIDGTIVSRHPEKAVT---FVENHDT-----OPQSLSESTQVTFKPLAVAFI 351
DB 1003 MRKIDRISDBRYDAQNTNGVIFDNNHVKFPLNDASKPGANDDKMQL---KALGFT 1059
QY 352 LTRSGYQVQYGVDMYGTGTSPEKIPSLKDNIEPILAKREYAVGPOHDYIDHPVIGW 411
DB 1060 LT-SRGIPIIYQGTQGYSG--GDDPANRENNM-----FNANHDLVYQYIAKLNY 1105
QY 412 TREGSSAKSGLALITDGGSGKRWYAGLKNGETWYD-----ITGRSPTVTKGS 464
DB 1106 VRANHPAL-----QNGSOR-----EKWVDSFYSFGSKXGDEAIYVPI 1144
QY 465 DGM-----GEF-----HVNDGSVSI 479
DB 1145 NSMNSQRTIGNFMDLSNGTRLTNQLSNDVSQINNQSITV 1184

RESULT 11
AM3B_ORYSA STANDARD; PRT; 438 AA.
ID AM3B_ORYSA P27937;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Alpha-amylase isozyme 3B precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
DE glucanohydrolase).
GN Amyl. 6 OR Amy3B.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae;
OC Ehrhacroidae; Oryzaceae; Oryza.
OC NCBI_TaxID=4530;
OX RN
RX SEQUENCE FROM N.A.
RX STRAIN=cv. Japonica M202; TISSUE=Etolated leaf;
RX MEDLINE=91329692; PubMed=1714318;
RX Sutliff T.D., Huang N., Lites J.C., Rodriguez R.L.;
```

```
RT "Characterization of an alpha-amylase multi-gene cluster in rice."
RL Plant Mol. Biol. 16:579-591(1991).
RN (2)
RP SEQUENCE FROM N.A.
RA Sutliff T.D., Huang N., Rodriguez R.L.
Submitted (May-1993) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: Important for breakdown of endosperm starch during
CC germination.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -1- COFACTOR: Binds 3 calcium ions per subunit (By similarity).
CC -1- SUBUNIT: Monomer.
CC -1- TISSUE SPECIFICITY: Germinating seeds.
CC -1- DEVELOPMENTAL STAGE: Expressed at a high level during germination
CC in the aleurone cells under the control of the plant hormone
CC gibberellic acid and in the developing grains at a low level.
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
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CC or send an email to license@isb-sib.ch).
CC
DR EMBL: X56337; CAA39777.1; -
DR EMBL: X24941; AAA3897.1; -
DR PIR: S14957; S14957.
DR HSSP: P04063; IAVA.
DR Gramene; P27937; -.
DR InterPro: IPR006589; Alp.amyl.cat.sub.
DR InterPro: IPR006047; Alpha.amyl.cat.
DR InterPro: IPR006046; Glyco_Hydro_13.
DR Pfam: PF00128; alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Amyy; 1.
KW Carbohydrate metabolism; Hydrolyase; Glycosidase; Calcium-binding;
KW signal; Multigene family.
FT SIGNAL 1 26
FT CHAIN 1 438
FT ACT SITE 205 303
FT ACT SITE 313 313
FT ACT SITE 117 117
FT METAL 117 117 CALCIUM 1 (BY SIMILARITY).
FT METAL 134 134 CALCIUM 2 (BY SIMILARITY).
FT METAL 137 137 CALCIUM 2 (BY SIMILARITY).
FT METAL 139 139 CALCIUM 2 (BY SIMILARITY).
FT METAL 143 143 CALCIUM 3 (BY SIMILARITY).
FT METAL 153 153 CALCIUM 3 (BY SIMILARITY).
FT METAL 164 164 CALCIUM 3 (VIA CARBONYL OXYGEN) (BY
FT METAL 167 167 SIMILARITY).
FT METAL 168 168 CALCIUM 1 (BY SIMILARITY).
FT METAL 169 169 CALCIUM 1 (VIA CARBONYL OXYGEN) (BY
FT METAL 172 172 CALCIUM 3 (VIA CARBONYL OXYGEN) (BY
FT METAL 174 174 CALCIUM 3 (VIA CARBONYL OXYGEN) (BY
SQ SEQUENCE 438 AA, 48591 MM, B9DE0D5ABC63F9C CRC64;

Query Match 12.2%; Score 319; DB 1; Length 438;
Best Local Similarity 24.5%; Pred. No. 2,4e-15;
Matches 108; Conservative 54; Mismatches 136; Indels 142; Gaps 16;
```

```
QY 5 LMOYFMYTNDQHWKRLQNDAEHLSDIGITAVWIIPRAYKGLSQSDNGYGPY 57
DB 29 LPOGFNW-----ESWKQGGWYNFLGHVDDIAATGVTHWLP--PSHSAVAPQGYMBG 80
QY 58 DLVDLGEFGQKGVRRKYGTSKSELQDAIGSLHSRVQYGVYDLVNLHKKAGADATEDVTAVE 117
DB 81 RLVDLD-----ASKYTGALRLSLIAFHSKGIKVADIVINRC----- 120
QY 118 VNPANRQETSERYQIKANTDRFRPGKNTYSDFKMHYHFDGADWDSEKRSRIKFRG 177
```


AC P27934;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Alpha-amylase isozyme 3B precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
glucanohydrolase).
GN AM1.4 OR AM13E.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhacidae; Oryzaeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Japonica M202; TISSUE=Etisolated leaf;
RX MEDLINE=9108278; PubMed=2263460;
RA Huang N., Koizumi N., Reini S., Rodriguez R.L.;
RT "Structural organization and differential expression of rice alpha-
amylase genes.";
RL Nucleic Acids Res. 18:7007-7014 (1990).
CC -1- FUNCTION: Important for breakdown of endosperm starch during
CC germination.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -1- COFACTOR: Binds 3 calcium ions per subunit (By similarity).
CC -1- SUBUNIT: Monomer.
CC -1- TISSUE SPECIFICITY: More abundant in germinating seeds than in
CC young roots, young leaves and callus.
CC -1- DEVELOPMENTAL STAGE: Expressed at a high level during germination
CC in the aleurone cells under the control of the plant hormone
CC gibberellic acid and in the developing grains at a low level.
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL: M59352; AAA33896.1; -
CC PIR: J09463; J09463.
CC HSSP: P04063; J09463.
DR Gramene; P27934; -
DR InterPro; IPR006589; Alp_ami1_cat_sub.
DR InterPro; IPR006047; Alpha_ami1_cat.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAMYLASE.
DR SMART; SM00642; Amy; 1.
KW Carbohydrate metabolism; Hydrolyase; Glycosidase; Calcium-binding;
KW Signal; Multigene family.
FT SIGNAL 1 25
FT CHAIN 26 437 POTENTIAL. ALPHA-AMYLASE ISOZYME 3B.
FT ACT_SITE 204 204 BY SIMILARITY.
FT ACT_SITE 312 312 BY SIMILARITY.
FT METAL 116 116 CALCIUM 1 (BY SIMILARITY).
FT METAL 133 133 CALCIUM 2 (BY SIMILARITY).
FT METAL 136 136 CALCIUM 2 (BY SIMILARITY).
FT METAL 138 138 CALCIUM 2 (BY SIMILARITY).
FT METAL 142 142 CALCIUM 2 (BY SIMILARITY).
FT METAL 152 152 CALCIUM 3 (BY SIMILARITY).
FT METAL 153 153 CALCIUM 3 (BY SIMILARITY).
FT METAL 163 163 CALCIUM 3 (VIA CARBONYL OXYGEN) (BY
FT METAL 166 166 CALCIUM 3 (VIA CARBONYL OXYGEN) (BY
FT METAL 168 168 CALCIUM 1 (VIA CARBONYL OXYGEN) (BY
FT METAL 171 171 CALCIUM 3 (VIA CARBONYL OXYGEN) (BY
FT METAL 173 173 CALCIUM 1 AND 3 (BY SIMILARITY).
SQ SEQUENCE 437 AA; 48707 MW; C08276CCEA16602 CRC64;

Query Match 12.0%; Score 315.5; DB 1; Length 437;
Best Local Similarity 24.9%; Pred. No. 4.2e-15;
Matches 122; Conservative 54; Mismatches 146; Indels 167; Gaps 21;
QY 5 LMGFEWYIPNQGHWK-----LQNDAEHLSDIGTAWVIPPAYKSLQSQDNQGY 57
DB LFGQFW-----ESRKQGWTFHEKVEELASGATHWLP--BSHSVPGQYMG 79
QY 58 DLYDICEFOQKGTVRTKRYGTSKELDQAGSLHSRVQYGVYLVNKKAGADATEDVAVE 117
DB RLYDLD-----ASKYGTAEELKELIAFHDKNVECLADIVINRC----- 119
QY 118 VNPANNQETSEYQKAWTDPRFPGNGTYSDFKMHWHPDGAQMDSEKXSRJFKFRG 177
DB 120 -----ADYKSRGYCYFEGGT 136
QY 178 EGRAMD-----EVSSENGND-----YLMADVDPDHPDYAEKTKGIWYANEL 223
DB 137 PGRLDWGPDMICSDDTQYNSNGRHRDTGAGGAAPDIDHLPVQRELTDWLNLRDLD 196
QY 224 SLGFRIDAKHKKFELADWQAVQATGKEMFYAEWQ-----NNACK----- 269
DB 197 GFGMRUDFPAKGYSAFLARIYDNTNPT-----FVGEIWSLLIYNGDESTNDADQ 251
QY 270 -LENYLNTKTSFNQSVDPVPLHFNILQAASSQGGYDMRLLDGT-----VSSHPEKAYTF 323
DB 252 ELVNWTEGVGKPAATDFTTKGLQA-VQG--ELMRLLDNGKAPGLMGMWPDQAVTF 307
QY 324 VEHNDTPQSGLESTVQTFKP-----LVAFLTPRESGYPOYFGDMYGTGSEKPEP 378
DB 308 VDMHDGTSQSL-----WPFPSDKVMQGYAYILT-HPDIFCIYDHF--DMNLQHELA 358
QY 379 SL-----KDNIEPLIKARKE-----AGPOHD-----YIDH-P 406
DB 359 TLEIISRNRHAEHLIDILKAGDLYVAMIDKATYTKGPRYDAGGILPSDFHVAHGN 418
QY 407 DVGWTRREG 415
DB 419 DYCWEREK 427
RESULT 14
AMY3_WHEAT STANDARD; PRT; 413 AA.
ID AMY3_WHEAT
AC P08117;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Alpha-amylase AMY3 precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
glucanohydrolase).
GN AMY1.1 OR ALPHA-AMY3.
OS Triticum aestivum (Wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Triticum.
OX NCBI_TaxID=4565;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Chinese Spring;
RA Baulcombe D.C., Huttly A.K., Martienssen R.A., Barker R.F.,
RA Jarvis M.G.;
RT "A novel wheat alpha-amylase gene (alpha-Amy1)." ;
RI Mol. Gen. Genet. 209:33-40 (1987).
CC -1- FUNCTION: Important for breakdown of endosperm starch during
CC germination.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -1- COFACTOR: Binds 3 calcium ions per subunit (By similarity).
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- DEVELOPMENTAL STAGE: Expressed at a high level during germination
CC in the aleurone cells under the control of the plant hormone
CC gibberellic acid and in the developing grains at a low level.
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.

RESULT 15	AMY1_HORVU	STANDARD;	PT;	438 AA.
ID	AMY1_HORVU	STANDARD;	PT;	438 AA.
AC	P00693;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Alpha-amyrase type A isozyme precursor (EC 3.2.1.1) (1.4-alpha-D-glucan 1-glucanohydrolase) (AMY1) (Low pI alpha-amyrase).			
GN	AMY1.1.			
OS	Hordeum vulgare (Barley).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;			
OC	Triticeae; Hordeum.			
OX	NCBI_TaxId=4513;			
ON	(1)			
RP	SEQUENCE FROM N.A.;			
RC	STRAIN=cv. Himalaya;			
RA	MEDLINE=83238423; PubMed=6190808;			
RT	Rogers J.C., Millman C.;			
RT	"Isolation and sequence analysis of a barley alpha-amyrase cDNA clone."			
RL	J. Biol. Chem. 258:8169-8174(1983).			
CC	-1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic linkages in oligosaccharides and polysaccharides.			
CC	-1- COFACTOR: Binds 3 calcium ions per subunit (By similarity).			
CC	-1- SUBUNIT: Monomer (By similarity).			
CC	-1- SUBCELLULAR LOCATION: Extracellular.			
CC	-1- DEVELOPMENTAL STAGE: Production of alpha-amyrase is hormonally regulated. Germinating embryos produce the hormone gibberellic acid, which within 10 hours stimulates the aleurone cells covering the endosperm of the seed to produce alpha-amyrase. The enzyme then degrades the starch within the endosperm for use by the developing plant embryo.			
CC	-1- MISCELLANEOUS: There are at least 4 types of alpha-amyrase in barley.			
CC	-1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; J01236; AAA92929.1; -.			
DR	PIR; A00846; ALBH.			
DR	HSSP; P04063; IAVA.			
DR	InterPro; IPR006589; Alp_amy1_cat_sub.			
DR	InterPro; IPR006047; Alpha_amy1_cat.			
DR	InterPro; IPR006046; Glyco_hydro_13.			
DR	Pfam; PF00128; alpha-amyrase, 1.			
DR	PRINTS; PR00110; ALPHAMYLASE.			
DR	SMART; SM00642; Amy; 1.			
KW	Germination; Carbohydrate metabolism; Hydrolase; Glycosidase; Seed; Calcium-binding; Signal; Multigene family.			
KW	Calcium-binding; Signal; Multigene family.			
FT	CHAIN	25	438	ALPHA-AMYLASE TYPE A ISOZYME.
FT	ACT_SITE	204	224	BY SIMILARITY.
FT	ACT_SITE	229	229	BY SIMILARITY.
FT	ACT_SITE	315	315	BY SIMILARITY.
FT	METAL	116	116	CALCIUM 1 (BY SIMILARITY).
FT	METAL	133	133	CALCIUM 2 (BY SIMILARITY).
FT	METAL	136	136	CALCIUM 2 (BY SIMILARITY).
FT	METAL	138	138	CALCIUM 2 (BY SIMILARITY).
FT	METAL	142	142	CALCIUM 3 (BY SIMILARITY).
FT	METAL	152	152	CALCIUM 3 (BY SIMILARITY).
FT	METAL	163	163	CALCIUM 3 (BY SIMILARITY).
FT	METAL	166	166	CALCIUM 3 (VIA CARBONYL OXYGEN) (BY SIMILARITY).

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FT METAL 167 167 CALCIUM 1 (BY SIMILARITY).
FT METAL 168 168 CALCIUM 1 (VIA CARBONYL OXYGEN) (BY
FT METAL 171 171 SIMILARITY).
FT METAL 171 171 CALCIUM 3 (VIA CARBONYL OXYGEN) (BY
FT METAL 173 173 SIMILARITY).
FT METAL 173 173 CALCIUM 1 AND 3 (BY SIMILARITY).
SQ SEQUENCE 438 AA; 47796 MW; 2393FDAC5180F51 CRC64;

Query Match 11.7%; Score 307.5; DB 1; Length 438;
Best Local Similarity 25.2%; Pred. No. 1.6e-14;
Matches 110; Conservative 51; Mismatches 131; Indels 145; Gaps 18;

QY 5 LMOVPEWYTPNDGQHMKR-----LQNDAEHLSDIGTAVWIPPAKGLSQSDNGYGPY 57
DB 28 LFGGNNW-----ESMKSGGMYNNMGKVDIAAGVTHWLP--PSHSVSNEGIMPG 79
QY 58 DLYDIGEPQKGTATKTKGTSELODAIGLSHRNVQYGVVNLNKAQADATEDVTAVE 117
DB 80 RLYDID-----ASKYGNAAELKSLIGALHGKGVQAIADIVINHRC----- 119
QY 118 VNPANRQGTSEBYQIKAWTDFRFGNGNTYSDFKHWYHFDGADWDSRKISRIFFKRG 177
DB 120 -----ADYKDSRGICYCFEGGT 136
QY 178 EGRKAWD-----EVSSSENGY---DYLMTADVDYDHPDVVAETKKMGIMYANEL 223
DB 137 SDGRLDWGPBMICRDDTKYSDGTANLDGADFAAPDIDHLDNDRYOREIKEMLLMKSDL 196
QY 224 SIDGRIDAAKIKRIFLBDWQAVROATGKEMFTVAEYMNNA-----GK----- 269
DB 197 GFDANRLDPRGYSPEMAKVYIDGTSFS-----LAAYEYMDMAFGDGDKENYDQDAHQ. 251
QY 270 -LENYLINKTSFNQS---VEDVPLHFNLOAASQGGGYDMRLLDGT-----VSRHPKKA 320
DB 252 NLVNVVDKVGGAASGMVDFPTTKGILNNA--VEG---ELMRLIDPQKAPGVMGWMPAKA 307
QY 321 VTFVENHDTQPGQSLESTVGTWFKP-----LAYAFILTRSGYRQVFGDMYGTGTSK 375
DB 308 ATFVNDHDT-----GSTQAMPFSDKVMQGYAYILT-HPGIFCLTFIDHFFNW----- 354
QY 376 EIPSLKDNIEPIIKARK 392
DB 355 ---GFKDQIALVALAIRK 368
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Search completed: May 3, 2004, 20:51:14
Job time: 12.3995 secs

Query Match 100.0%; Score 2847; DB 2; Length 514;
 Best Local Similarity 100.0%; Pred. No. 3.8e-245;
 Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAFNGTMMQYFEMWLPDDGTLMTKVANEANNLSLGIITLMLPAPYKGTSRSDVGYGY 60
 DB 1 AAFNGTMMQYFEMWLPDDGTLMTKVANEANNLSLGIITLMLPAPYKGTSRSDVGYGY 60
 QY 61 DLYDGEFNQKVTATKTKYTAQYLOAIOAAHAAQYVADVFDHKGADGTEWDAVE 120
 DB 61 DLYDGEFNQKVTATKTKYTAQYLOAIOAAHAAQYVADVFDHKGADGTEWDAVE 120
 QY 121 VNPSDRNOEISGTVOIOAWTKFDFPGRGNTYSSFKRWYHFDGVWDESRKLSRIYKFRG 180
 DB 121 VNPSDRNOEISGTVOIOAWTKFDFPGRGNTYSSFKRWYHFDGVWDESRKLSRIYKFRG 180
 QY 181 IGRAMWEDVTENGNDYLMYADLMDHPEVVTBLKNGKMYVNTNIDGFRDLAVYHIK 240
 DB 181 IGRAMWEDVTENGNDYLMYADLMDHPEVVTBLKNGKMYVNTNIDGFRDLAVYHIK 240
 QY 241 FSPFPMLSYVSQTKPLFTVGEWYSYDINKLHNYITKTDGMSLFPAPLNKRYTASK 300
 DB 241 FSPFPMLSYVSQTKPLFTVGEWYSYDINKLHNYITKTDGMSLFPAPLNKRYTASK 300
 QY 301 SGGAFDMRTLMNTLMKQPTLAVTFVNDHDEPQALQSWDPMFKPLAVAFILTRQEG 360
 DB 301 SGGAFDMRTLMNTLMKQPTLAVTFVNDHDEPQALQSWDPMFKPLAVAFILTRQEG 360
 QY 361 YPCVFYGDYIGIPQYNISLSKIDPLIARDYAVGTQHDYLDHSDIIGWTRBGTEKP 420
 DB 361 YPCVFYGDYIGIPQYNISLSKIDPLIARDYAVGTQHDYLDHSDIIGWTRBGTEKP 420
 QY 421 GSGIALIITDGGSGKMYVQKQHAGKVFYDLTGNSDVTIINSOGWGEFKNVGSVSW 480
 DB 421 GSGIALIITDGGSGKMYVQKQHAGKVFYDLTGNSDVTIINSOGWGEFKNVGSVSW 480
 QY 481 VPRKTTVSTIARPIITRPWTGEFVRWTEBRLVAM 514
 DB 481 VPRKTTVSTIARPIITRPWTGEFVRWTEBRLVAM 514

RESULT 2

AAR72449
 ID AAR72449 standard; protein; 515 AA.

AC AAR72449;
 XX
 DT 16-OCT-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 01-DEC-1995 (first entry)
 XX
 DE Bacillus stearothermophilus alpha amylase (mature protein).
 XX
 KW Alpha amylase; variant; enzyme; detergent; additive; dishwashing;
 KW washing; Bacillus licheniformis; Bacillus subtilis; Bacillus
 KW Bacillus stearothermophilus; dyeing; bleaching; scouring; textile;
 KW thermostable.
 XX
 OS Geobacillus stearothermophilus.
 XX
 PN WO9510603-A1.
 XX
 PD 20-APR-1995.
 XX
 PF 05-OCT-1994; 94WO-DK000370.
 XX
 PR 08-OCT-1993; 93DK-00001133.
 PR 02-FEB-1994; 94DK-00000140.
 XX
 PA (NOVO) NOVO-NORDISK AS.
 XX
 PI Borchert TV, Bisgard-Franzen H, Svendsen A, Thellersen M;

PI Van Der Zee P;
 XX
 DR WPI, 1995-161790/21.
 DR N-PSDB; AAQ88068.
 XX
 PT New Bacillus derived alpha-amylase variants - having amino acid
 PT modifications to improve washing and/or dishwashing performance.
 XX
 PS Claim 34; Page 11-12; 105pp; English.

CC Variant alpha amylase enzymes which have improved washing and/or as
 CC detergent additives. The enzymes have one or more amino acid residues
 CC added, deleted or substituted. The variants can also be used for textile
 CC desizing prior to scouring, bleaching and dyeing. The variants have
 CC improved thermostability, acid/alkaline stability, low temperature
 CC optimum; pH optimum; higher hydrolysis velocity and improved tolerance to
 CC other composition constituents, e.g. oxidation agents. (updated on 25-MAR
 CC -2003 to correct PN field.) (updated on 25-MAR-2003 to correct PI field.)
 CC (updated on 16-OCT-2003 to standardise OS field)
 XX
 SQ Sequence 515 AA;

Query Match 100.0%; Score 2847; DB 2; Length 515;
 Best Local Similarity 100.0%; Pred. No. 3.8e-245;
 Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAFNGTMMQYFEMWLPDDGTLMTKVANEANNLSLGIITLMLPAPYKGTSRSDVGYGY 60
 DB 1 AAFNGTMMQYFEMWLPDDGTLMTKVANEANNLSLGIITLMLPAPYKGTSRSDVGYGY 60
 QY 61 DLYDGEFNQKVTATKTKYTAQYLOAIOAAHAAQYVADVFDHKGADGTEWDAVE 120
 DB 61 DLYDGEFNQKVTATKTKYTAQYLOAIOAAHAAQYVADVFDHKGADGTEWDAVE 120
 QY 121 VNPSDRNOEISGTVOIOAWTKFDFPGRGNTYSSFKRWYHFDGVWDESRKLSRIYKFRG 180
 DB 121 VNPSDRNOEISGTVOIOAWTKFDFPGRGNTYSSFKRWYHFDGVWDESRKLSRIYKFRG 180
 QY 181 IGRAMWEDVTENGNDYLMYADLMDHPEVVTBLKNGKMYVNTNIDGFRDLAVYHIK 240
 DB 181 IGRAMWEDVTENGNDYLMYADLMDHPEVVTBLKNGKMYVNTNIDGFRDLAVYHIK 240
 QY 241 FSPFPMLSYVSQTKPLFTVGEWYSYDINKLHNYITKTDGMSLFPAPLNKRYTASK 300
 DB 241 FSPFPMLSYVSQTKPLFTVGEWYSYDINKLHNYITKTDGMSLFPAPLNKRYTASK 300
 QY 301 SGGAFDMRTLMNTLMKQPTLAVTFVNDHDEPQALQSWDPMFKPLAVAFILTRQEG 360
 DB 301 SGGAFDMRTLMNTLMKQPTLAVTFVNDHDEPQALQSWDPMFKPLAVAFILTRQEG 360
 QY 361 YPCVFYGDYIGIPQYNISLSKIDPLIARDYAVGTQHDYLDHSDIIGWTRBGTEKP 420
 DB 361 YPCVFYGDYIGIPQYNISLSKIDPLIARDYAVGTQHDYLDHSDIIGWTRBGTEKP 420
 QY 421 GSGIALIITDGGSGKMYVQKQHAGKVFYDLTGNSDVTIINSOGWGEFKNVGSVSW 480
 DB 421 GSGIALIITDGGSGKMYVQKQHAGKVFYDLTGNSDVTIINSOGWGEFKNVGSVSW 480
 QY 481 VPRKTTVSTIARPIITRPWTGEFVRWTEBRLVAM 514
 DB 481 VPRKTTVSTIARPIITRPWTGEFVRWTEBRLVAM 514

RESULT 3

AAM31406
 ID AAM31406 standard; protein; 515 AA.

AC AAM31406;
 XX
 DT 17-OCT-2003 (revised)
 DT 11-MAY-1998 (first entry)
 XX
 DE Bacillus stearothermophilus Teramyl-1-like alpha-amylase.

XX Termamyl; alpha-amylase; enzyme engineering; protein engineering; starch;
 KW liquefaction; saccharification; sweetener; textile desizing;
 KM detergent additive; ss.
 XX Geobacillus stearothermophilus.
 XX WO9741213-A1.
 PN 06-NOV-1997.
 PD 30-APR-1997; 97WO-DK000197.
 PF 30-APR-1996; 96DK-00000515.
 XX 28-JUN-1996; 96DK-00000712.
 PR 11-JUL-1996; 96DK-00000775.
 PR 08-NOV-1996; 96DK-00001263.
 XX (NOVO) NOVO-NORDISK AS.
 XX Svendsen A, Borchert TV, Bisgard-Frantzen H;
 PI WPI; 1997-549718/50.
 DR N-PSDB; AAV02473.
 XX Termamyl-like alpha-amylase variants with improved properties - e.g.
 PT increased stability at low pH and low calcium, useful as detergent
 PT additives and in industrial starch processing e.g. liquefaction.
 XX Disclosure; Page 86; 101pp; English.
 PS
 XX This protein comprises the Termamyl-like alpha-amylase of Bacillus
 CC steothermophilus. The invention relates to novel variants of Termamyl-
 CC like alpha-amylases that have alpha-amylase activity and exhibit an
 CC alteration in at least one property selected from: substrate specificity;
 CC binding or cleavage pattern; thermal stability; pH/activity or
 CC pH/stability profile; stability towards oxidation; Ca²⁺ dependency and
 CC specific activity. The variant has one or more mutations from those
 CC listed in the specification in relation to Bacillus licheniformis
 CC Termamyl (see AAW31404). Also claimed are constructs comprising DNA
 CC encoding the variant (see AAV02471-73), and recombinant expression
 CC vectors and transformed cells containing the DNA. The Termamyl-like alpha
 CC in industrial starch processing e.g. liquefaction (claimed) or
 CC saccharification to produce sweeteners, and in textile desizing
 CC (claimed). (Updated on 17-OCT-2003 to standardise OS field)
 CC
 XX
 SQ Sequence 515 AA;

Query Match 100.0%; Score 2847; DB 2; Length 515;
 Best Local Similarity 100.0%; Pred. No. 3.8e-245;
 Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAFNGTMMQYFEMWLPDDGLMTKVAEANNLSIGITATLWLPAYKGTSHSDVGYVY 60
 DB 1 AAFNGTMMQYFEMWLPDDGLMTKVAEANNLSIGITATLWLPAYKGTSHSDVGYVY 60

QY 61 DLYDGEFNGKGTATKTKYKTAQYLOAQOAAHAAGQYADVPFHKGAGDTEWDAVE 120
 DB 61 DLYDGEFNGKGTATKTKYKTAQYLOAQOAAHAAGQYADVPFHKGAGDTEWDAVE 120

QY 121 VNPSPRNGEISGTYOIQAWTKFDFPGRGNTYSSFFKRWYHPFGVMDSESKLSRIYKFRG 180
 DB 121 VNPSPRNGEISGTYOIQAWTKFDFPGRGNTYSSFFKRWYHPFGVMDSESKLSRIYKFRG 180

QY 181 ICKADMEVDTENGNYDYIMYADLMDHPEVYTELKNGKRYVNTTNDGFFLDVVKIK 240
 DB 181 ICKADMEVDTENGNYDYIMYADLMDHPEVYTELKNGKRYVNTTNDGFFLDVVKIK 240

QY 241 FSEFPDMISYASQGTGKPLFTVGEYWSYDINKLHNYITKTDGTMGLFPAFLNKKRYTASK 300
 DB 241 FSEFPDMISYASQGTGKPLFTVGEYWSYDINKLHNYITKTDGTMGLFPAFLNKKRYTASK 300

QY 301 SGCAFPMKRTIMTMTLKKDQPTLAVTFVDNHDTEPGQALQSWDPKPKPLAYAFILTRQEG 360
 DB 301 SGCAFPMKRTIMTMTLKKDQPTLAVTFVDNHDTEPGQALQSWDPKPKPLAYAFILTRQEG 360

QY 361 YPCVFYGDYIGIPQYNIPLSKSKIDPELLIARRDYAGTQHDYDHSIDIIGMREGGTEKP 420
 DB 361 YPCVFYGDYIGIPQYNIPLSKSKIDPELLIARRDYAGTQHDYDHSIDIIGMREGGTEKP 420

QY 421 GSGIALALITDGPQSGSKWYTGKQAGKRYFDLTGNRSPTVTINSDDWGEFPKNGSSVSW 480
 DB 421 GSGIALALITDGPQSGSKWYTGKQAGKRYFDLTGNRSPTVTINSDDWGEFPKNGSSVSW 480

QY 481 VPKRTVSTIARPIITRPMTGEFVFWTEPRLVAM 514
 DB 481 VPKRTVSTIARPIITRPMTGEFVFWTEPRLVAM 514

RESULT 4
 ID AAY99770 standard; protein; 515 AA.
 XX AAY99770
 AC AAY99770
 DT 12-SEP-2003 (revised)
 DT 04-SEP-2000 (first entry)
 XX
 DE Bacillus stearothermophilus Termamyl-like alpha-amylase #2.
 XX
 KW Bacillus; alpha-amylase; washing; textile desizing; starch liquefaction;
 KM saccharification; muten; mutant; enzyme stability; hydrid.
 XX
 XX Geobacillus stearothermophilus.
 OS WO200029560-A1.
 PN 25-MAY-2000.
 PD 16-NOV-1999; 99WO-DK000628.
 PF 16-NOV-1998; 98DK-00001495.
 PR 16-NOV-1998; 98DK-00001495.
 XX
 PA (NOVO) NOVO-NORDISK AS.
 XX
 FI Svendsen A, Kjærulff S, Bisgard-Frantzen H, Andersen C;
 XX WPI; 2000-387777/33.
 DR N-PSDB; AAA48482.
 XX
 PT Variant of parent termamyl-like alpha amylase useful for washing, textile
 PT desizing and starch liquefaction, comprising alterations in one or more
 PT solvent exposed amino acid residues.
 XX
 XX Claim 8; Fig 1; 80pp; English.
 PS
 XX The present sequence is a parent alpha-amylase from which mutants with
 CC increased stability at acidic pH, low calcium concentration and high
 CC temperatures have been derived. A variant may contain mutations in one or
 CC more solvent exposed amino acid residues to increase the overall
 CC hydrophobicity of the enzyme or the overall number of methyl groups in
 CC the side chains of exposed residues may be increased. The mutations can
 CC be incorporated by site-directed mutagenesis or by random mutagenesis. As
 CC a result of their increased stability, the variants are suitable for the
 CC industrial processing of starch, i.e. starch liquefaction and
 CC saccharification. They may also be useful for washing, dishwashing and
 CC textile desizing. Hybrid alpha-amylases comprising partial amino acid
 CC sequences derived from two or more alpha-amylases have also been created
 CC in order to increase enzyme stability. Note: According to the
 CC specification, the present sequence and the sequence shown in AAY99604
 CC are the same. (Updated on 12-SEP-2003 to standardise OS field)
 XX
 SQ Sequence 515 AA;

Query Match 100.0%; Score 2847; DB 3; Length 515;

Tue May 4 14:34:48 2004

us-10-644-187-6.rag

Page 4

Best Local Similarity 100.0%; Pred. No. 3.8e-245;
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAPFNGTMMQYFEMWLPDDGTLMTKVNANNNLSLIGTALMLPPAYKGSRSVDVGYV 60
D 1 AAPFNGTMMQYFEMWLPDDGTLMTKVNANNNLSLIGTALMLPPAYKGSRSVDVGYV 60
QY 61 DLYDLGEFNOGKTVRTKTKYKAQYLOAIQAHAAGMQUYADVDPHKGADGTEWDAVE 120
D 61 DLYDLGEFNOGKTVRTKTKYKAQYLOAIQAHAAGMQUYADVDPHKGADGTEWDAVE 120
QY 121 VNPSDRNOISGTYOIAQMTKFPFGKNTYSSFKKRWYHPGVMDSEKLSRIYKFRG 180
D 121 VNPSDRNOISGTYOIAQMTKFPFGKNTYSSFKKRWYHPGVMDSEKLSRIYKFRG 180
QY 181 IGRAMDEVDTENGNDYDLYADLMDHDEBVYTELKNMGKMYVNTNIDGFRDLAVKIK 240
D 181 IGRAMDEVDTENGNDYDLYADLMDHDEBVYTELKNMGKMYVNTNIDGFRDLAVKIK 240
QY 241 FSFPDMLSYVRSQTKPLFTVGEYWSYDINKLHNITKTGMSLFDAPLHNKRYTAS 300
D 241 FSFPDMLSYVRSQTKPLFTVGEYWSYDINKLHNITKTGMSLFDAPLHNKRYTAS 300
QY 241 FSFPDMLSYVRSQTKPLFTVGEYWSYDINKLHNITKTGMSLFDAPLHNKRYTAS 300
D 241 FSFPDMLSYVRSQTKPLFTVGEYWSYDINKLHNITKTGMSLFDAPLHNKRYTAS 300
QY 301 SGGAEDMRMTMTNLMKOPTLAVTFVNDHDEPQALQSVDWPFKPLAVAFILTRQEG 360
D 301 SGGAEDMRMTMTNLMKOPTLAVTFVNDHDEPQALQSVDWPFKPLAVAFILTRQEG 360
QY 361 YPCVFGDYDYGIPQYNIPSLKSKIDPLLIARDYAVGTHDYLDSHDIIGWTRGTEKP 420
D 361 YPCVFGDYDYGIPQYNIPSLKSKIDPLLIARDYAVGTHDYLDSHDIIGWTRGTEKP 420
QY 421 GSGLAALITDGPGGSKMYVKGKQAKVYDITGNRSDVTYVINSOGWGEFKNQGSVSW 480
D 421 GSGLAALITDGPGGSKMYVKGKQAKVYDITGNRSDVTYVINSOGWGEFKNQGSVSW 480
QY 481 VPKRTVSTIARPIITRPWTGEFVWTEPRLVAM 514
D 481 VPKRTVSTIARPIITRPWTGEFVWTEPRLVAM 514
RESULT 5
ID AA97547 standard; protein; 515 AA.
XX AA97547;
DT 11-SEP-2003 (revised)
DT 12-FEB-2001 (first entry)
XX B. steaerotherophilus termamyl-like alpha amylase.
XX Termamyl-like alpha-amylase; variant; starch liquefaction; fuel;
XX detergent composition; laundry cleaning composition; ethanol production;
XX dish washing cleaning composition; hard surface cleaning composition;
XX industrial ethanol production; textile desizing.
XX Geobacillus steaerotherophilus.
XX WO200060059-A2.
XX 12-OCT-2000.
XX 28-MAR-2000; 2000WO-DK000148.
XX 30-MAR-1999; 99DK-00000437.
XX (NOVO) NOVO NORDISK AS.
XX Andersen C, Jorgensen CT, Bisgard-Frantzen H, Svendsen A;
XX Kjaerulff S;
XX WPI: 2001-015656/02.
XX N-PSDB; AAA37851.

XX New variants of parent Termamyl-like alpha-amylase, useful in starch
PT liquefaction, in detergent compositions and in ethanol production,
PT exhibit altered cleavage pattern relative to the parent.
PS Claim 17; Page 69-70; 78pp; English.
XX This sequence represents a termamyl-like alpha amylase. The invention
CC relates to a variant (I) of parent termamyl-like alpha-amylase comprising
CC alteration at one or more of the positions W13, G48, T49, S50, Q51, A52,
CC D53, V54, G57, G107, G108, A111, S166 and M197. The alterations in (I)
CC are independently an insertion of an amino acid downstream of the amino
CC acid which occupies the position of deletion or substitution of the amino
CC acid which occupies the position with a different amino acid. The variant
CC has alpha-amylase activity, (I) or compositions containing it are useful
CC in starch liquefaction, in detergent compositions such as laundry, dish
CC washing and hard surface cleaning compositions, ethanol production, desizing of
CC textiles, fabrics or garments. (I) exhibits a reduced capability of
CC cleaving a substrate close to the branching point, and further exhibits
CC improved substrate specificity and/or improved specific activity relative
CC to the parent alpha-amylase. (updated on 11-SEP-2003 to standardise OS
CC field)
XX
XX . Sequence 515 AA;
XX
Query Match 100.0%; Score 2847; DB 4; Length 515;
Best Local Similarity 100.0%; Pred. No. 3.8e-245;
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAPFNGTMMQYFEMWLPDDGTLMTKVNANNNLSLIGTALMLPPAYKGSRSVDVGYV 60
D 1 AAPFNGTMMQYFEMWLPDDGTLMTKVNANNNLSLIGTALMLPPAYKGSRSVDVGYV 60
QY 61 DLYDLGEFNOGKTVRTKTKYKAQYLOAIQAHAAGMQUYADVDPHKGADGTEWDAVE 120
D 61 DLYDLGEFNOGKTVRTKTKYKAQYLOAIQAHAAGMQUYADVDPHKGADGTEWDAVE 120
QY 121 VNPSDRNOISGTYOIAQMTKFPFGKNTYSSFKKRWYHPGVMDSEKLSRIYKFRG 180
D 121 VNPSDRNOISGTYOIAQMTKFPFGKNTYSSFKKRWYHPGVMDSEKLSRIYKFRG 180
QY 181 IGRAMDEVDTENGNDYDLYADLMDHDEBVYTELKNMGKMYVNTNIDGFRDLAVKIK 240
D 181 IGRAMDEVDTENGNDYDLYADLMDHDEBVYTELKNMGKMYVNTNIDGFRDLAVKIK 240
QY 241 FSFPDMLSYVRSQTKPLFTVGEYWSYDINKLHNITKTGMSLFDAPLHNKRYTAS 300
D 241 FSFPDMLSYVRSQTKPLFTVGEYWSYDINKLHNITKTGMSLFDAPLHNKRYTAS 300
QY 301 SGGAEDMRMTMTNLMKOPTLAVTFVNDHDEPQALQSVDWPFKPLAVAFILTRQEG 360
D 301 SGGAEDMRMTMTNLMKOPTLAVTFVNDHDEPQALQSVDWPFKPLAVAFILTRQEG 360
QY 361 YPCVFGDYDYGIPQYNIPSLKSKIDPLLIARDYAVGTHDYLDSHDIIGWTRGTEKP 420
D 361 YPCVFGDYDYGIPQYNIPSLKSKIDPLLIARDYAVGTHDYLDSHDIIGWTRGTEKP 420
QY 421 GSGLAALITDGPGGSKMYVKGKQAKVYDITGNRSDVTYVINSOGWGEFKNQGSVSW 480
D 421 GSGLAALITDGPGGSKMYVKGKQAKVYDITGNRSDVTYVINSOGWGEFKNQGSVSW 480
QY 481 VPKRTVSTIARPIITRPWTGEFVWTEPRLVAM 514
D 481 VPKRTVSTIARPIITRPWTGEFVWTEPRLVAM 514
RESULT 6
ID ABB06935 standard; protein; 515 AA.
XX ABB06935;
XX ABB06935;

DT 29-AUG-2003 (revised)
 DT 19-JUN-2002 (first entry)
 XX
 XX B. stearothermophilus termamyl-like alpha-amylase protein SEQ ID NO:6.
 DE Bacillus; termamyl-like alpha-amylase; alpha-amylase; EC 3.2.1.1;
 KM variant; mutant; enzyme; protein co-ordinate data; cleaning; detergent;
 KM washing; sweetener; ethanol; starch.
 XX Geobacillus stearothermophilus.
 OS
 XX MO20016712-A2.
 XX 13-SEP-2001.
 PD
 XX 07-MAR-2001; 2001WO-DK000144.
 PF
 XX 08-MAR-2000; 2000DK-00000376.
 PR 15-MAR-2000; 2000US-0189857P.
 PR 23-FEB-2001; 2001DK-00000303.
 PR 26-FEB-2001; 2001US-0271382P.
 XX
 XX (NOVO) NOVOZYMES AS.
 PA
 XX Andersen C, Borchert TV, Nielsen BR;
 PI WPI; 2002-239612/29.
 DR N-PSDB; ABL50566.
 XX
 XX Novel variant of parent termamyl-like alpha-amylase useful as a component
 PT in washing and dishwashing compositions, for textile desizing, for starch
 PT liquefaction, and for producing sweeteners and ethanol from starch.
 XX
 PS Claim 8; Page 138-139; 153pp; English.
 XX
 XX The present invention describes a variant of a parent termamyl-like alpha
 CC -amylase (EC 3.2.1.1) (I) comprising an alteration at one or more
 CC positions of a group of 31 possible amino acid positions. The alteration
 CC in (I) may be at Arg28, Arg118, Arg174, Arg181, Gly182, Asp183, Gly184,
 CC Gly186, Trp189, Asn195, Met202, Tyr298, Asn299, Lys302, Ser303, Asn306,
 CC Arg310, Asn314, Arg320, His324, Gly345, Tyr396, Arg400, Trp439, Arg444,
 CC Asn445, Lys446, Glu449, Arg458, Asn471, or Asn484. (I) can be used for
 CC washing and/or dishwashing, textile desizing, and starch liquefaction.
 CC (I) is useful as a component in hard surface cleaning detergent
 CC composition, and for producing sweeteners and ethanol from starch. (I)
 CC has altered solubility, preferably increased solubility, in particular
 CC under washing, dish washing or hard surface cleaning conditions. The
 CC present sequence represents a Bacillus stearothermophilus termamyl-like
 CC alpha-amylase which is used in the exemplification of the present
 CC invention. (Updated on 29-AUG-2003 to standardise OS field)
 CC
 XX
 SQ Sequence 515 AA:
 Query Match 100.0%; Score 2847; DB 5; Length 515;
 Best Local Similarity 100.0%; Pred. No. 3,8e-245;
 Matches 515; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAPNGNTMOYFEWYLEDGGTLMTKVNENANNLSLGLTLMTPRAYKGSRDVGVGY 60
 DB 1 AAPNGNTMOYFEWYLEDGGTLMTKVNENANNLSLGLTLMTPRAYKGSRDVGVGY 60
 QY DLYDLGFNKGKGTATKTKGTAQVLAIOAAHAGMOVADVVDHKGADGTEWDAVE 120
 DB 61 DLYDLGFNKGKGTATKTKGTAQVLAIOAAHAGMOVADVVDHKGADGTEWDAVE 120
 QY 121 VNPSDRAQISGTYQIOAMTKFDPFGKNTYSSFKMWYHFDGDWDESKLSRIYKRG 180
 DB 121 VNPSDRAQISGTYQIOAMTKFDPFGKNTYSSFKMWYHFDGDWDESKLSRIYKRG 180
 QY 181 IGMAMDEVDTEENGVYDLAMADJDMHPEVTEELKMGKMYVNTTIDGFRLDVAVKIK 240
 DB 181 IGMAMDEVDTEENGVYDLAMADJDMHPEVTEELKMGKMYVNTTIDGFRLDVAVKIK 240

QY 241 FSPFEDMLSVRSQGTGKPLFTVGEYMSYDINKAHNTTKDGTMSLFDAPLHNKFTYAK 300
 DB 241 FSPFEDMLSVRSQGTGKPLFTVGEYMSYDINKAHNTTKDGTMSLFDAPLHNKFTYAK 300
 QY 301 SGGAFFDMRTIMTLMKDQPTLAVTFVDNHDTEPGALQSWDPWPKPLAVAFILTRQEG 360
 DB 301 SGGAFFDMRTIMTLMKDQPTLAVTFVDNHDTEPGALQSWDPWPKPLAVAFILTRQEG 360
 QY 361 YPCVFYDDYGIPOYNIPLSKIDPILLARRAYAGTODYLDHSDIIGMTSEGGTERK 420
 DB 361 YPCVFYDDYGIPOYNIPLSKIDPILLARRAYAGTODYLDHSDIIGMTSEGGTERK 420
 QY 421 GSGIALIITDGGGSKMYVQKQAGKVFYDLTGNSDPTVTINSDGGEFKVNGSSVSVM 480
 DB 421 GSGIALIITDGGGSKMYVQKQAGKVFYDLTGNSDPTVTINSDGGEFKVNGSSVSVM 480
 QY 481 VPKRTVSTIARPTTPWTGEPVWTEPRLVAM 514
 DB 481 VPKRTVSTIARPTTPWTGEPVWTEPRLVAM 514
 RESULT 7
 ID AAU12151 standard; protein: 515 AA.
 XX AAU12151;
 AC 29-AUG-2003 (revised)
 DT 09-APR-2002 (first entry)
 PT
 PT
 XX
 XX Bacillus TERMAMYL-like alpha-amylase BSG.
 DE
 XX TERMAMYL; alpha-amylase; detergent; dishwashing; textile desizing;
 KM starch liquefaction; ethanol production; hard surface cleaner; sweetener;
 KM amylopectin; limit dextrin; NOVAMYL; BSG.
 XX
 OS Geobacillus stearothermophilus.
 XX
 XX WO20018107-A2.
 XX 22-NOV-2001.
 PD 10-MAY-2001; 2001WO-DK00023.
 PF 12-MAY-2000; 2000DK-00000779.
 PR
 XX (NOVO) NOVOZYMES AS.
 PA Svendsen A, Jorgensen CT, Nielsen BR;
 PI WPI; 2002-106123/14.
 DR N-PSDB; AAS20024.
 DR
 XX
 XX New variant of parent Termamyl-like alpha-amylase for use as a component
 PT in washing and dishwashing compositions, for textile desizing, for starch
 PT liquefaction, and for producing sweeteners and ethanol from starch.
 PT
 XX
 XX Claim 5; Fig 1; 84pp; English.
 XX
 XX The invention relates to a variant of parent TERMAMYL-like alpha- amylase
 CC comprising an alteration at regions 186-193, 261-276, 283-293 or 334-339,
 CC or at position 234, where the variant has alpha-amylase activity and each
 CC position corresponds to a position of a parent Termamyl-like alpha-
 CC amylase sequence having a Bacillus licheniformis alpha-amylase sequence
 CC of 483 amino acids, given in specification. The variant alpha- amylase, a
 CC detergent additive, comprising the variant or a detergent composition
 CC comprising the variant, is useful for washing and/or dishwashing or
 CC textile desizing. The alpha-amylase is useful for starch liquefaction or
 CC ethanol production and as a component in a hard surface cleaning
 CC detergent composition, and for producing sweeteners from starch. The
 CC variant has altered alpha-1, 6-D-glucosidic branch linkage cleavage
 CC activity on amylopectin, preferably increased alpha-1, 6-D-glucosidic
 CC branch linkage cleavage activity of amylopectin or a limit dextrin

CC prepared by TERAMYL (RTM) or NOVAMYL (RTM). The present sequence is a
 CC natural variant of the TERAMYL alpha-amylase, BSG. (Updated on 29-AUG-
 CC 2003 to standardise OS field)

XX Sequence 515 AA;

Query Match 100.0%; Score 2847; DB 5; Length 515;
 Best Local Similarity 100.0%; Pred. No. 3.8e-245;
 Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC 1 AAFNGTMMQYFEMWLPDDGTLMTKANEANNLSLGTALMLPAYKGRSRSDVGYGY 60
 DB 1 AAFNGTMMQYFEMWLPDDGTLMTKANEANNLSLGTALMLPAYKGRSRSDVGYGY 60
 CC 61 DLYDGEFNQKGTVRTKGTAKOYLQAIQAHAAGMOYADVDFHKGADGTEWDAVE 120
 DB 61 DLYDGEFNQKGTVRTKGTAKOYLQAIQAHAAGMOYADVDFHKGADGTEWDAVE 120
 CC 121 VNPEDRNOEISGTYOIQAMTKFDFPGRGNTYSSFKRWYHFDGVDWDESRKLSRIYKFRG 180
 DB 121 VNPEDRNOEISGTYOIQAMTKFDFPGRGNTYSSFKRWYHFDGVDWDESRKLSRIYKFRG 180
 CC 181 IGRAMDWEVDTENGVNYLYMADLMDHPEVTELEKMGKRYVNTNIDGFRDLAVKHIK 240
 DB 181 IGRAMDWEVDTENGVNYLYMADLMDHPEVTELEKMGKRYVNTNIDGFRDLAVKHIK 240
 CC 241 FSPFPDMLSYRSQTKPLFTVGEWYSYDINKLHNYITKTGMSLFDAPLHNFYASK 300
 DB 241 FSPFPDMLSYRSQTKPLFTVGEWYSYDINKLHNYITKTGMSLFDAPLHNFYASK 300
 CC 301 SGGAFFMRRLMTNLTMKOQPLAVTFVDNHDTEPGALQSWDPMFKPLAVAFILTRQEG 360
 DB 301 SGGAFFMRRLMTNLTMKOQPLAVTFVDNHDTEPGALQSWDPMFKPLAVAFILTRQEG 360
 CC 361 YPCVFYGDYGIPOYNIPSLKSKIDPLIARRDYAVGTHDYLDHSDIIGWTRGTEKP 420
 DB 361 YPCVFYGDYGIPOYNIPSLKSKIDPLIARRDYAVGTHDYLDHSDIIGWTRGTEKP 420
 CC 421 GSGLAALITDPPGSKMYVKGQAKGVFDLTGNSDVTITNSDGMGEFKVNGSVSW 480
 DB 421 GSGLAALITDPPGSKMYVKGQAKGVFDLTGNSDVTITNSDGMGEFKVNGSVSW 480
 CC 481 VPKRTVSTIARPIITRPWTGEFVWTEPRLVAM 514
 DB 481 VPKRTVSTIARPIITRPWTGEFVWTEPRLVAM 514

RESULT 8

ID AAB47852 standard; protein; 515 AA.

XX AAB47852;

XX 29-AUG-2003 (revised)

XX 02-APR-2002 (first entry)

XX Bacillus alpha amylase BSG.

XX Alpha amylase; Bacillus; Teramyl-like; maltodextrin; glucose syrup;
 KW starch; food; feed; pharmaceutical; confectionery; candy; isotonic drink;
 KW bakery; cereal bar; ice cream; coffee whitener; salad dressing;
 KW cured meat; fermented meat; spice.

XX Geobacillus stearothermophilus.

XX MO200196537-A2.

XX 20-DEC-2001.

XX 13-JUN-2001; 2001WO-DK000404.

XX 14-JUN-2000; 2000DK-00000917.

XX 20-JUN-2000; 2000US-0212852P.

XX (NOVO) NOVOZYMES AS.
 PA Nielsen BR, Welbye M;
 XX WPI; 2002-098064/13.
 DR N-PSDB; AAI72213.
 DR
 XX New modified alpha-amylase derived from the genus Bacillus and/or is a
 PT Teramyl-like alpha-amylase, which has been pre-oxidized for producing
 PT maltodextrin or glucose syrup.
 PS Claim 5; Page 32-33; 47pp; English.

CC The sequences given in AAB47850-56 show modified alpha-amylases derived
 CC from the genus Bacillus. These alpha amylases are Teramyl-like alpha-
 CC amylase and they have been pre-oxidized. The alpha amylase is useful for
 CC producing a maltodextrin or glucose syrup, by treating starch with a pre-
 CC oxidized alpha-amylase until a product with a DE between 5-45 has been
 CC provided and/or until a product with a molecular weight of between 5-30
 CC kDa has been provided. The product comprises a maltodextrin with a DE of
 CC 18.5 and/or a maltodextrin with a molecular weight of 14-16 kDa. The
 CC alpha amylase is useful for producing a maltodextrin or glucose syrup,
 CC where the glucose syrup is useful as an ingredient in food, feed or
 CC pharmaceuticals. Glucose syrup is useful in confectionery such as
 CC candies, beverages such as isotonic drinks, bakery such as cereal bars,
 CC dairy and ice cream such as coffee whiteners, conventional foods such as
 CC salad dressings, and food ingredients and preparations such as cured
 CC meat, fermented meat, spices and seasoning encapsulated flavours.
 CC (Updated on 29-AUG-2003 to standardise OS field)

XX Sequence 515 AA;

Query Match 100.0%; Score 2847; DB 5; Length 515;
 Best Local Similarity 100.0%; Pred. No. 3.8e-245;
 Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC 1 AAFNGTMMQYFEMWLPDDGTLMTKANEANNLSLGTALMLPAYKGRSRSDVGYGY 60
 DB 1 AAFNGTMMQYFEMWLPDDGTLMTKANEANNLSLGTALMLPAYKGRSRSDVGYGY 60
 CC 61 DLYDGEFNQKGTVRTKGTAKOYLQAIQAHAAGMOYADVDFHKGADGTEWDAVE 120
 DB 61 DLYDGEFNQKGTVRTKGTAKOYLQAIQAHAAGMOYADVDFHKGADGTEWDAVE 120
 CC 121 VNPEDRNOEISGTYOIQAMTKFDFPGRGNTYSSFKRWYHFDGVDWDESRKLSRIYKFRG 180
 DB 121 VNPEDRNOEISGTYOIQAMTKFDFPGRGNTYSSFKRWYHFDGVDWDESRKLSRIYKFRG 180
 CC 181 IGRAMDWEVDTENGVNYLYMADLMDHPEVTELEKMGKRYVNTNIDGFRDLAVKHIK 240
 DB 181 IGRAMDWEVDTENGVNYLYMADLMDHPEVTELEKMGKRYVNTNIDGFRDLAVKHIK 240
 CC 241 FSPFPDMLSYRSQTKPLFTVGEWYSYDINKLHNYITKTGMSLFDAPLHNFYASK 300
 DB 241 FSPFPDMLSYRSQTKPLFTVGEWYSYDINKLHNYITKTGMSLFDAPLHNFYASK 300
 CC 301 SGGAFFMRRLMTNLTMKOQPLAVTFVDNHDTEPGALQSWDPMFKPLAVAFILTRQEG 360
 DB 301 SGGAFFMRRLMTNLTMKOQPLAVTFVDNHDTEPGALQSWDPMFKPLAVAFILTRQEG 360
 CC 361 YPCVFYGDYGIPOYNIPSLKSKIDPLIARRDYAVGTHDYLDHSDIIGWTRGTEKP 420
 DB 361 YPCVFYGDYGIPOYNIPSLKSKIDPLIARRDYAVGTHDYLDHSDIIGWTRGTEKP 420
 CC 421 GSGLAALITDPPGSKMYVKGQAKGVFDLTGNSDVTITNSDGMGEFKVNGSVSW 480
 DB 421 GSGLAALITDPPGSKMYVKGQAKGVFDLTGNSDVTITNSDGMGEFKVNGSVSW 480
 CC 481 VPKRTVSTIARPIITRPWTGEFVWTEPRLVAM 514
 DB 481 VPKRTVSTIARPIITRPWTGEFVWTEPRLVAM 514

RESULT 9
 ABB76588
 ID ABB76588 standard; protein; 515 AA.
 AC ABB76588;
 DT 29-AUG-2003 (revised)
 DT 19-AUG-2002 (first entry)
 DE Termamyl-like-alpha-amylase #3.
 XX Termamyl; alpha amylase; starch liquefaction; ethanol production;
 KW textile desizing; detergent; enzyme.
 OS Geobacillus stearothermophilus.
 XX
 PN WO200210355-A2.
 PD 07-FEB-2002.
 PF 12-JUL-2001; 2001WO-DK000488.
 PR 01-AUG-2000; 2000DK-00001160.
 PR 12-SEP-2000; 2000DK-00001354.
 PR 10-NOV-2000; 2000DK-00001887.
 PR 26-APR-2001; 2001DK-00000655.
 XX
 PA (NOVO) NOVOZYMES AS.
 PI Thisted T, Kjaerulf S, Andersen C, Englaug CC;
 DR WPI: 2002-28063/32.
 DR N-PSDB; ABL96209.
 XX
 PT Variant of parent Termamyl-like alpha amylase, useful in detergent
 PT compositions, for starch liquefaction, ethanol production, washing and/or
 PT dish washing, and textile desizing.
 PS Claim 4; Fig 5; 90pp; English.
 XX
 CC This invention relates to variants of a parent Termamyl-like alpha-
 CC amylases. These are used for starch liquefaction, ethanol production,
 CC detergent, and textile desizing. The amylases have altered stability,
 CC particularly at high temperatures from 70-120plusoc and low pH in the
 CC range from pH 4.0-6.0. The present sequence is a termamyl-like-alpha-
 CC amylase. (Updated on 29-AUG-2003 to standardise OS field)
 CC
 XX Sequence 515 AA.
 SO
 Query Match 100.0%; Score 2847; DB 5; Length 515;
 Best Local Similarity 100.0%; Pred. No. 3,8e-245;
 Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 301 SGGAFPMRLMTNTLMKQPTLAVTFVNDHDEPGQALQSWDPMFKPLAVAFILITOE 360
 DB 301 SGGAFPMRLMTNTLMKQPTLAVTFVNDHDEPGQALQSWDPMFKPLAVAFILITOE 360
 QY 361 YPCVFYGDYGGTPOVNIPELKSIDPLIARDVYVGTQHPDLBSPDILGTRGGTEKP 420
 DB 361 YPCVFYGDYGGTPOVNIPELKSIDPLIARDVYVGTQHPDLBSPDILGTRGGTEKP 420
 QY 421 GSGIALITDGGGSKMTVSGKQAHGKVPYDITGNRSUTVTIINSDGCEFFVNGGSVW 480
 DB 421 GSGIALITDGGGSKMTVSGKQAHGKVPYDITGNRSUTVTIINSDGCEFFVNGGSVW 480
 QY 481 VPKRTVSTIARPIITRPWTGSEFVWTEPRLVW 514
 DB 481 VPKRTVSTIARPIITRPWTGSEFVWTEPRLVW 514
 RESULT 10
 ABB03090
 ID ABB03090 standard; protein; 549 AA.
 AC ABB03090;
 DT 21-JAN-2003 (first entry)
 DE Alpha amylase polypeptide #51.
 XX
 KW Alpha amylase; enzyme; starch linkage hydrolysis; starch liquefaction;
 KW starch breakdown catalysts; textile desizing; lignocellulosic fibre;
 KW enzymatic de-linking; recycled paper; high-maltose syrup; dough;
 KW high glucose syrup; cornwet milling process; detergent; baking process;
 KW beverage; oil field; fuel ethanol; brewing process; scaling;
 XX starch modification.
 OS Unidentified.
 XX
 PN WO200268589-A2.
 PD 06-SEP-2002.
 PR 21-FEB-2002; 2002WO-US005068.
 PR 21-FEB-2001; 2001US-0270495P.
 PR 21-FEB-2001; 2001US-0270496P.
 PR 14-MAY-2001; 2001US-0291122P.
 XX
 PA (DIVE-) DIVERSA CORP.
 PI Callen W, Richardson T, Frey G;
 DR WPI: 2003-018656/01.
 DR N-PSDB; ABX08461.
 XX
 PT Novel purified polypeptide with alpha-amylase activity, useful e.g. for
 PT liquefying starch, for textile desizing, for creating lignocellulosic
 PT fibers, and for producing high-maltose or high-glucose syrup.
 PS Claim 30; Fig 16; 301pp; English.
 XX
 CC The invention relates to a purified polypeptide with alpha-amylase
 CC activity and the polynucleotide encoding it. The polypeptide is useful
 CC for hydrolyzing starch linkages, for catalyzing the breakdown of a
 CC starch, for modifying small molecules, for liquefying starch, for washing
 CC an object, for textile desizing, for creating lignocellulosic fibers, for
 CC improving fibre properties, for enzymatic de-linking of recycled paper
 CC pulp, for producing a high-maltose or high-glucose syrup or a mixed
 CC syrup, and for increasing the flow of production fluids from a
 CC subterranean formation by removing a viscous, starch-containing
 CC fluid formed during production operations and found within the
 CC subterranean formation which surrounds a completed well bore. The
 CC polypeptide is also useful for preparing a dough or a baked product
 CC prepared from the dough and in corn-wet milling processes, detergents,

CC baking processes, beverages, oil fields (fuel ethanol), brewing processes
 CC and starch modification in the paper and pulp industry, for removing
 CC starch containing strains from a material and for reducing staling of
 CC bakery products. Sequences AB003040-AB003144 represent alpha amylase
 CC polypeptides of the invention
 CC
 XX
 SQ Sequence 549 AA;
 Query Match 99.4%; Score 2829; DB 6; Length 549;
 Best Local Similarity 99.4%; Pred. No. 1.7e-243; Indels 0; Gaps 0;
 Matches 511; Conservative 2; Mismatches 1;
 QY 1 AAPENGIMQYFEWYLPDDGLMTKRVANEANNISLIGITALMLPAYKGTSRSDVGYGVY 60
 DB 35 AAPENGIMQYFEWYLPDDGLMTKRVANEANNISLIGITALMLPAYKGTSRSDVGYGVY 94
 QY 61 DLYDLGEFNQKGTARKTKYQAOYLQALQAHAAGMOYVADVDPHKGADGTEWDAVE 120
 DB 95 DLYDLGEFNQKGTARKTKYQAOYLQALQAHAAGMOYVADVDPHKGADGTEWDAVE 154
 QY 121 VNPSDRNOEISGTYOIQAMTKFDFPGRGNTYSSEFKRWYHFDGVWDSEKRLSRITYKFRG 180
 DB 155 VNPSDRNOEISGTYOIQAMTKFDFPGRGNTYSSEFKRWYHFDGVWDSEKRLSRITYKFRG 214
 QY 181 IGAAMDVEVDTEENGNDYDLMYADLDMHPEVYTELKMGKRYVNTTINDGFRDLDAVGHK 240
 DB 215 IGAAMDVEVDTEENGNDYDLMYADLDMHPEVYTELKMGKRYVNTTINDGFRDLDAVGHK 274
 QY 241 FSFFPDMLSYRSQTKPLFTVGEYWSYDINKLHNYITKEDGTMSLFADPLANKFYTASK 300
 DB 275 FSFFPDMLSYRSQTKPLFTVGEYWSYDINKLHNYITKEDGTMSLFADPLANKFYTASK 334
 QY 301 SGGAFDKRLMTNTLMKQOPTLAFTVDNHDTEBPQALQSWDPMFKPLAYAFILTRQEG 360
 DB 335 SGGAFDKRLMTNTLMKQOPTLAFTVDNHDTEBPQALQSWDPMFKPLAYAFILTRQEG 394
 QY 361 YPCVYGYDYGIPOYNIPSLKSKIDPLIARDVAYGTOHDYLDHSDIIGTRREGTEKP 420
 DB 395 YPCVYGYDYGIPOYNIPSLKSKIDPLIARDVAYGTOHDYLDHSDIIGTRREGTEKP 454
 QY 421 GSGLAALITDGPQSKMYVQKQAGKVFYDLTGNSDPTVTINSDDGCEFKVNGSVSVW 480
 DB 455 GSGLAALITDGPQSKMYVQKQAGKVFYDLTGNSDPTVTINSDDGCEFKVNGSVSVW 514
 QY 481 VPKRTTASTIARPIITRPMTGFEVWTEPRLVAV 514
 DB 515 VPKRTTASTIARPIITRPMTGFEVWTEPRLVAV 548
 RESULT 11
 AB003084
 ID AB003084 standard; protein; 549 AA.
 AC AB003084;
 XX
 XX 21-JAN-2003 (first entry)
 DE Alpha amylase polypeptide #45.
 XX
 XX Alpha amylase; enzyme; starch linkage hydrolysis; starch liquefaction;
 KM starch breakdown catalysts; textile desizing; lignocellulosic fibres;
 KM enzymatic de-linking; recycled paper; high-maltose syrup; dough;
 KM high glucose syrup; corn-wet milling process; detergent; baking process;
 KM beverage; oil field; fuel ethanol; brewing process; staling;
 KM starch modification.
 XX
 OS Unidentified.
 XX
 XX WO200268589-A2.
 XX
 PD 06-SEP-2002.
 XX
 PF 21-FEB-2002; 2002WO-US005068.

XX
 PR 21-FEB-2001; 2001US-0270495P.
 PR 21-FEB-2001; 2001US-0270496P.
 PR 14-MAY-2001; 2001US-0291122P.
 XX
 XX (DIVE-) DIVERSA CORP.
 PA Callen W, Richardson T, Frey G;
 PI
 XX
 DR WPI: 2003-018656/01.
 N-PSDB; ABX08455.
 XX
 PT Novel purified polypeptide with alpha-amylase activity, useful e.g. for
 PT liquefying starch, for textile desizing, for treating lignocellulosic
 PT fibers, and for producing high-maltose or high-glucose syrup.
 XX
 PS Claim 30; Fig 16; 301pp; English.
 XX
 CC The invention relates to a purified polypeptide with alpha-amylase
 CC activity and the polynucleotide encoding it. The polypeptide is useful
 CC for hydrolysing starch linkages, for catalysing the breakdown of a
 CC starch, for modifying small molecules, for liquefying starch, for washing
 CC an object for textile desizing, for treating lignocellulosic fibers, for
 CC improving fibre properties, for enzymatic de-linking of recycled paper
 CC pulp, for producing a high-maltose or high-glucose syrup or a mixed
 CC syrup, and for increasing the flow of production fluids from a
 CC substrate. The polypeptide is a viscous, starch-containing, damaging
 CC fluid formed during production operations and found within the
 CC substrate. The polypeptide is also useful for preparing a dough or a baked product
 CC prepared from the dough and in corn-wet milling processes, detergents,
 CC baking processes, beverages, oil fields (fuel ethanol), brewing processes
 CC and starch modification in the paper and pulp industry, for removing
 CC starch containing strains from a material and for reducing staling of
 CC bakery products. Sequences AB003040-AB003144 represent alpha amylase
 CC polypeptides of the invention
 CC
 XX
 SQ Sequence 549 AA;
 Query Match 99.2%; Score 2825; DB 6; Length 549;
 Best Local Similarity 99.4%; Pred. No. 3.9e-243; Indels 0; Gaps 0;
 Matches 511; Conservative 1; Mismatches 2;
 QY 1 AAPENGIMQYFEWYLPDDGLMTKRVANEANNISLIGITALMLPAYKGTSRSDVGYGVY 60
 DB 35 AAPENGIMQYFEWYLPDDGLMTKRVANEANNISLIGITALMLPAYKGTSRSDVGYGVY 94
 QY 61 DLYDLGEFNQKGTARKTKYQAOYLQALQAHAAGMOYVADVDPHKGADGTEWDAVE 120
 DB 95 DLYDLGEFNQKGTARKTKYQAOYLQALQAHAAGMOYVADVDPHKGADGTEWDAVE 154
 QY 121 VNPSDRNOEISGTYOIQAMTKFDFPGRGNTYSSEFKRWYHFDGVWDSEKRLSRITYKFRG 180
 DB 155 VNPSDRNOEISGTYOIQAMTKFDFPGRGNTYSSEFKRWYHFDGVWDSEKRLSRITYKFRG 214
 QY 181 IGAAMDVEVDTEENGNDYDLMYADLDMHPEVYTELKMGKRYVNTTINDGFRDLDAVGHK 240
 DB 215 IGAAMDVEVDTEENGNDYDLMYADLDMHPEVYTELKMGKRYVNTTINDGFRDLDAVGHK 274
 QY 241 FSFFPDMLSYRSQTKPLFTVGEYWSYDINKLHNYITKEDGTMSLFADPLANKFYTASK 300
 DB 275 FSFFPDMLSYRSQTKPLFTVGEYWSYDINKLHNYITKEDGTMSLFADPLANKFYTASK 334
 QY 301 SGGAFDKRLMTNTLMKQOPTLAFTVDNHDTEBPQALQSWDPMFKPLAYAFILTRQEG 360
 DB 335 SGGAFDKRLMTNTLMKQOPTLAFTVDNHDTEBPQALQSWDPMFKPLAYAFILTRQEG 394
 QY 361 YPCVYGYDYGIPOYNIPSLKSKIDPLIARDVAYGTOHDYLDHSDIIGTRREGTEKP 420
 DB 395 YPCVYGYDYGIPOYNIPSLKSKIDPLIARDVAYGTOHDYLDHSDIIGTRREGTEKP 454
 QY 421 GSGLAALITDGPQSKMYVQKQAGKVFYDLTGNSDPTVTINSDDGCEFKVNGSVSVW 480

Db 455 GGGAAALITDGGGSKMAYVGHAKGVFYDLTGNSDTVTINSDDGGEFKVNGSVSW 514

QY 481 VPRKTVSTIARPIITRPWTGEFVWTEPRLVAM 514

Db 515 VPRKTVSTIARPIITRPWTGEFVWTEPRLVAM 548

RESULT 12

AA70338

ID AAP70338 standard; protein; 549 AA.

XX AAP70338;

AC 24-OCT-2003 (revised)

DT 25-MAR-2003 (revised)

DT 12-MAR-1991 (first entry)

XX Alpha-amylase gene product.

DE Bacillus licheniformis.

XX

XX Geobacillus stearothermophilus.

XX

XX EP208491-A.

XX

XX 14-JAN-1987.

XX

XX 30-JUN-1986; 86EP-00305057.

XX

XX 03-JUL-1985; 85US-00752267.

XX

XX (GENEV) GENENCOR INC.

XX

XX Gray GL;

PI

XX WPI, 1987-009126/02.

DR N-PSDB; AAN70538.

XX

XX Hybrid DNA sequence prodn. - by forming a circular vector from 3 DNA

PT sequences and transforming a rec positive microorganism with the vector.

XX

XX

PS Disclosure; Fig 2; 54pp; English.

XX

XX A method is claimed for transforming a host with a recombinant Bacillus

CC alpha-amylase gene, made up of a steaothermophilus N-terminal and a

CC licheniformis C-terminal. The method involves constructing a plasmid with

CC a sequence separating the two terminals containing a unique restriction

CC site which may be cut allowing the plasmid to recombine. See also

CC AAN70539. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 24-

CC OCT-2003 to standardise OS field)

XX

XX Sequence 549 AA;

SQ

Query Match 98.4%; Score 2801; DB 1; Length 549;

Best Local Similarity 98.6%; Pred. No. 5.4e-241;

Matches 507; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 AAPFNCTMQYFWMYLPDDGTLMTKYANFANNLSLGTALMLPPAYKGTSSDVGYGY 60

Db 35 AAPFNCTMQYFWMYLPDDGTLMTKYANFANNLSLGTALMLPPAYKGTSSDVGYGY 94

QY 61 DLYDLGEFNQKGVTRTKYGTAKQYLOAIOAANAAGQYVADVFDHKGAGDGTEWDAVE 120

Db 95 DLYDLGEFNQKGVTRTKYGTAKQYLOAIOAANAAGQYVADVFDHKGAGDGTEWDAVE 154

QY 121 VAFSDNQEISGTGYIOAWTKPDPGRGNTYSSFKRWTHFDGVDWDESRKLSRIYKFRG 180

Db 155 VAFSDNQEISGTGYIOAWTKPDPGRGNTYSSFKRWTHFDGVDWDESRKLSRIYKFRG 214

QY 181 IGAAMDEVDTEGNTGYADLMDHPEVVTETLKNWGMVNTNIGFRLDAVKHIX 240

Db 215 IGAAMDEVDTEGNTGYADLMDHPEVVTETLKNWGMVNTNIGFRLDAVKHIX 274

QY 241 FSEFPDWLSYRSQOTKPLFTVGEVWSYDINKLANYITKTDGMSLFDAPLHNKFTASK 300

Db 275 FSEFPDWLSYRSQOTKPLFTVGEVWSYDINKLANYITKTDGMSLFDAPLHNKFTASK 334

QY 301 SGCAFDMRTMTMTLTKMDQPTLAVTEVDNHDTEFGQALQSWDPWPKPLAYAFILTRQSG 360

Db 335 SGCAFDMRTMTMTLTKMDQPTLAVTEVDNHDTEFGQALQSWDPWPKPLAYAFILTRQSG 394

QY 361 YPCVTFYGDYIGIPQNNIPSLKSKIDPELLARPDYAGTQHDYLDHSDITGMTRREGTEKP 420

Db 395 YPCVTFYGDYIGIPQNNIPSLKSKIDPELLARPDYAGTQHDYLDHSDITGMTRREGTEKP 454

QY 421 GSGLAALITDGGGSKMAYVGHAKGVFYDLTGNSDTVTINSDDGGEFKVNGSVSW 480

Db 455 GSGLAALITDGGGSKMAYVGHAKGVFYDLTGNSDTVTINSDDGGEFKVNGSVSW 514

QY 481 VPRKTVSTIARPIITRPWTGEFVWTEPRLVAM 514

Db 515 VPRKTVSTIARPIITRPWTGEFVWTEPRLVAM 548

RESULT 13

AA71295

ID AA71295 standard; protein; 514 AA.

XX AA71295;

XX

XX 16-OCT-2003 (revised)

DT 07-APR-1997 (first entry)

XX

XX Alpha-amylase.

XX

XX Alpha-amylase; detergent; thermal stability; oxidation stability; enzyme;

XX calcium ion dependency; alpha-amylolytic activity; washing composition;

XX textile desizing; papermaking; beer-making; ethanol production;

XX sweetener.

XX

XX Geobacillus stearothermophilus.

OS

XX WO9623873-A1.

XX

XX 08-AUG-1996.

XX

XX 05-FEB-1996; 96WO-DK000056.

XX

XX 03-FEB-1995; 95DK-00000126.

XX

XX 29-MAR-1995; 95DK-00000336.

XX

XX 29-SEP-1995; 95DK-00001097.

XX

XX 06-OCT-1995; 95DK-00001121.

XX

XX (NOVO) NOVO-NORDISK AS.

XX

XX Biesgaard-Frantzen H, Svendsen A, Borchert T;

PI

XX WPI, 1996-371423/37.

XX

XX Alpha-amylase variants - with improved thermal and oxidation stability

PT and reduced calcium ion dependency.

XX

XX Disclosure; Page 86-88; 11pp; English.

XX

XX AA71295, AA71296, AA71835 and AA71836 represent the parent alpha-

CC amylases used to create the variants of the invention (such as AA712098-

CC M1131). This sequence represents the alpha-amylase from Bacillus

CC stearothermophilus. The variants of the invention were created using site

CC directed, or random, mutagenesis of the DNA sequences encoding these

CC parent alpha-amylases. The variants of the invention can have improved

CC thermal stability (such as at temperatures in the range of 40-70 degrees

CC Celsius), and/or oxidation stability, and/or reduced calcium ion

CC dependency. The variants can also have increased alpha-amylolytic

CC activity (especially at pH values in the range of 8.5-10.5), and improved

CC binding of a particular substrate. The variant alpha-amylases also

CC possess improved specificity to a particular substrate, and/or improved

CC specificity with respect to cleavage of substrate. The variants can be
 CC used in detergent and washing compositions, and for textile desizing. The
 CC alpha-amylase variants can also be used in papermaking and beer-making
 CC processes. The variants of the invention can also be used in the
 CC production of sweeteners and ethanol from starch. (Updated on 16-OCT-2003
 CC to standardise OS field)

XX Sequence 514 AA;

Query Match 97.6%; Score 2780; DB 2; Length 514;
 Best Local Similarity 98.1%; Pred. No. 3.7e-239;
 Matches 504; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 AAPFNGTMQYFEMWLPDDGTLMTKVNANLSSIGITALLPAPAYKTSRSDVGYGY 60
 DB 1 AAPFNGTMQYFEMWLPDDGTLMTKVNANLSSIGITALLPAPAYKTSRSDVGYGY 60
 QY 61 DLYDLGEFNQKGVTRTKYGTAKYLOAIQAAHAGQYADVDPHKGADGTEWDAVE 120
 DB 61 DLYDLGEFNQKGVTRTKYGTAKYLOAIQAAHAGQYADVDPHKGADGTEWDAVE 120
 QY 121 VNPSDRNOEISGTYOIOAWTKPDPGRGNTYSSFKRWYHPFGVWDESRKLSRIYKFRG 180
 DB 121 VNPSDRNOEISGTYOIOAWTKPDPGRGNTYSSFKRWYHPFGVWDESRKLSRIYKFRG 180
 QY 181 IGRAMDWEVDTENGNVDYLMYADLDMDEPVEVTELSKMGKMYNTNIDGFRDAVKHIX 240
 DB 181 IGRAMDWEVDTENGNVDYLMYADLDMDEPVEVTELSKMGKMYNTNIDGFRDAVKHIX 240
 QY 241 FSPFPDWLSYVSQSGKPLFTVGEYMSYDINKLHNYITKTDGMSLFDAPLHNKFTYASK 300
 DB 241 FSPFPDWLSYVSQSGKPLFTVGEYMSYDINKLHNYITKTDGMSLFDAPLHNKFTYASK 300
 QY 301 SGGAFDMRTIMNTNLTLMKQPTLAVTFVDNHDTEPGALQSWDPMFKPLAFAFILTROEG 360
 DB 301 SGGAFDMRTIMNTNLTLMKQPTLAVTFVDNHDTEPGALQSWDPMFKPLAFAFILTROEG 360
 QY 361 YPCVFGDYGYGIPQVNIPLSKKIDPILLARBYAGTQHDYLDHSDIIGWTRREGVTEKP 420
 DB 361 YPCVFGDYGYGIPQVNIPLSKKIDPILLARBYAGTQHDYLDHSDIIGWTRREGVTEKP 420
 QY 421 GSGIALIITDGPQSGKMYVKGQAHGKVYDITGNRSDVTYINSDGWGEFKVNGGSVSW 480
 DB 421 GSGIALIITDGPQSGKMYVKGQAHGKVYDITGNRSDVTYINSDGWGEFKVNGGSVSW 480
 QY 481 VPRKTVSTIARPIITRPWTGEFVRWTEPRLVAM 514
 DB 481 VPRKTVSTIARPIITRPWTGEFVRWTEPRLVAM 514

RESULT 14

AA15417
 ID AA15417 standard; protein; 514 AA.

AC AA15417;

DT 17-OCT-2003 (revised)
 DT 22-JUL-1999 (first entry)

DE Bacillus stearothermophilus alpha-amylase protein.

XX Termamyl-like; alpha-amylase; variant; washing; dishwashing; production;
 KW sweetener; ethanol; starch; textile desizing; starch liquefaction;
 XX saccharification process.

OS Geobacillus stearothermophilus.

FN WO9923211-A1.

PD 14-MAY-1999.

PF 30-OCT-1998; 98WO-DK000471.

XX

PR 30-OCT-1997; 97DK-00001240.
 PR 14-JUL-1998; 98DK-00000936.
 PA (NOVO) NOVO-NORDISK AS.
 XX Borchert TV, Svendsen A, Andersen C, Nielsen BR, Nissen TL;
 PI Kjaerulff S;
 DR WPI; 1998-326987/27.
 XX
 PT New Termamyl-like alpha-amylase variants.
 PS Claim 38; Page 81-82; 115pp; English.

XX The specification describes termamyl-like alpha-amylase variants that
 CC have altered amino acid sequences to improve properties. The variants are
 CC produced by creating one or more of the following mutations in amino acid
 CC sequence of the parent termamyl-like alpha-amylase: T141, K142, F143,
 CC D144, F145, P146, G147, R148, G149, Q174, R181, G182, D183, Q184, K185,
 CC A186, W189, S193, N195, H107, K108, G109, D166, W167, D168, Q169, S170,
 CC R171, Q172, F173, F268, K268, N270, D271, L272, G273, A274, L275,
 CC K311, E346, K385, G456, W457, K458, P459, G460, T461, V462, T463. The
 CC variants can be used for washing and/or dishwashing. They can also be
 CC used in the production of sweeteners and ethanol from starch, and/or for
 CC textile desizing, and in starch liquefaction and/or saccharification
 CC processes. The present amylase can function as the parent sequence in the
 CC production of the variants of the invention. (Updated on 17-OCT-2003 to
 CC standardise OS field)

SO Sequence 514 AA;

Query Match 97.6%; Score 2780; DB 2; Length 514;
 Best Local Similarity 98.1%; Pred. No. 3.7e-239;
 Matches 504; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 AAPFNGTMQYFEMWLPDDGTLMTKVNANLSSIGITALLPAPAYKTSRSDVGYGY 60
 DB 1 AAPFNGTMQYFEMWLPDDGTLMTKVNANLSSIGITALLPAPAYKTSRSDVGYGY 60
 QY 61 DLYDLGEFNQKGVTRTKYGTAKYLOAIQAAHAGQYADVDPHKGADGTEWDAVE 120
 DB 61 DLYDLGEFNQKGVTRTKYGTAKYLOAIQAAHAGQYADVDPHKGADGTEWDAVE 120
 QY 121 VNPSDRNOEISGTYOIOAWTKPDPGRGNTYSSFKRWYHPFGVWDESRKLSRIYKFRG 180
 DB 121 VNPSDRNOEISGTYOIOAWTKPDPGRGNTYSSFKRWYHPFGVWDESRKLSRIYKFRG 180
 QY 181 IGRAMDWEVDTENGNVDYLMYADLDMDEPVEVTELSKMGKMYNTNIDGFRDAVKHIX 240
 DB 181 IGRAMDWEVDTENGNVDYLMYADLDMDEPVEVTELSKMGKMYNTNIDGFRDAVKHIX 240
 QY 241 FSPFPDWLSYVSQSGKPLFTVGEYMSYDINKLHNYITKTDGMSLFDAPLHNKFTYASK 300
 DB 241 FSPFPDWLSYVSQSGKPLFTVGEYMSYDINKLHNYITKTDGMSLFDAPLHNKFTYASK 300
 QY 301 SGGAFDMRTIMNTNLTLMKQPTLAVTFVDNHDTEPGALQSWDPMFKPLAFAFILTROEG 360
 DB 301 SGGAFDMRTIMNTNLTLMKQPTLAVTFVDNHDTEPGALQSWDPMFKPLAFAFILTROEG 360
 QY 361 YPCVFGDYGYGIPQVNIPLSKKIDPILLARBYAGTQHDYLDHSDIIGWTRREGVTEKP 420
 DB 361 YPCVFGDYGYGIPQVNIPLSKKIDPILLARBYAGTQHDYLDHSDIIGWTRREGVTEKP 420
 QY 421 GSGIALIITDGPQSGKMYVKGQAHGKVYDITGNRSDVTYINSDGWGEFKVNGGSVSW 480
 DB 421 GSGIALIITDGPQSGKMYVKGQAHGKVYDITGNRSDVTYINSDGWGEFKVNGGSVSW 480
 QY 481 VPRKTVSTIARPIITRPWTGEFVRWTEPRLVAM 514
 DB 481 VPRKTVSTIARPIITRPWTGEFVRWTEPRLVAM 514

RESULT 15

GenCore version 5.1.6
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CM protein - protein search, using sw model

Run on: May 3, 2004, 20:34:58 ; Search time 48.7475 Seconds

(without alignments)
2782.151 Million cell updates/sec

Title: US-10-644-187-4

Perfect score: 2624
Sequence: 1 VNGTLNQYFEWYTPNDQHW.....KIGSDGGEFHVNDGSVSIY 480

Scoring table:

BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: A_Geneseq_29Jan04:*

- 1: geneseqp1960s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2624	100.0	480	2 AAR78268	Aar78268 Bacillus
2	2624	100.0	480	2 AAR78268	Aar78268 Bacillus
3	2624	100.0	480	2 AAR78268	Aar78268 Bacillus
4	2624	100.0	480	2 AAR78268	Aar78268 Bacillus
5	2624	100.0	480	2 AAR78268	Aar78268 Bacillus
6	2624	100.0	480	2 AAR78268	Aar78268 Bacillus
7	2624	100.0	480	2 AAR78268	Aar78268 Bacillus
8	2624	100.0	480	2 AAR78268	Aar78268 Bacillus
9	2624	100.0	480	2 AAR78268	Aar78268 Bacillus
10	2624	100.0	480	2 AAR78268	Aar78268 Bacillus
11	2624	100.0	480	2 AAR78268	Aar78268 Bacillus
12	2624	100.0	480	2 AAR78268	Aar78268 Bacillus
13	2624	100.0	480	2 AAR78268	Aar78268 Bacillus
14	2624	100.0	480	2 AAR78268	Aar78268 Bacillus
15	2624	100.0	480	2 AAR78268	Aar78268 Bacillus
16	2624	100.0	480	2 AAR78268	Aar78268 Bacillus
17	2624	100.0	480	2 AAR78268	Aar78268 Bacillus
18	2624	100.0	480	2 AAR78268	Aar78268 Bacillus
19	2624	100.0	480	2 AAR78268	Aar78268 Bacillus
20	2624	100.0	480	2 AAR78268	Aar78268 Bacillus
21	2624	100.0	480	2 AAR78268	Aar78268 Bacillus
22	2624	100.0	480	2 AAR78268	Aar78268 Bacillus
23	2624	100.0	480	2 AAR78268	Aar78268 Bacillus
24	2624	100.0	480	2 AAR78268	Aar78268 Bacillus
25	2624	100.0	480	2 AAR78268	Aar78268 Bacillus

26	2600	99.1	480	3 AAY99771	Aay99771 Bacillus
27	2584	98.5	483	6 ABP60493	Abp60493 Bacillus
28	2559	97.5	485	6 ABP60492	Abp60492 Bacillus
29	2427	92.5	483	6 ABP60492	Abp60492 Bacillus
30	2330	88.8	483	6 ABP60495	Abp60495 Bacillus
31	2279	86.9	481	6 ABP60491	Abp60491 Bacillus
32	2244	85.5	481	6 ABP60490	Abp60490 Bacillus
33	2214	84.4	481	6 ABP60489	Abp60489 Bacillus
34	2202	83.9	483	2 AAW57979	Aaw57979 Bacillus
35	2202	83.8	482	4 AAW57952	Aaw57952 Bacillus
36	2200	83.8	483	2 AAW57975	Aaw57975 Bacillus
37	2200	83.8	512	4 AAW57956	Aaw57956 Bacillus
38	2199	83.8	483	2 AAW57976	Aaw57976 Bacillus
39	2199	83.8	483	2 AAW57978	Aaw57978 Bacillus
40	2199	83.8	512	4 AAW57954	Aaw57954 Bacillus
41	2197	83.7	483	2 AAW57971	Aaw57971 Bacillus
42	2197	83.7	483	2 AAW57981	Aaw57981 Bacillus
43	2197	83.7	483	2 AAW57973	Aaw57973 Bacillus
44	2197	83.7	483	2 AAW57973	Aaw57973 Bacillus
45	2197	83.7	512	4 AAW57951	Aaw57951 Bacillus

ALIGNMENTS

RESULT 1

ID AAR78268 standard; protein; 480 AA.

XX AAR78268;

DT 17-JAN-1996 (first entry)

XX Bacillus amyloliquefaciens alpha amylase (mature protein).

XX Alpha amylase; oxidation; desizing; bleaching; scouring; fabric; starch;

KW thermostable; methionine; Bacillus licheniformis;

KM Bacillus amyloliquefaciens; Bacillus stearothermophilus.

XX Bacillus amyloliquefaciens.

XX W05521247-A1.

XX 10-AUG-1995.

XX 05-OCT-1994; 94MO-DK000371.

XX 02-FEB-1994; 94DK-00000141.

XX (NOVO) NOVO-NORDISK AS.

XX Toft AH, Marcher D, Pedersen HH, Nilsson TE;

XX WPI; 1995-283767/37.

XX N-PSDB; AAC95032.

XX Use of an oxidation stable alpha-amylase - for simultaneous desizing and

XX bleaching or scouring of fabrics contg. starch or starch derive.

XX Claim 7, Page 24, 37pp; English.

XX Oxidation stable alpha amylases can be used for the simultaneous desizing

XX and bleaching or scouring of a fabric comprising starch or starch

XX derivatives. They exhibit a better heat stability, especially in the

XX presence of oxidizing agents. They are obtained from a parent alpha

XX amylase by replacing one or more methionine residues with any amino acid

XX different from Cys or Met, preferably Leu, Thr, Ala, Gly, Ser, Ile or

XX Asp. The parent alpha amylase is derived from a Bacillus species. This

XX sequence is the wild type (unmodified) alpha amylase

XX Sequence 480 AA;

XX Query Match 100.0%; Score 2624; DB 2; Length 480;

DR WPI; 1996-371424/37.

XX Alpha-amylase variants and methods of production - have altered
PT properties such as calcium dependency, substrate binding and stability.
XX

PS Disclosure; Page 86; 177pp; English.

XX The present sequence is the mature *Bacillus amyloliquefaciens* alpha-
CC amylase (A). Variants of parent termamyl-like alpha-amylases (and methods
CC of constructing them) are claimed. Examples of variants are featured
CC above. At least one of the amino acids of the parent, which is present in
CC a fragment identified above, is/are deleted or replaced with one or more
CC residues, which is/are present in a fragment corresponding to a fragment
CC of AAM14500 (*Aspergillus oryzae* fungamyl alpha-amylase). The variants
CC have altered properties such as calcium dependency, substrate binding and
CC stability. Also one or more proline or cysteine residues in the variant
CC is modified or replaced with a non-proline or non-cysteine residue such as
CC alanine. The variants can be used for (dish)washing, as detergent
CC additives or for fabric desizing or starch liquefaction. They can also be
CC used for the production of sweeteners and ethanol from starch. See also
CC AAM14498 and AAM14500
CC

XX Sequence 480 AA;

Query Match 100.0%; Score 2624; DB 2; Length 480;
Best Local Similarity 100.0%; Pred. No. 8.1e-218;

Matches 480; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 VNGTLMOYFEWYTPNDGQHWKRLQNDAEHLSDIGITAWIPPAKYKLSQSDNGYGPYDLY 60

1 VNGTLMOYFEWYTPNDGQHWKRLQNDAEHLSDIGITAWIPPAKYKLSQSDNGYGPYDLY 60

61 DLGEFOQKGTAVTKYKGTSELQDAIGSLHRSRVQYGVVYLNHKGADATEDVTAVERN 120

61 DLGEFOQKGTAVTKYKGTSELQDAIGSLHRSRVQYGVVYLNHKGADATEDVTAVERN 120

121 ANRNOETSEBYQIKAWTDFRPPRGNTYSDFKMHWYHFDGADWDSRKISRIKFRGECK 180

121 ANRNOETSEBYQIKAWTDFRPPRGNTYSDFKMHWYHFDGADWDSRKISRIKFRGECK 180

181 AMDWVSSENGNDYLYAVDVYDHPDVVAETKKMGWYANELSLDGFRIIDAKHIKFSF 240

181 AMDWVSSENGNDYLYAVDVYDHPDVVAETKKMGWYANELSLDGFRIIDAKHIKFSF 240

241 LRDWVAVRQATGKEMFTVAEYQWNNAGKLENTYLNKTSFNQSVFDPVPLHFNLOAASQGG 300

241 LRDWVAVRQATGKEMFTVAEYQWNNAGKLENTYLNKTSFNQSVFDPVPLHFNLOAASQGG 300

301 GYDMRRLDGTIVSRHPEKAVTFVENHDTQPGQSLSTVQVTFKPLAFAFILTRESGYPO 360

301 GYDMRRLDGTIVSRHPEKAVTFVENHDTQPGQSLSTVQVTFKPLAFAFILTRESGYPO 360

361 VFYGDWYGTGTSPEKIPSLKDNIEPILKARKEVAVGPQHDYIDHPDVIGWTRGDSAA 420

361 VFYGDWYGTGTSPEKIPSLKDNIEPILKARKEVAVGPQHDYIDHPDVIGWTRGDSAA 420

421 KSGIALALITDGPQSKMYAGLKNAGETWDTIGNRSDTYKISDQWGEFHVNDGSVSIY 480

421 KSGIALALITDGPQSKMYAGLKNAGETWDTIGNRSDTYKISDQWGEFHVNDGSVSIY 480

RESULT 3

AA15419 standard; protein; 480 AA.

XX AA15419;

XX 22-JUL-1999 (first entry)

DE *Bacillus amyloliquefaciens* alpha-amylase protein.

XX Termamyl-like; alpha-amylase; variant; washing; dishwashing; production;
KW sweetener; ethanol; starch; textile desizing; starch liquefaction;

KM saccharification process.

OS *Bacillus amyloliquefaciens*.

XX WO9923211-A1.

XX 14-MAY-1999.

XX 30-OCT-1998; 98WO-DK000471.

XX 30-OCT-1997; 97DK-00001240.

XX 14-JUL-1998; 98DK-00000936.

XX (NOVO) NOVO-NORDISK AS.

XX Borchert TV, Svendsen A, Andersen C, Nielsen BR, Nissen TL;

XX Kjaerulf S;

XX WPI; 1999-326987/27.

XX New Termamyl-like alpha-amylase variants.

XX Claim 38; Page 84-86; 115pp; English.

XX The specification describes termamyl-like alpha-amylase variants that
CC have altered amino acid sequences to improve properties. The variants are
CC produced by creating one or more of the following mutations in amino acid
CC sequence of the parent termamyl-like alpha-amylase: T141, K142, F143,
CC D144, F145, P146, G147, R148, Q174, R181, G182, D183, G184, K185,
CC A186, W189, S193, N195, H107, K108, G109, D167, D168, Q169, S170,
CC R171, Q172, F173, F267, W268, K269, N270, D271, L272, G272, A274, L275,
CC K311, E346, K385, G456, N457, K458, P459, G460, T461, V462, T463. The
CC variants can be used for washing and/or dishwashing. They can also be
CC used in the production of sweeteners and ethanol from starch, and/or for
CC textile desizing, and in starch liquefaction and/or saccharification
CC processes. The present amylase can function as the parent sequence in the
CC production of the variants of the invention
CC

XX Sequence 480 AA;

Query Match 100.0%; Score 2624; DB 2; Length 480;
Best Local Similarity 100.0%; Pred. No. 8.1e-218;

Matches 480; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 VNGTLMOYFEWYTPNDGQHWKRLQNDAEHLSDIGITAWIPPAKYKLSQSDNGYGPYDLY 60

1 VNGTLMOYFEWYTPNDGQHWKRLQNDAEHLSDIGITAWIPPAKYKLSQSDNGYGPYDLY 60

61 DLGEFOQKGTAVTKYKGTSELQDAIGSLHRSRVQYGVVYLNHKGADATEDVTAVERN 120

61 DLGEFOQKGTAVTKYKGTSELQDAIGSLHRSRVQYGVVYLNHKGADATEDVTAVERN 120

121 ANRNOETSEBYQIKAWTDFRPPRGNTYSDFKMHWYHFDGADWDSRKISRIKFRGECK 180

121 ANRNOETSEBYQIKAWTDFRPPRGNTYSDFKMHWYHFDGADWDSRKISRIKFRGECK 180

181 AMDWVSSENGNDYLYAVDVYDHPDVVAETKKMGWYANELSLDGFRIIDAKHIKFSF 240

181 AMDWVSSENGNDYLYAVDVYDHPDVVAETKKMGWYANELSLDGFRIIDAKHIKFSF 240

241 LRDWVAVRQATGKEMFTVAEYQWNNAGKLENTYLNKTSFNQSVFDPVPLHFNLOAASQGG 300

241 LRDWVAVRQATGKEMFTVAEYQWNNAGKLENTYLNKTSFNQSVFDPVPLHFNLOAASQGG 300

301 GYDMRRLDGTIVSRHPEKAVTFVENHDTQPGQSLSTVQVTFKPLAFAFILTRESGYPO 360

301 GYDMRRLDGTIVSRHPEKAVTFVENHDTQPGQSLSTVQVTFKPLAFAFILTRESGYPO 360

361 VFYGDWYGTGTSPEKIPSLKDNIEPILKARKEVAVGPQHDYIDHPDVIGWTRGDSAA 420

361 VFYGDWYGTGTSPEKIPSLKDNIEPILKARKEVAVGPQHDYIDHPDVIGWTRGDSAA 420

421 KSGIALALITDGPQSKMYAGLKNAGETWDTIGNRSDTYKISDQWGEFHVNDGSVSIY 480

421 KSGIALALITDGPQSKMYAGLKNAGETWDTIGNRSDTYKISDQWGEFHVNDGSVSIY 480

Db 421 KSGLAALITDPGSGSKMYAGLKNAGETWYDITGNRSDTYKISGDGGEFHVNDGSVSIY 480

RESULT 4

AA07385
ID AA07385 standard; protein; 480 AA.

AA07385;
AC

DT 16-JUN-1999 (first entry)

DE Wild type Termamyl(RTM)-like alpha-amylase protein #5.

XX Variant; Termamyl; alpha-amylase; mutation; Bacillus; detergent;
KW dishwashing; laundry; textile; desizing; starch liquefaction; sweetener;
KM ethanol.

XX Bacillus sp.

OS Key Location/Qualifiers

FT Misc-difference 176, 179 /note= "optionally 1, 2, 3 or all residues are deleted"

FT Misc-difference 190 /note= "optionally altered to any amino acid except an

FT Misc-difference 201 /note= "optionally altered to any amino acid except a Val

FT Misc-difference 207 /note= "optionally altered to any amino acid except a

FT Misc-difference 211 /note= "optionally altered to any amino acid except a Glu

FT Misc-difference 264 /note= "optionally altered to any amino acid except a Glu

FT residue" /note= "optionally altered to any amino acid except a Glu

XX WO9919467-A1.

XX 22-APR-1999.

XX 13-OCT-1998; 98WO-DK000444.

XX 13-OCT-1997; 97DK-00001172.

XX (NOVO) NOVO-NORDISK AS.

XX Svendsen A, Borchert TV, Bisgard-Frantzen H;

XX MPI; 1999-277632/23.

XX Variant alpha-amylases - useful as detergents or for textile desizing or

XX starch liquefaction.

XX Claim 1; Page 69-70; 93pp; English.

XX This sequence represents the parent sequence for new variants of a parent
CC Termamyl-like alpha-amylase with alpha-amylase activity. The variants
CC comprise mutations in 2-6 regions/positions relative to an alpha-amylase
CC from either of two Bacillus species in WO9526397, B. stearothermophilus,
CC B. licheniformis, B. amyloliquefaciens or Bacillus sp. #707. The alpha-
CC amylase variants are detergent additives for use in detergents for
CC dishwashing, manual or automatic laundry. The variants can also be used
CC for textile desizing or starch liquefaction (e.g. for production of
CC sweeteners or ethanol).

XX Sequence 480 AA;

Query Match 100.0%; Score 2624; DB 2; Length 480;
Best Local Similarity 100.0%; Pred. No. 8, 1e-216; Indels 0; Gaps 0;
Matches 480; Conservative 0; Mismatches 0;

QY 1 VNGTLMQFFEWYTPNDGQHWKRLQNDAEHLSDIGITAWIIPPAYKGLSQSDNGYGPYDLY 60
Db 1 VNGTLMQFFEWYTPNDGQHWKRLQNDAEHLSDIGITAWIIPPAYKGLSQSDNGYGPYDLY 60

QY 61 DIGEFQOQGVTRTKYKTSSELDQAIIGSLHSNNVQYGVDTLNRKAGADATEDVAVENP 120
Db 61 DIGEFQOQGVTRTKYKTSSELDQAIIGSLHSNNVQYGVDTLNRKAGADATEDVAVENP 120

QY 121 ANRQETSESEYQIKAWTDFRFPGRGNTYSDPKMWYHFDGADMDSEKRSIIFKRGEGK 180
Db 121 ANRQETSESEYQIKAWTDFRFPGRGNTYSDPKMWYHFDGADMDSEKRSIIFKRGEGK 180

QY 181 AMDWEVSSSENGYDYLMAVDYDHPDVAAETKKWGIYANESLDDGRIDAAKHIFSF 240
Db 181 AMDWEVSSSENGYDYLMAVDYDHPDVAAETKKWGIYANESLDDGRIDAAKHIFSF 240

QY 241 LRDWTQAVRQATGKMFVVAEYQWNNAGKLENYLNKTSFNQSVDFVPLHFNILQAASQGG 300
Db 241 LRDWTQAVRQATGKMFVVAEYQWNNAGKLENYLNKTSFNQSVDFVPLHFNILQAASQGG 300

QY 301 GYDWERLLDGVVSSHPEKAVTFVENHDTQPGQSLSESTVQTFWFLAFAFLTRBSGTPQ 360
Db 301 GYDWERLLDGVVSSHPEKAVTFVENHDTQPGQSLSESTVQTFWFLAFAFLTRBSGTPQ 360

QY 361 VFGYDWTGKTSPEKIPSLKONIEPILKAREYVGPQHDYIDHPVIGWTRBSGSA 420
Db 361 VFGYDWTGKTSPEKIPSLKONIEPILKAREYVGPQHDYIDHPVIGWTRBSGSA 420

QY 421 KSGLAALITDPGSGSKMYAGLKNAGETWYDITGNRSDTYKISGDGGEFHVNDGSVSIY 480
Db 421 KSGLAALITDPGSGSKMYAGLKNAGETWYDITGNRSDTYKISGDGGEFHVNDGSVSIY 480

RESULT 5
AA099606
ID AA099606 standard; protein; 480 AA.

XX AA099606;

XX 04-SEP-2000 (first entry)

XX Bacillus amyloliquefaciens Termamyl-like alpha-amylase.

XX Bacillus; alpha-amylase; washing; textile desizing; starch liquefaction;
KW saccharification; mutain; mutant; enzyme stability; hybrid.

XX Bacillus amyloliquefaciens.

XX WO200029560-A1.

XX 25-MAY-2000.

XX 16-NOV-1999; 99WO-DK000628.

XX 16-NOV-1998; 98DK-00001495.

XX (NOVO) NOVO-NORDISK AS.

XX Svendsen A, Kjaerulff S, Bisgard-Frantzen H, Andersen C;

XX MPI; 2000-38777/33.

XX N-PSDB; AAA46484.

XX Variant of parent termamyl-like alpha amylase useful for washing, textile
PT desizing and starch liquefaction, comprising alterations in one or more
PT solvent exposed amino acid residues.

XX Claim 8; Page 59-60; 80pp; English.
XX The present sequence is a parent alpha-amylase from which mutants with
CC increased stability at acidic pH, low calcium concentration and high
CC temperatures have been derived. The sequence encoding this enzyme was

CC Isolated from a *Bacillus amyloliquefaciens* genomic DNA library. A variant
CC may contain mutations in one or more solvent exposed amino acid residues
CC to increase the overall hydrophobicity of the enzyme or the overall
CC number of methyl groups in the side chains of exposed residues may be
CC increased. The mutations can be incorporated by site-directed mutagenesis
CC or by random mutagenesis. As a result of their increased stability, the
CC variants are suitable for the industrial processing of starch, i.e.
CC starch liquefaction and saccharification. They may also be useful for
CC washing, dishwashing and textile desizing. Hybrid alpha-amylases
CC comprising partial amino acid sequences derived from two or more alpha-
CC amylases have also been created in order to increase enzyme stability
XX

SQ Sequence 480 AA;

Query Match 100.0%; Score 2624; DB 3; Length 480;
Best Local Similarity 100.0%; Pred. No. 8,1e-218;
Matches 480; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNGTLMQYFEMWTPNDGQHWKRLQNDAEHLSDIGITAWIPPAVKGLSGSDNGYGPYDLY 60
DB 1 VNGTLMQYFEMWTPNDGQHWKRLQNDAEHLSDIGITAWIPPAVKGLSGSDNGYGPYDLY 60
QY 61 DLGEFOQKGTVRKTKGTSKSELQDAGSLHSRNQVYGVVLANHKAQADATEDVTAVERN 120
DB 61 DLGEFOQKGTVRKTKGTSKSELQDAGSLHSRNQVYGVVLANHKAQADATEDVTAVERN 120
QY 121 ANRNGTSESEYQIKAWTDFRFGKNTYSDFKMWHYFDGADWDSRKISRIFKRGEGK 180
DB 121 ANRNGTSESEYQIKAWTDFRFGKNTYSDFKMWHYFDGADWDSRKISRIFKRGEGK 180
QY 181 AMDWEVSSSENGNDYLMYADVDDHPVVAETKKMGITWANEISLDGFRIDAKKIKFSF 240
DB 181 AMDWEVSSSENGNDYLMYADVDDHPVVAETKKMGITWANEISLDGFRIDAKKIKFSF 240
QY 241 LRDWVQAVRQATGKEMFTVAEYQWNNAGKLENTKTSFNQSVFVPLHFNLOAASSQGG 300
DB 241 LRDWVQAVRQATGKEMFTVAEYQWNNAGKLENTKTSFNQSVFVPLHFNLOAASSQGG 300
QY 301 GYDMRRLDGTIVSRHPEKAVTFVENHDTOPGQSLSTVQTFKPLAVAFILTRREGYPQ 360
DB 301 GYDMRRLDGTIVSRHPEKAVTFVENHDTOPGQSLSTVQTFKPLAVAFILTRREGYPQ 360
QY 361 VFYGDWYGTGTSKPEKIPSLKDNIEPILKARKEVAYGPQHDYIDHPDIVGWTREGDSSAA 420
DB 361 VFYGDWYGTGTSKPEKIPSLKDNIEPILKARKEVAYGPQHDYIDHPDIVGWTREGDSSAA 420
QY 421 KSGLAALITDGPQGSKMYAGLKNAGETWYDITGNRSPTYKIGSDGGEFFHNDGSVSIY 480
DB 421 KSGLAALITDGPQGSKMYAGLKNAGETWYDITGNRSPTYKIGSDGGEFFHNDGSVSIY 480

RESULT 6

ID AAR72448 standard; protein; 483 AA.

XX AAR72448;

XX 25-MAR-2003 (revised)
DT 01-DEC-1995 (first entry)XX *Bacillus amyloliquefaciens* alpha amylase (mature protein).

XX Alpha amylase; variant; enzyme; detergent; additive; dishwashing;
KM washing; *Bacillus licheniformis*; *Bacillus amyloliquefaciens*;
KM *Bacillus stearothermophilus*; dyeing; bleaching; scouring; textile;
thermostable.

OS *Bacillus amyloliquefaciens*.

XX WO9510603-A1.

XX 20-APR-1995.

XX

PF 05-OCT-1994; 94WO-DK000370.
XX
XX 08-OCT-1993; 93DK-00001133.
PR 02-FEB-1994; 94DK-00000140.
XX
XX (NOVO) NOVO-NORDISK AS.
PA
PI Borchert TV, Bisgard-Frantzen H, Svendsen A, Thellersen M;
PI Van Der Zee P;
XX WPI; 1995-161790/21.
DR N-PSDB; AAQ88067.
XX
XX New *Bacillus* derived alpha-amylase variants - having amino acid
PT modifications to improve washing and/or dishwashing performance.
XX
PS Claim 34; Page 11-12; 105pp; English.

Variant alpha amylase enzymes which have improved washing and/or as
CC detergent additives. The enzymes have one or more amino acid residues
CC added, deleted or substituted. The variants can also be used for textile
CC desizing, prior to scouring, bleaching and dyeing. The variants have
CC improved thermostability, acid/alkaline stability; low temperature
CC optimum; pH optimum; higher hydrolysis velocity and improved tolerance to
CC other composition constituents, e.g. oxidation agents. (Updated on 25-MAR
CC -2003 to correct PN field.) (Updated on 25-MAR-2003 to correct PI field.)
XX

SQ Sequence 483 AA;

Query Match 100.0%; Score 2624; DB 2; Length 483;
Best Local Similarity 100.0%; Pred. No. 8,2e-218;
Matches 480; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNGTLMQYFEMWTPNDGQHWKRLQNDAEHLSDIGITAWIPPAVKGLSGSDNGYGPYDLY 60
DB 1 VNGTLMQYFEMWTPNDGQHWKRLQNDAEHLSDIGITAWIPPAVKGLSGSDNGYGPYDLY 60
QY 61 DLGEFOQKGTVRKTKGTSKSELQDAGSLHSRNQVYGVVLANHKAQADATEDVTAVERN 120
DB 61 DLGEFOQKGTVRKTKGTSKSELQDAGSLHSRNQVYGVVLANHKAQADATEDVTAVERN 120
QY 121 ANRNGTSESEYQIKAWTDFRFGKNTYSDFKMWHYFDGADWDSRKISRIFKRGEGK 180
DB 121 ANRNGTSESEYQIKAWTDFRFGKNTYSDFKMWHYFDGADWDSRKISRIFKRGEGK 180
QY 181 AMDWEVSSSENGNDYLMYADVDDHPVVAETKKMGITWANEISLDGFRIDAKKIKFSF 240
DB 181 AMDWEVSSSENGNDYLMYADVDDHPVVAETKKMGITWANEISLDGFRIDAKKIKFSF 240
QY 241 LRDWVQAVRQATGKEMFTVAEYQWNNAGKLENTKTSFNQSVFVPLHFNLOAASSQGG 300
DB 241 LRDWVQAVRQATGKEMFTVAEYQWNNAGKLENTKTSFNQSVFVPLHFNLOAASSQGG 300
QY 301 GYDMRRLDGTIVSRHPEKAVTFVENHDTOPGQSLSTVQTFKPLAVAFILTRREGYPQ 360
DB 301 GYDMRRLDGTIVSRHPEKAVTFVENHDTOPGQSLSTVQTFKPLAVAFILTRREGYPQ 360
QY 361 VFYGDWYGTGTSKPEKIPSLKDNIEPILKARKEVAYGPQHDYIDHPDIVGWTREGDSSAA 420
DB 361 VFYGDWYGTGTSKPEKIPSLKDNIEPILKARKEVAYGPQHDYIDHPDIVGWTREGDSSAA 420
QY 421 KSGLAALITDGPQGSKMYAGLKNAGETWYDITGNRSPTYKIGSDGGEFFHNDGSVSIY 480
DB 421 KSGLAALITDGPQGSKMYAGLKNAGETWYDITGNRSPTYKIGSDGGEFFHNDGSVSIY 480

RESULT 7

ID AAM31405 standard; protein; 483 AA.

XX AAM31405;

XX 11-MAY-1998 (first entry)

XX

XX DE Bacillus amyloliquefaciens Termamy1-like alpha-amylase.
 XX KM Termamy1; alpha-amylase; enzyme engineering; protein engineering; starch;
 XX KW liquefaction; saccharification; sweetener; textile desizing;
 XX KM detergent additive; ss.
 XX OS Bacillus amyloliquefaciens.
 XX PN MO9741213-A1.
 XX PD 06-NOV-1997.
 XX PF 30-APR-1997; 97WO-DK000197.
 XX PR 30-APR-1996; 96DX-00000515.
 XX PR 28-JUN-1996; 96DX-00000712.
 XX PR 11-JUL-1996; 96DX-00000775.
 XX PR 08-NOV-1996; 96DX-00001263.
 XX PA (NOVO) NOVO-NORDISK AS.
 XX PI Svendsen A, Borchert TV, Bisgard-Frantzen H;
 XX DR WPI: 1997-549718/50.
 XX DR N-PsDB; AAV02472.
 XX PT Termamy1-like alpha-amylase variants with improved properties - e.g.
 XX PT increased stability at low pH and low calcium, useful as detergent
 XX PT additives and in industrial starch processing e.g. liquefaction.
 XX PS Disclosure; Page 84; 101pp; English.
 CC This protein comprises the Termamy1-like alpha-amylase of Bacillus
 CC amyloliquefaciens. The invention relates to novel variants of Termamy1-
 CC like alpha-amylases that have alpha-amylase activity and exhibit an
 CC alteration in at least one property selected from: substrate specificity;
 CC binding or cleavage pattern; thermal stability; pH/activity or
 CC pH/stability profile; stability towards oxidation; Ca2+ dependency and
 CC specific activity. The variant has one or more mutations from those
 CC listed in the specification in relation to Bacillus licheniformis
 CC Termamy1 (see AAW31404). Also claimed are constructs comprising DNA
 CC encoding the variant (see AAV02471-73), and recombinant expression
 CC vectors and transformed cells containing the DNA. The Termamy1-like alpha
 CC -amylase variant is useful as a detergent additive and can also be used
 CC in industrial starch processing e.g. liquefaction (claimed) or
 CC saccharification to produce sweeteners, and in textile desizing (claimed)
 CC XX
 XX SQ Sequence 483 AA;
 Query Match 100.0%; Score 2624; DB 2; Length 483;
 Best Local Similarity 100.0%; Pred. No. 8.2e-218; Mismatches 0; Gaps 0;
 Matches 480; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 301 GYDMRLLDGTGVSRRPEKAVTFVFNHDPQPGQSLESTVQWFKPLAYAFILITRESSGYQ 360
 DB 301 GYDMRLLDGTGVSRRPEKAVTFVFNHDPQPGQSLESTVQWFKPLAYAFILITRESSGYQ 360
 QY 361 VFYGDWYGTGTSPEKIPSLKONIEPIILAKREYVAGQHDYIDHPDYIGWTRBGSSAA 420
 DB 361 VFYGDWYGTGTSPEKIPSLKONIEPIILAKREYVAGQHDYIDHPDYIGWTRBGSSAA 420
 QY 421 KSGLLALITDGPQGSRRMAYGKAGETWYDITGRSDTWKIGSGWGEFHYNDSSVLY 480
 DB 421 KSGLLALITDGPQGSRRMAYGKAGETWYDITGRSDTWKIGSGWGEFHYNDSSVLY 480
 421 KSGLLALITDGPQGSRRMAYGKAGETWYDITGRSDTWKIGSGWGEFHYNDSSVLY 480
 RESULT 8
 ID AAY97546
 ID AAY97546 standard; protein; 483 AA.
 AC AAY97546;
 XX 12-FEB-2001 (first entry)
 DE B. amyloliquefaciens termamy1-like alpha amylase.
 XX KM Termamy1-like alpha-amylase; variant; starch liquefaction; fuel;
 XX KM detergent composition; laundry cleaning composition; ethanol production;
 XX KM dish washing composition; composition; hard surface cleaning composition;
 XX KM industrial ethanol production; textile desizing.
 OS Bacillus amyloliquefaciens.
 XX PN WO200060059-A2.
 XX PD 12-OCT-2000.
 XX PF 28-MAR-2000; 2000WO-DK000148.
 XX PR 30-MAR-1999; 99DX-00000437.
 XX PA (NOVO) NOVO NORDISK AS.
 XX PI Andersen C, Jorgensen CT, Bisgard-Frantzen H, Svendsen A;
 XX PI Kjaerulf S;
 XX WPI: 2001-015666/02.
 XX DR N-PsDB; AAW37850.
 XX PT New variants of parent Termamy1-like alpha-amylase, useful in starch
 XX PT liquefaction, in detergent compositions and in ethanol production,
 XX PT exhibit altered cleavage pattern relative to the parent.
 XX PS Claim 9; Page 64-67; 78pp; English.
 XX XX
 CC This sequence represents a termamy1-like alpha amylase. The invention
 CC relates to a variant (I) of parent Termamy1-like alpha-amylase comprising
 CC alteration at one or more of the positions W13, G48, T49, S50, Q51, A52,
 CC D53, V54, G57, G107, G108, A111, S168 and M197. The alterations in (I)
 CC are independently an insertion of an amino acid downstream of the amino
 CC acid which occupies the position or deletion or substitution of the amino
 CC acid which occupies the position with a different amino acid. The variant
 CC has alpha-amylase activity. (I) or compositions containing it are useful
 CC in starch liquefaction, in detergent compositions such as laundry, dish
 CC washing and hard surface cleaning compositions, ethanol production
 CC as fuel, drinking and industrial ethanol production, desizing of
 CC textiles, fabrics or garments. (I) exhibits a reduced capability of
 CC cleaving a substrate close to the branching point, and further exhibits
 CC improved substrate specificity and/or improved specific activity relative
 CC to the parent alpha-amylase
 CC XX
 XX SQ Sequence 483 AA;
 Query Match 100.0%; Score 2624; DB 4; Length 483;
 Best Local Similarity 100.0%; Pred. No. 8.2e-218;

Matches 480; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNGTLMQYFEMWTPNDGQHWKRLQNDAEHLSDIGITAWMIPPAYKGLSOSDNGYGPYDLY 60
 DB 1 VNGTLMQYFEMWTPNDGQHWKRLQNDAEHLSDIGITAWMIPPAYKGLSOSDNGYGPYDLY 60
 QY 61 DLGEFOQKGTVRTKTKYKTSKSELQDAIGSLHSRNVOYGVGVVLAHKAQADATEDVTAVERN 120
 DB 61 DLGEFOQKGTVRTKTKYKTSKSELQDAIGSLHSRNVOYGVGVVLAHKAQADATEDVTAVERN 120
 QY 121 ANRNOETSEBYQIKAWTDPRFPGRGNTYSPFKMWHFHDGADWDESKISRIFFKRGSK 180
 DB 121 ANRNOETSEBYQIKAWTDPRFPGRGNTYSPFKMWHFHDGADWDESKISRIFFKRGSK 180
 QY 181 AMDWEVSSENGNDYLMYADVDYDHPDVVAETKKMGIMYANELSLDGRIDAAXHKKFSF 240
 DB 181 AMDWEVSSENGNDYLMYADVDYDHPDVVAETKKMGIMYANELSLDGRIDAAXHKKFSF 240
 QY 241 LRDWVQAVROATGKEMFTVAEYWNNAKLENTLNTKTSFNQSVFDPVPLHFNLOAASSQGG 300
 DB 241 LRDWVQAVROATGKEMFTVAEYWNNAKLENTLNTKTSFNQSVFDPVPLHFNLOAASSQGG 300
 QY 301 GYDMRRLDGTIVSRHPEKAVTFVENHDTQPGQSLSTVQTFWFKPLAVAFILTRBSGYPO 360
 DB 301 GYDMRRLDGTIVSRHPEKAVTFVENHDTQPGQSLSTVQTFWFKPLAVAFILTRBSGYPO 360
 QY 361 VFYGDWYGTGTSKPEIPLSKDNTEPIILKAKREYAYGQCHYIDHPDVIGMTRESDSSAA 420
 DB 361 VFYGDWYGTGTSKPEIPLSKDNTEPIILKAKREYAYGQCHYIDHPDVIGMTRESDSSAA 420
 QY 421 KSGLAALITDGPQSGSKRYAGLKNAGETWYDITGNRSPTYKISGSDGGEFFHVNDGSVSIY 480
 DB 421 KSGLAALITDGPQSGSKRYAGLKNAGETWYDITGNRSPTYKISGSDGGEFFHVNDGSVSIY 480

RESULT 9

ABR06937 ID ABR06937 standard; protein; 483 AA.

XX ABR06937;

XX 19-JUN-2002 (first entry)

DE B. amyloliquefaciens termamy1-like alpha-amylase protein SEQ ID NO:10.

XX Bacillus; termamy1-like alpha-amylase; alpha-amylase; EC 3.2.1.1;

KW variant; mutant; enzyme; protein co-ordinate data; cleaning; detergent;

XX washing; sweetener; ethanol; starch.

OS Bacillus amyloliquefaciens.

XX WO20016712-A2.

XX 13-SEP-2001.

XX 07-MAR-2001; 2001WO-DK000144.

XX 08-MAR-2000; 2000DK-00000376.

XX 15-MAR-2000; 2000US-0189857P.

XX 23-FEB-2001; 2001DK-00000303.

XX 26-FEB-2001; 2001US-0271382P.

XX (NOVO) NOVOZYMES AS.

XX Andersen C, Borchert TV, Nielsen BR;

XX WPI; 2002-239612/29.

XX N-PSDB; ABL50568.

XX Novel variant of parent termamy1-like alpha-amylase useful as a component in washing and dishwashing compositions, for textile desizing, for starch liquefaction, and for producing sweeteners and ethanol from starch.

PS Claim 8; Page 145-146; 153pp; English.

XX The present invention describes a variant of a parent termamy1-like alpha
 CC -amylase (EC 3.2.1.1) (I) comprising an alteration at one or more
 CC positions of a group of 31 possible amino acid positions. The alteration
 CC in (I) may be at Arg28, Arg118, Asn174, Asn182, Asp183, Gly184,
 CC Arg186, Trp189, Asn195, Met202, Tyr298, Asn299, Lys302, Asn306,
 CC Arg310, Asn314, Arg320, His324, Glu345, Tyr396, Arg400, Trp439, Arg444,
 CC Asn445, Lys446, Glu449, Arg458, Asn471, or Asn484. (I) can be used for
 CC washing and/or dishwashing, textile desizing, and starch liquefaction.
 CC (I) is useful as a component in hard surface cleaning detergent
 CC composition, and for producing sweeteners and ethanol from starch. (I)
 CC has altered solubility, preferably increased solubility, in particular
 CC under washing, dish washing or hard surface cleaning conditions. The
 CC present sequence represents a Bacillus amyloliquefaciens termamy1-like
 CC alpha-amylase which is used in the exemplification of the present
 CC invention

XX Sequence 483 AA;

XX Query Match 100.0%; Score 2624; DB 5; Length 483;

XX Best Local Similarity 100.0%; Pred. No. 8.2e-218; Indels 0; Gaps 0;

XX Matches 480; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNGTLMQYFEMWTPNDGQHWKRLQNDAEHLSDIGITAWMIPPAYKGLSOSDNGYGPYDLY 60

DB 1 VNGTLMQYFEMWTPNDGQHWKRLQNDAEHLSDIGITAWMIPPAYKGLSOSDNGYGPYDLY 60

QY 61 DLGEFOQKGTVRTKTKYKTSKSELQDAIGSLHSRNVOYGVGVVLAHKAQADATEDVTAVERN 120

DB 61 DLGEFOQKGTVRTKTKYKTSKSELQDAIGSLHSRNVOYGVGVVLAHKAQADATEDVTAVERN 120

QY 121 ANRNOETSEBYQIKAWTDPRFPGRGNTYSPFKMWHFHDGADWDESKISRIFFKRGSK 180

DB 121 ANRNOETSEBYQIKAWTDPRFPGRGNTYSPFKMWHFHDGADWDESKISRIFFKRGSK 180

QY 181 AMDWEVSSENGNDYLMYADVDYDHPDVVAETKKMGIMYANELSLDGRIDAAXHKKFSF 240

DB 181 AMDWEVSSENGNDYLMYADVDYDHPDVVAETKKMGIMYANELSLDGRIDAAXHKKFSF 240

QY 241 LRDWVQAVROATGKEMFTVAEYWNNAKLENTLNTKTSFNQSVFDPVPLHFNLOAASSQGG 300

DB 241 LRDWVQAVROATGKEMFTVAEYWNNAKLENTLNTKTSFNQSVFDPVPLHFNLOAASSQGG 300

QY 301 GYDMRRLDGTIVSRHPEKAVTFVENHDTQPGQSLSTVQTFWFKPLAVAFILTRBSGYPO 360

DB 301 GYDMRRLDGTIVSRHPEKAVTFVENHDTQPGQSLSTVQTFWFKPLAVAFILTRBSGYPO 360

QY 361 VFYGDWYGTGTSKPEIPLSKDNTEPIILKAKREYAYGQCHYIDHPDVIGMTRESDSSAA 420

DB 361 VFYGDWYGTGTSKPEIPLSKDNTEPIILKAKREYAYGQCHYIDHPDVIGMTRESDSSAA 420

QY 421 KSGLAALITDGPQSGSKRYAGLKNAGETWYDITGNRSPTYKISGSDGGEFFHVNDGSVSIY 480

DB 421 KSGLAALITDGPQSGSKRYAGLKNAGETWYDITGNRSPTYKISGSDGGEFFHVNDGSVSIY 480

RESULT 10

AAU12153 ID AAU12153 standard; protein; 483 AA.

XX AAU12153;

XX 09-APR-2002 (first entry)

XX Bacillus TERMAMY1-like alpha-amylase BAN.

XX TERMAMY1; alpha-amylase; detergent; dishwashing; textile desizing;

XX starch liquefaction; ethanol production; hard surface cleaner; sweetener;

XX amylopectin; limit dextrin; NOVAMY1, BAN.

XX Bacillus amyloliquefaciens.

PN WO200186107-A2.
 XX
 PD 22-NOV-2001.
 XX
 PF 10-MAY-2001; 2001WO-DK000323.
 XX
 PR 12-MAY-2000; 2000DK-00000779.
 XX
 PA (NOVO) NOVOZYMES AS.
 XX
 PI Svendsen A, Jorgensen CT, Nielsen BR;
 XX
 DR WPI; 2002-106123/14.
 DR N-PSDB; AAS20026.
 XX
 PT New variant of parent Termamyl-like alpha-amylase for use as a component
 PT in washing and dishwashing compositions, for textile desizing, for starch
 PT liquefaction, and for producing sweeteners and ethanol from starch.
 XX

Claim 5; Fig 1; 84pp; English.

PS The invention relates to a variant of parent TERMAMYL-like alpha-amylase
 CC comprising an alteration at regions 186-193, 261-276, 283-293 or 334-339,
 CC or at position 234, where the variant has alpha-amylase activity and each
 CC position corresponds to a position of a parent Termamyl-like alpha-
 CC amylase sequence having a Bacillus licheniformis alpha-amylase sequence
 CC of 483 amino acids, given in specification. The variant alpha-amylase, a
 CC detergent additive comprising the variant or a detergent composition
 CC comprising the variant, is useful for washing and/or dishwashing or
 CC textile desizing. The alpha-amylase is useful for starch liquefaction or
 CC ethanol production and as a component in a hard surface cleaning
 CC detergent composition, and for producing sweeteners from starch. The
 CC variant has altered alpha-1, 6-D-glucosidic branch linkage cleavage
 CC activity on amylopectin, preferably increased alpha-1, 6-D-glucosidic
 CC branch linkage cleavage activity of amylopectin or a limit dextrin
 CC prepared by TERMAMYL (RTM) or NOVAMYL (RTM). The present sequence is a
 CC natural variant of the TERMAMYL alpha-amylase, BAN
 CC
 XX

Sequence 483 AA;

Query Match 100.0%; Score 2624; DB 5; Length 483;

Best Local Similarity 100.0%; Pred. No. 8, 2e-218; Indels 0; Gaps 0;

Matches 480; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNGTLMQYFEMWYTPNDGQHWKRLONDAEHLSDIGITAVWIPRAYKGLSOSDNGYGPYDLY 60
 DB 1 VNGTLMQYFEMWYTPNDGQHWKRLONDAEHLSDIGITAVWIPRAYKGLSOSDNGYGPYDLY 60
 QY 61 DLGEFOQKGVRTKYGTGKSELQDAIGLSHRNVQVGDVVLNHRKAGADATEDVTAVERN 120
 DB 61 DLGEFOQKGVRTKYGTGKSELQDAIGLSHRNVQVGDVVLNHRKAGADATEDVTAVERN 120
 QY 121 ANRNOETSEBYQIKAWTDFRPPRGNTYSDPKWMTYHPGADWDESRIKSRIFKPERGECK 180
 DB 121 ANRNOETSEBYQIKAWTDFRPPRGNTYSDPKWMTYHPGADWDESRIKSRIFKPERGECK 180
 QY 181 ANRMEVSSSENGANDYLYADVDYDHPVVAETKKMGITWANEISLDFGFIIDAKHKIKESF 240
 DB 181 ANRMEVSSSENGANDYLYADVDYDHPVVAETKKMGITWANEISLDFGFIIDAKHKIKESF 240
 QY 241 LRDMVQAVROATGKEMFTVAEYQWONNAGKLENTYKTSFQSVFDPVLFHNLQPAASQGG 300
 DB 241 LRDMVQAVROATGKEMFTVAEYQWONNAGKLENTYKTSFQSVFDPVLFHNLQPAASQGG 300
 QY 301 GYDMRLLDGTIVSRHEKAVTEVENHDITOPGOSLSSTVQWTKPLAVAFILTRREGGYQ 360
 DB 301 GYDMRLLDGTIVSRHEKAVTEVENHDITOPGOSLSSTVQWTKPLAVAFILTRREGGYQ 360
 QY 361 VFYGDWYGTGTSFKELPSLKDNIEPILKARKEAYVPOHDYIDHPVDIGMTREGDSAA 420
 DB 361 VFYGDWYGTGTSFKELPSLKDNIEPILKARKEAYVPOHDYIDHPVDIGMTREGDSAA 420
 QY 421 KSGLAALITDGPQGSKMYAGLKNAGETWYDITGNRSDTYKIGSDGGEFHVNDGSVLY 480

DB 421 KSGLAALITDGPQGSKMYAGLKNAGETWYDITGNRSDTYKIGSDGGEFHVNDGSVLY 480

RESULT 11

AA047854
 ID AAB47854 standard; protein; 483 AA.

XX AAB47854;

AC 02-APR-2002 (first entry)

DE Bacillus alpha amylase BAN.

XX Alpha amylase; Bacillus; Termamyl-like; maltodextrin; glucose syrup;
 KM starch; food; feed; pharmaceutical; confectionery; candy; isotonic drink;
 KM bakery; cereal bar; ice cream; coffee whitener; salad dressing;
 KM cured meat; fermented meat; spice.

XX Bacillus amyloliquefaciens.

XX WO200196537-A2.

PN 20-DEC-2001.

XX 13-JUN-2001; 2001WO-DK000404.

XX 14-JUN-2000; 2000DK-00000917.

PR 20-JUN-2000; 2000US-0212852P.

XX (NOVO) NOVOZYMES AS.

PI Nielsen BR, Welbye M;

DR WPI; 2002-098064/13.

XX N-PSDB; AAI72215.

PT New modified alpha-amylase derived from the genus Bacillus and/or is a
 PT Termamyl-like alpha-amylase, which has been pre-oxidized for producing
 PT maltodextrin or glucose syrup.

XX Claim 5; Page 39-41; 47pp; English.

CC The sequences given in AAB47850-56 show modified alpha-amylases derived
 CC from the genus Bacillus. These alpha amylases are Termamyl-like alpha-
 CC amylase and they have been pre-oxidized. The alpha amylase is useful for
 CC producing a maltodextrin or glucose syrup, by treating starch with a pre-
 CC oxidized alpha-amylase until a product with a DE between 5-45 has been
 CC provided and/or until a product with a molecular weight of between 5-30
 CC kDa has been provided. The product comprises a maltodextrin with a DE of
 CC 18.5 and/or a maltodextrin with a molecular weight of 14-16 kDa. The
 CC alpha amylase is useful for producing a maltodextrin or glucose syrup,
 CC where the glucose syrup is useful as an ingredient in food, feed or
 CC pharmaceuticals. Glucose syrup is useful in confectionery such as
 CC candies, beverages such as isotonic drinks, bakery such as cereal bars,
 CC dairy and ice cream such as coffee whiteners, conventional foods such as
 CC salad dressings, and food ingredients and preparations such as cured
 CC meat, fermented meat, spices and seasoning encapsulated flavours

Sequence 483 AA;

Query Match 100.0%; Score 2624; DB 5; Length 483;

Best Local Similarity 100.0%; Pred. No. 8, 2e-218; Indels 0; Gaps 0;

Matches 480; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNGTLMQYFEMWYTPNDGQHWKRLONDAEHLSDIGITAVWIPRAYKGLSOSDNGYGPYDLY 60
 DB 1 VNGTLMQYFEMWYTPNDGQHWKRLONDAEHLSDIGITAVWIPRAYKGLSOSDNGYGPYDLY 60
 QY 61 DLGEFOQKGVRTKYGTGKSELQDAIGLSHRNVQVGDVVLNHRKAGADATEDVTAVERN 120
 DB 61 DLGEFOQKGVRTKYGTGKSELQDAIGLSHRNVQVGDVVLNHRKAGADATEDVTAVERN 120

QY 121 ANRNOETSEBYQIKAMTDFRFGNGTYSDFKHMWHYFPGADWDESRKISRIFKFRGEGK 180
 DB 121 ANRNOETSEBYQIKAMTDFRFGNGTYSDFKHMWHYFPGADWDESRKISRIFKFRGEGK 180
 QY 181 AMDWEVSSSENGNYDYLMTADVDYDHPDVAETKKGIMWYANELSLDGRIDAARHIFKFSF 240
 DB 181 AMDWEVSSSENGNYDYLMTADVDYDHPDVAETKKGIMWYANELSLDGRIDAARHIFKFSF 240
 QY 241 LRDWVQAVRQATGKEMFTVAEYKONNAGKLENTSPFQSVFVPLHFNLOAASSQGG 300
 DB 241 LRDWVQAVRQATGKEMFTVAEYKONNAGKLENTSPFQSVFVPLHFNLOAASSQGG 300
 QY 301 GYDMRRLDGTIVVSRHPEKAVTFVENHDTQPGQSLSTVQTWFKPLAVAFILTRREGYPQ 360
 DB 301 GYDMRRLDGTIVVSRHPEKAVTFVENHDTQPGQSLSTVQTWFKPLAVAFILTRREGYPQ 360
 QY 361 VFYGDWYGTGTSKPEIPSLKDNIEPLTKARKEVAYGPOHDYIDHPDVGWTRREGSSAA 420
 DB 361 VFYGDWYGTGTSKPEIPSLKDNIEPLTKARKEVAYGPOHDYIDHPDVGWTRREGSSAA 420
 QY 421 KSGIALALITDGPQSGSKMYAGLKNAGETWYDITGNRSJTYKIGSDGWSGFHVNDGSVSIIY 480
 DB 421 KSGIALALITDGPQSGSKMYAGLKNAGETWYDITGNRSJTYKIGSDGWSGFHVNDGSVSIIY 480
 RESULT 12
 ABB76590
 ID ABB76590 standard; protein; 483 AA.
 AC ABB76590;
 XX 19-AUG-2002 (first entry)
 DE Termamyl-1-like-alpha-amylase #5.
 XX Termamyl-1-like-alpha-amylase #5.
 KM Textile desizing; detergent; enzyme.
 XX Bacillus amyloliquefaciens.
 OS WO200210355-A2.
 EN 07-FEB-2002.
 PD 12-JUL-2001; 2001WO-DK000488.
 XX 01-AUG-2000; 2000DK-00001160.
 PR 12-SEP-2000; 2000DK-00001354.
 PR 10-NOV-2000; 2000DK-00001687.
 PR 26-APR-2001; 2001DK-00000655.
 XX (NOVO) NOVOZYMES AS.
 PA Thisted T, Kjaerulff S, Andersen C, Fuglsang CC;
 PI WPI; 2002-280633/32.
 DR N-PSDB; ABL96211.
 XX Variant of parent Termamyl-1-like alpha amylase, useful in detergent
 PT composition, for starch liquefaction, ethanol production, washing and/or
 PT dish washing, and textile desizing.
 PS Claim 4; Fig 3; 90pp; English.
 XX This invention relates to variants of a parent Termamyl-1-like alpha-
 CC amylases. These are used for starch liquefaction, ethanol production,
 CC detergent, and textile desizing. The amylases have altered stability,
 CC particularly at high temperatures from 70-120pH and low pH in the
 CC range from pH 4.0-6.0. The present sequence is a termamyl-1-like-alpha-
 CC amylase
 SQ Sequence 483 AA;

Query Match 100.0%; Score 2624; DB 5; Length 483;
 Best Local Similarity 100.0%; Pred. No. 8.2e-216; Indels 0; Gaps 0;
 Matches 480; Conservative 0; Mismatches 0;
 QY 1 VNGTLQYFEMWYTPNPGHKKLQNDAEHLSDIGTAVWIPPAVKGLSQSDNGYGPYDLY 60
 DB 1 VNGTLQYFEMWYTPNPGHKKLQNDAEHLSDIGTAVWIPPAVKGLSQSDNGYGPYDLY 60
 QY 61 DLGEFOCKGTATKTKYGTSELODAISGLHSRNQVYTGIVYLHKAQADATEDVTAENV 120
 DB 61 DLGEFOCKGTATKTKYGTSELODAISGLHSRNQVYTGIVYLHKAQADATEDVTAENV 120
 QY 121 ANRNOETSEBYQIKAMTDFRFGNGTYSDFKHMWHYFPGADWDESRKISRIFKFRGEGK 180
 DB 121 ANRNOETSEBYQIKAMTDFRFGNGTYSDFKHMWHYFPGADWDESRKISRIFKFRGEGK 180
 QY 181 AMDWEVSSSENGNYDYLMTADVDYDHPDVAETKKGIMWYANELSLDGRIDAARHIFKFSF 240
 DB 181 AMDWEVSSSENGNYDYLMTADVDYDHPDVAETKKGIMWYANELSLDGRIDAARHIFKFSF 240
 QY 241 LRDWVQAVRQATGKEMFTVAEYKONNAGKLENTSPFQSVFVPLHFNLOAASSQGG 300
 DB 241 LRDWVQAVRQATGKEMFTVAEYKONNAGKLENTSPFQSVFVPLHFNLOAASSQGG 300
 QY 301 GYDMRRLDGTIVVSRHPEKAVTFVENHDTQPGQSLSTVQTWFKPLAVAFILTRREGYPQ 360
 DB 301 GYDMRRLDGTIVVSRHPEKAVTFVENHDTQPGQSLSTVQTWFKPLAVAFILTRREGYPQ 360
 QY 361 VFYGDWYGTGTSKPEIPSLKDNIEPLTKARKEVAYGPOHDYIDHPDVGWTRREGSSAA 420
 DB 361 VFYGDWYGTGTSKPEIPSLKDNIEPLTKARKEVAYGPOHDYIDHPDVGWTRREGSSAA 420
 QY 421 KSGIALALITDGPQSGSKMYAGLKNAGETWYDITGNRSJTYKIGSDGWSGFHVNDGSVSIIY 480
 DB 421 KSGIALALITDGPQSGSKMYAGLKNAGETWYDITGNRSJTYKIGSDGWSGFHVNDGSVSIIY 480
 RESULT 13
 ABB60488
 ID ABB60488 standard; protein; 483 AA.
 AC ABB60488;
 XX 10-MAY-2003 (first entry)
 DE Bacillus amyloliquefaciens alpha-amylase SEQ ID NO 4.
 XX Bacillus amyloliquefaciens; alpha-amylase; washing; cleaning; textile;
 KM dishwashing machine; starch-based capsule; EC 3.2.1.1; enzyme.
 XX Bacillus amyloliquefaciens.
 OS WO2003014358-A2.
 EN 20-FEB-2003.
 PD 27-JUL-2002; 2002WO-EP008391.
 XX 07-AUG-2001; 2001DE-01038753.
 PR (HENK) HENKEL KGAA.
 PA Kotwitz B, Breves R, Maurer K;
 PI WPI; 2003-278480/27.
 DR N-PSDB; ABE59264.
 XX Washing and cleaning composition, useful for laundry and hard surface
 PT cleaning, contains hybrid amylase derived from two Bacillus enzymes.
 PS Claim 4; Fig 2; 118pp; German.
 XX The invention relates to a washing and cleaning composition (A)
 CC

CC containing an amylolytic hybrid protein (I) containing sequences from the
 CC alpha-amylases (BC 3.2.1.1) of *Bacillus amyloliquefaciens* and B.
 CC licheniformis. (A) are used for cleaning textiles (by hand or machine) or
 CC hard surfaces (metal, glass, plastic etc.), especially in dishwashing
 CC machines. (I) can also be used to release other components of the
 CC compositions from starch-based capsules. The present sequence is that of
 CC the *Bacillus amyloliquefaciens* alpha-amylase of the invention

XX
 CC Sequence 483 AA;

Query Match 100.0%; Score 2624; DB 6; Length 483;
 Best Local Similarity 100.0%; Pred. No. 8.2e-218;
 Matches 480; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNGTLMQYFEMWTPNDGQHKRLQNDAEHLSDIGITAWIPPAKGLSDSDNGYGYDLY 60
 DB 1 VNGTLMQYFEMWTPNDGQHKRLQNDAEHLSDIGITAWIPPAKGLSDSDNGYGYDLY 60
 QY 61 DLGEFOQKGTVRTKTKGKSELQDAIGSLHSRNQYGVYVLAHKAQADATEDVTAVEVNP 120
 DB 61 DLGEFOQKGTVRTKTKGKSELQDAIGSLHSRNQYGVYVLAHKAQADATEDVTAVEVNP 120
 QY 121 ANNRQETSEBYOIKAWTDFRPPGRGNTYSDFKMHWHPGADWDSRKISRIFFKFRGEGK 180
 DB 121 ANNRQETSEBYOIKAWTDFRPPGRGNTYSDFKMHWHPGADWDSRKISRIFFKFRGEGK 180
 QY 181 AMDWEVSSSENGNDYLMYADVDDHPDVVAETKKQGIWYANELSLDGFRIIDAKHIKFSF 240
 DB 181 AMDWEVSSSENGNDYLMYADVDDHPDVVAETKKQGIWYANELSLDGFRIIDAKHIKFSF 240
 QY 241 LRDVWQAVROATGKEMFTVAEYQNNAGKLENYLNTKTSFNQSVFDPVPLHFNLOAASSQGG 300
 DB 241 LRDVWQAVROATGKEMFTVAEYQNNAGKLENYLNTKTSFNQSVFDPVPLHFNLOAASSQGG 300
 QY 301 GYDMRRLDGTIVVSRHPEKAVTFVENHDTQPGSLSTVQTWFKPLAVAFILTRBSGYPQ 360
 DB 301 GYDMRRLDGTIVVSRHPEKAVTFVENHDTQPGSLSTVQTWFKPLAVAFILTRBSGYPQ 360
 QY 361 VFYGDWYGTGKTSPEKIPSLKDNIEPILKARKEVYAGPQHDYIDHPDVIQWTRREGDSSAA 420
 DB 361 VFYGDWYGTGKTSPEKIPSLKDNIEPILKARKEVYAGPQHDYIDHPDVIQWTRREGDSSAA 420
 QY 421 KSGILAALITDGPQGSKRMVAGLKNAGETWYDITGNNSDTYKISGDMGGEFHVNDGSVSIY 480
 DB 421 KSGILAALITDGPQGSKRMVAGLKNAGETWYDITGNNSDTYKISGDMGGEFHVNDGSVSIY 480

RESULT 14
 AAY29853
 ID AAY29853 standard; protein; 514 AA.

XX AC AAY29853;
 XX DT 18-NOV-1999 (first entry)
 XX DE *Bacillus amyloliquefaciens* Termamyl-1-like alpha-amylase.
 XX KW Alpha-amylase; Termamyl-1-like alpha-amylase; glucose syrup; starch.
 XX OS *Bacillus amyloliquefaciens*.

XX Key Location/Qualifiers
 XX FT Peptide 1..31
 XX FT 32..514 /label= signal
 XX FT Protein /label= Termamyl-1-like_alpha-amylase

XX PN W09946399-A1.
 XX PD 16-SEP-1999.
 XX PF 08-MAR-1999; 99W0-DK000114.

PR 09-MAR-1998; 98DK-00000321.

XX PA (NOVO) NOVO-NORDISK AS.
 XX PI Norman BE, Hendriksen HV;
 XX PT WPI; 1999-551422/46.
 XX DR N-PSDB; AAZ21079.

XX PT Preparation of a glucose syrup, using a Termamyl-1-like alpha-amylase.
 XX PS Disclosure; Page 32-34; 36pp; English.

CC A method has been developed for the preparation of a glucose syrup using
 CC a Termamyl-1-like alpha-amylase containing a substitution at Val(54). The
 CC glucose syrup obtained by the process is useful as an ingredient in food
 CC products. The Termamyl-1-like alpha-amylase facilitates the preparation of
 CC glucose syrups suitable for the food industry, previously only possible
 CC using acid hydrolysis. The present sequence represents *Bacillus*
 CC *amyloliquefaciens* Termamyl-1-like alpha-amylase

XX
 CC Sequence 514 AA;

Query Match 100.0%; Score 2624; DB 2; Length 514;
 Best Local Similarity 100.0%; Pred. No. 9e-218;
 Matches 480; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNGTLMQYFEMWTPNDGQHKRLQNDAEHLSDIGITAWIPPAKGLSDSDNGYGYDLY 60
 DB 32 VNGTLMQYFEMWTPNDGQHKRLQNDAEHLSDIGITAWIPPAKGLSDSDNGYGYDLY 91
 QY 61 DLGEFOQKGTVRTKTKGKSELQDAIGSLHSRNQYGVYVLAHKAQADATEDVTAVEVNP 120
 DB 92 DLGEFOQKGTVRTKTKGKSELQDAIGSLHSRNQYGVYVLAHKAQADATEDVTAVEVNP 151
 QY 121 ANNRQETSEBYOIKAWTDFRPPGRGNTYSDFKMHWHPGADWDSRKISRIFFKFRGEGK 180
 DB 152 ANNRQETSEBYOIKAWTDFRPPGRGNTYSDFKMHWHPGADWDSRKISRIFFKFRGEGK 211
 QY 181 AMDWEVSSSENGNDYLMYADVDDHPDVVAETKKQGIWYANELSLDGFRIIDAKHIKFSF 240
 DB 212 AMDWEVSSSENGNDYLMYADVDDHPDVVAETKKQGIWYANELSLDGFRIIDAKHIKFSF 271
 QY 241 LRDVWQAVROATGKEMFTVAEYQNNAGKLENYLNTKTSFNQSVFDPVPLHFNLOAASSQGG 300
 DB 272 LRDVWQAVROATGKEMFTVAEYQNNAGKLENYLNTKTSFNQSVFDPVPLHFNLOAASSQGG 331
 QY 301 GYDMRRLDGTIVVSRHPEKAVTFVENHDTQPGSLSTVQTWFKPLAVAFILTRBSGYPQ 360
 DB 332 GYDMRRLDGTIVVSRHPEKAVTFVENHDTQPGSLSTVQTWFKPLAVAFILTRBSGYPQ 391
 QY 361 VFYGDWYGTGKTSPEKIPSLKDNIEPILKARKEVYAGPQHDYIDHPDVIQWTRREGDSSAA 420
 DB 392 VFYGDWYGTGKTSPEKIPSLKDNIEPILKARKEVYAGPQHDYIDHPDVIQWTRREGDSSAA 451
 QY 421 KSGILAALITDGPQGSKRMVAGLKNAGETWYDITGNNSDTYKISGDMGGEFHVNDGSVSIY 480
 DB 452 KSGILAALITDGPQGSKRMVAGLKNAGETWYDITGNNSDTYKISGDMGGEFHVNDGSVSIY 511

RESULT 15
 AAB12433
 ID AAB12433 standard; protein; 514 AA.

XX AC AAB12433;
 XX DT 19-OCT-2000 (first entry)
 XX DE *Bacillus amyloliquefaciens* amylase protein SEQ ID NO:9.
 XX KW *Bacillus amyloliquefaciens*; alpha-amylase; thermostable; bread.

XX OS *Bacillus amyloliquefaciens*.

Job time : 49.7475 secs

XX JP2000135093-A.

XX 16-MAY-2000.

XX 20-AUG-1999; 99JP-00234813.

XX 24-AUG-1998; 98JP-00237839.

XX (DAIW) DAIWA KASEI KK.

XX MPI; 2000-403584/35.

PT Novel thermostable alpha-amylase, useful for improving the preparation of
PT bread, comprises alpha-amylase activity with less than 80% activity after
PT treatment at 65degrec for 30 min.

PS Claim 1; Page 18-19; 22pp; Japanese.

CC The present invention describes a thermostable alpha-amylase (I)
CC comprising the sequence given in AAB12433 (A) or deletions, replacements
CC or insertions of one or more amino acid(s) in the sequence and alpha-
CC amylase activity with less than 80% activity after treatment at 65 plus
CC degrees Celsius for 30 minutes. Also described are: (1) DNAs encoding (I)
CC ; (2) DNAs containing one of 4 nucleotide sequences comprising 1545 base
CC pairs (see AAA60576 to AAA60579); (3) expression vectors containing the
CC above mentioned DNAs; (4) host cells containing the above mentioned
CC expression vectors; (5) preparation of a polypeptide having alpha-amylase
CC activity by culture of the recombinant host cells; and (6) preparation of
CC bread including a process to add (I) to the dough. (I) is useful in the
CC preparation of bread. (I) improves the soft volume of the bread and
CC prevents it aging

SQ Sequence 514 AA:

Query Match 100.0%; Score 2624; DB 3; Length 514;

Best Local Similarity 100.0%; Pred. No. 9e-218; Mismatches 0; Indels 0; Gaps 0;

Matches 480; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAWIPPAYKGLSQSDNGYGPYDLY 60
DB 32 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAWIPPAYKGLSQSDNGYGPYDLY 91
QY 61 DLGEPOQKGTVRTKTKYKSELDQAIQSLHSRNVQYGDVYLNHKAQADATEDVTAENVP 120
DB 92 DLGEPOQKGTVRTKTKYKSELDQAIQSLHSRNVQYGDVYLNHKAQADATEDVTAENVP 151
QY 121 ANRQETSEFYQIKAWTDFFRFGKNTYSDPKWTHYHFDGADWDESKISRIFFKRGEGK 180
DB 152 ANRQETSEFYQIKAWTDFFRFGKNTYSDPKWTHYHFDGADWDESKISRIFFKRGEGK 211
QY 181 AMDWEVSENGNVDYLMADVDYDHPDVAAETKKGIVYANELSLDGFRIIDAKHIFSF 240
DB 212 AMDWEVSENGNVDYLMADVDYDHPDVAAETKKGIVYANELSLDGFRIIDAKHIFSF 271
QY 241 LRDWVOAAROATGKEMFTVAEYQWNNAGKLENYLNKTSFNQSVFDPVLAHFNLOAASSQGG 300
DB 272 LRDWVOAAROATGKEMFTVAEYQWNNAGKLENYLNKTSFNQSVFDPVLAHFNLOAASSQGG 331
QY 301 GYDMRLLDGTIVSSHPEKAVTFVENHDTOPQGSLESTVQTFEKLAYAFILITRESGYPQ 360
DB 332 GYDMRLLDGTIVSSHPEKAVTFVENHDTOPQGSLESTVQTFEKLAYAFILITRESGYPQ 391
QY 361 VVEGMYGTGKTSPEKIPSLKDNIEPIILKARKEYAYGPOHDYIDHPDVIQWTRREGSSAA 420
DB 392 VVEGMYGTGKTSPEKIPSLKDNIEPIILKARKEYAYGPOHDYIDHPDVIQWTRREGSSAA 451
QY 421 KSGLAALITDGPQGSKRYTAGLKNAGETWYDITGNRSDTVKIGSDGMBFHYNDGSVSIY 480
DB 452 KSGLAALITDGPQGSKRYTAGLKNAGETWYDITGNRSDTVKIGSDGMBFHYNDGSVSIY 511
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Search completed: May 3, 2004, 20:50:30

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 3, 2004, 20:29:27 ; Search time 16.2492 Seconds
(without alignments)
1525.031 Million cell updates/sec

Title: US-10-644-187-4

Perfect score: 2624 1 VNGTLMQYFEMTTPDQGMW.....KISDNGEFTVNDGSVSIY 480

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Issued Patents AA:
1: /cgn2_6/prodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/prodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/prodata/2/iaa/5A_COMB.pep:*
4: /cgn2_6/prodata/2/iaa/5B_COMB.pep:*
5: /cgn2_6/prodata/2/iaa/PTUS_COMB.pep:*
6: /cgn2_6/prodata/2/iaa/backfill.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2624	100.0	480	3	US-09-182-859-4
2	2624	100.0	480	3	US-09-170-670-5
3	2624	100.0	480	3	US-09-193-068-5
4	2624	100.0	480	3	US-09-183-412-5
5	2624	100.0	480	3	US-09-290-734-5
6	2624	100.0	480	4	US-09-672-459-4
7	2624	100.0	480	4	US-09-545-586-5
8	2624	100.0	480	4	US-10-186-042-4
9	2624	100.0	480	4	US-09-769-864-5
10	2624	100.0	483	4	US-09-291-023A-16
11	2624	100.0	483	4	US-09-537-168-6
12	2624	100.0	483	4	US-09-381-687-6
13	2624	100.0	483	4	US-09-540-715A-16
14	2624	100.0	514	1	US-08-720-899-4
15	2624	100.0	514	1	US-08-459-610-4
16	2624	100.0	514	2	US-08-343-804-4
17	2624	100.0	514	2	US-08-687-399-4
18	2624	100.0	514	2	US-08-600-908A-4
19	2624	100.0	514	2	US-08-683-838A-4
20	2624	100.0	514	3	US-09-264-057-4
21	2624	100.0	514	3	US-09-636-252A-4
22	2624	100.0	520	1	US-08-468-700-36
23	2624	100.0	520	1	US-08-645-971-4
24	2624	100.0	520	2	US-08-468-220-34
25	2624	100.0	520	2	US-08-468-698-34
26	2624	100.0	520	2	US-08-704-706A-36
27	2624	100.0	520	3	US-08-890-383-5

28	2624	100.0	520	3	US-08-914-679A-5
29	2624	100.0	520	3	US-08-985-659-37
30	2624	100.0	520	3	US-08-194-664A-34
31	2624	100.0	520	5	PCT-US94-01553A-34
32	2624	100.0	520	5	PCT-US95-10426-34
33	2475	94.3	483	2	US-08-600-908A-13
34	2475	94.3	483	2	US-08-683-838A-13
35	2475	94.3	483	4	US-09-636-252A-13
36	2190	83.5	481	4	US-09-537-168-2
37	2176	82.9	483	1	US-08-468-700-34
38	2176	82.9	483	1	US-08-645-971-2
39	2176	82.9	483	2	US-08-468-220-32
40	2176	82.9	483	2	US-08-468-698-32
41	2176	82.9	483	2	US-08-704-706A-34
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43	2176	82.9	483	3	US-08-914-679A-3
44	2176	82.9	483	3	US-08-985-659-35
45	2176	82.9	483	3	US-08-194-664A-32

ALIGNMENTS

RESULT 1				
US-09-182-859-4				
Sequence 4, Application US/09182859				
Patent No. 6143708				
GENERAL INFORMATION:				
APPLICANT: Svendsen, Allan				
APPLICANT: Borchert, Torben				
APPLICANT: Bisgaard-Friantzen, Henrik				
TITLE OF INVENTION: Alpha-Amylase Mutants				
FILE REFERENCE: 4796.204-US				
CURRENT APPLICATION NUMBER: US/09/182,859				
CURRENT FILING DATE: 1998-10-29				
EARLIER APPLICATION NUMBER: 0515/96				
EARLIER FILING DATE: 1996-04-30				
EARLIER APPLICATION NUMBER: 0712/96				
EARLIER FILING DATE: 1996-06-28				
EARLIER APPLICATION NUMBER: 0775/96				
EARLIER FILING DATE: 1996-07-11				
EARLIER APPLICATION NUMBER: 1263/96				
EARLIER FILING DATE: 1996-11-08				
NUMBER OF SEQ ID NOS: 37				
SOFTWARE: FASTSEQ For Windows Version 3.0				
SEQ ID NO 4				
LENGTH: 480				
TYPE: PRT				
ORGANISM: Bacillus amyloliquefaciens				
US-09-182-859-4				
Query Match				
Best Local Similarity 100.0%; Pred. No. 3.6e-230; Length 480;				
Matches 480; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	1	VNGTLMQYFEMTTPDQGMWRLQNDALHSLDIGITAWIPPAKGLSQSDNGGYDYLY	60	Sequence 5, Appl
DB	1	VNGTLMQYFEMTTPDQGMWRLQNDALHSLDIGITAWIPPAKGLSQSDNGGYDYLY	60	Sequence 37, Appl
QY	61	DIGEEQOGKTVRTKTKGTSELODAIGSLHSNNVQYGVVTLNHRAGADATDVAVENP	120	Sequence 34, Appl
DB	61	DIGEEQOGKTVRTKTKGTSELODAIGSLHSNNVQYGVVTLNHRAGADATDVAVENP	120	Sequence 34, Appl
QY	61	DIGEEQOGKTVRTKTKGTSELODAIGSLHSNNVQYGVVTLNHRAGADATDVAVENP	120	Sequence 13, Appl
DB	61	DIGEEQOGKTVRTKTKGTSELODAIGSLHSNNVQYGVVTLNHRAGADATDVAVENP	120	Sequence 13, Appl
QY	121	ARNQETSEYQIKAMTDFRFGKNTYSDPKMWHYFDGADWDSRKISIFKRGSGK	180	Sequence 2, Appl
DB	121	ARNQETSEYQIKAMTDFRFGKNTYSDPKMWHYFDGADWDSRKISIFKRGSGK	180	Sequence 2, Appl
QY	181	AMDWEVSSNGYDYLVMTADVDPDYVAETKKKGIYANLSDGERIDAAKIKRSF	240	Sequence 32, Appl
DB	181	AMDWEVSSNGYDYLVMTADVDPDYVAETKKKGIYANLSDGERIDAAKIKRSF	240	Sequence 32, Appl
QY	181	AMDWEVSSNGYDYLVMTADVDPDYVAETKKKGIYANLSDGERIDAAKIKRSF	240	Sequence 34, Appl
DB	181	AMDWEVSSNGYDYLVMTADVDPDYVAETKKKGIYANLSDGERIDAAKIKRSF	240	Sequence 34, Appl
QY	241	LADWQVAVQATGKEMFTVAEYQNNAGKLSEYLNKTSFNOSVDPDPLHFNLOAASQGG	300	Sequence 3, Appl
DB	241	LADWQVAVQATGKEMFTVAEYQNNAGKLSEYLNKTSFNOSVDPDPLHFNLOAASQGG	300	Sequence 3, Appl

Tue May 4 14:34:46 2004

us-10-644-187-4.ra1

Page 2

Db 241 LRDWQAVRQATGKEMFTVAEYQNNAGKLENTKTSFNQSVFDPVLFHFNLOAASSQGG 300
QY 301 GYDMRRLDGTIVSRHPEKAVTFVENHDTQPGQSLSTVQTFKPLAFAFILTRESGYPO 360
Db 301 GYDMRRLDGTIVSRHPEKAVTFVENHDTQPGQSLSTVQTFKPLAFAFILTRESGYPO 360
QY 361 VFYGDWYGTGTSPEKIPSLKDNIEPILKARKEVAYGPOHDYIDHPDYIGWTRBGSSAA 420
Db 361 VFYGDWYGTGTSPEKIPSLKDNIEPILKARKEVAYGPOHDYIDHPDYIGWTRBGSSAA 420
QY 421 KSGLAALITDGPQSGSKMYAGLKNAGETWYDITGNNSDTYKISDGMGEFHVNDGSVSIY 480
Db 421 KSGLAALITDGPQSGSKMYAGLKNAGETWYDITGNNSDTYKISDGMGEFHVNDGSVSIY 480

RESULT 2
US-09-170-670-5
Sequence 5, Application US/09170670
Patent No. 6187576
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Borchert, Torben
APPLICANT: Bisgaard-Frantzen, Henrik
TITLE OF INVENTION: Alpha-Amylase Mutants
FILE REFERENCE: 5276-200-US
CURRENT APPLICATION NUMBER: US/09/170,670
CURRENT FILING DATE: 1998-10-13
EARLIER APPLICATION NUMBER: 1172/97
EARLIER FILING DATE: 1997-10-13
EARLIER APPLICATION NUMBER: 60/063,306
EARLIER FILING DATE: 1997-10-28
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 5
LENGTH: 480
TYPE: PRT
ORGANISM: B. amyloliquefaciens
US-09-170-670-5

Query Match 100.0%; Score 2624; DB 3; Length 480;
Best Local Similarity 100.0%; Pred. No. 3.8e-230;
Matches 480; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNGTLMQYFEMWYTPNDQGHKRLQNDAEHLSDIGITAWIIPRAYKLSQSDNGYGPYDLY 60
Db 1 VNGTLMQYFEMWYTPNDQGHKRLQNDAEHLSDIGITAWIIPRAYKLSQSDNGYGPYDLY 60
QY 61 DLGEFOOKGTVRTKYGTGKSELQDAIGLSHRNVQYGVVLNHHKAGADATEDVTAVERNVP 120
Db 61 DLGEFOOKGTVRTKYGTGKSELQDAIGLSHRNVQYGVVLNHHKAGADATEDVTAVERNVP 120
QY 121 ANRNOETSEBYQIKAWTDFRFPGRGNTYSDFKMWHYHFGADWDESRKISRIFKFRGECK 180
Db 121 ANRNOETSEBYQIKAWTDFRFPGRGNTYSDFKMWHYHFGADWDESRKISRIFKFRGECK 180
QY 121 ANRNOETSEBYQIKAWTDFRFPGRGNTYSDFKMWHYHFGADWDESRKISRIFKFRGECK 180
Db 121 ANRNOETSEBYQIKAWTDFRFPGRGNTYSDFKMWHYHFGADWDESRKISRIFKFRGECK 180
QY 181 AMDEWSSSENGANDYLMYADVDDHPDYVAETKKGIWYANELSLDGFIDAKIKRSEF 240
Db 181 AMDEWSSSENGANDYLMYADVDDHPDYVAETKKGIWYANELSLDGFIDAKIKRSEF 240
QY 241 LRDWQAVRQATGKEMFTVAEYQNNAGKLENTKTSFNQSVFDPVLFHFNLOAASSQGG 300
Db 241 LRDWQAVRQATGKEMFTVAEYQNNAGKLENTKTSFNQSVFDPVLFHFNLOAASSQGG 300
QY 301 GYDMRRLDGTIVSRHPEKAVTFVENHDTQPGQSLSTVQTFKPLAFAFILTRESGYPO 360
Db 301 GYDMRRLDGTIVSRHPEKAVTFVENHDTQPGQSLSTVQTFKPLAFAFILTRESGYPO 360
QY 361 VFYGDWYGTGTSPEKIPSLKDNIEPILKARKEVAYGPOHDYIDHPDYIGWTRBGSSAA 420
Db 361 VFYGDWYGTGTSPEKIPSLKDNIEPILKARKEVAYGPOHDYIDHPDYIGWTRBGSSAA 420
QY 421 KSGLAALITDGPQSGSKMYAGLKNAGETWYDITGNNSDTYKISDGMGEFHVNDGSVSIY 480
Db 421 KSGLAALITDGPQSGSKMYAGLKNAGETWYDITGNNSDTYKISDGMGEFHVNDGSVSIY 480

Db 421 KSGLAALITDGPQSGSKMYAGLKNAGETWYDITGNNSDTYKISDGMGEFHVNDGSVSIY 480
RESULT 3
US-09-193-068-5
Sequence 5, Application US/09193068
Patent No. 6197565
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Kjullif, Soren
APPLICANT: Bisgaard-Frantzen, Henrik
TITLE OF INVENTION: -Amylase Variants
FILE REFERENCE: 5709,000-US
CURRENT APPLICATION NUMBER: US/09/193,068
CURRENT FILING DATE: 1998-11-16
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 5
LENGTH: 480
TYPE: PRT
ORGANISM: B. amyloliquefaciens
US-09-193-068-5

Query Match 100.0%; Score 2624; DB 3; Length 480;
Best Local Similarity 100.0%; Pred. No. 3.8e-230;
Matches 480; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNGTLMQYFEMWYTPNDQGHKRLQNDAEHLSDIGITAWIIPRAYKLSQSDNGYGPYDLY 60
Db 1 VNGTLMQYFEMWYTPNDQGHKRLQNDAEHLSDIGITAWIIPRAYKLSQSDNGYGPYDLY 60
QY 61 DLGEFOOKGTVRTKYGTGKSELQDAIGLSHRNVQYGVVLNHHKAGADATEDVTAVERNVP 120
Db 61 DLGEFOOKGTVRTKYGTGKSELQDAIGLSHRNVQYGVVLNHHKAGADATEDVTAVERNVP 120
QY 121 ANRNOETSEBYQIKAWTDFRFPGRGNTYSDFKMWHYHFGADWDESRKISRIFKFRGECK 180
Db 121 ANRNOETSEBYQIKAWTDFRFPGRGNTYSDFKMWHYHFGADWDESRKISRIFKFRGECK 180
QY 121 ANRNOETSEBYQIKAWTDFRFPGRGNTYSDFKMWHYHFGADWDESRKISRIFKFRGECK 180
Db 121 ANRNOETSEBYQIKAWTDFRFPGRGNTYSDFKMWHYHFGADWDESRKISRIFKFRGECK 180
QY 181 AMDEWSSSENGANDYLMYADVDDHPDYVAETKKGIWYANELSLDGFIDAKIKRSEF 240
Db 181 AMDEWSSSENGANDYLMYADVDDHPDYVAETKKGIWYANELSLDGFIDAKIKRSEF 240
QY 241 LRDWQAVRQATGKEMFTVAEYQNNAGKLENTKTSFNQSVFDPVLFHFNLOAASSQGG 300
Db 241 LRDWQAVRQATGKEMFTVAEYQNNAGKLENTKTSFNQSVFDPVLFHFNLOAASSQGG 300
QY 301 GYDMRRLDGTIVSRHPEKAVTFVENHDTQPGQSLSTVQTFKPLAFAFILTRESGYPO 360
Db 301 GYDMRRLDGTIVSRHPEKAVTFVENHDTQPGQSLSTVQTFKPLAFAFILTRESGYPO 360
QY 361 VFYGDWYGTGTSPEKIPSLKDNIEPILKARKEVAYGPOHDYIDHPDYIGWTRBGSSAA 420
Db 361 VFYGDWYGTGTSPEKIPSLKDNIEPILKARKEVAYGPOHDYIDHPDYIGWTRBGSSAA 420
QY 421 KSGLAALITDGPQSGSKMYAGLKNAGETWYDITGNNSDTYKISDGMGEFHVNDGSVSIY 480
Db 421 KSGLAALITDGPQSGSKMYAGLKNAGETWYDITGNNSDTYKISDGMGEFHVNDGSVSIY 480

RESULT 4
US-09-183-412-5
Sequence 5, Application US/09183412
Patent No. 6204232
GENERAL INFORMATION:
APPLICANT: Borchert, Torben V.
APPLICANT: Svendsen, Allan
APPLICANT: Andersen, Carsten
APPLICANT: Nielsen, Bjarne
APPLICANT: Nissen, Torben L.
TITLE OF INVENTION: Alpha-Amylase Mutants

FILE REFERENCE: 5368.200-US
CURRENT APPLICATION NUMBER: US/09/183,412
CURRENT FILING DATE: 1998-10-30
EARLIER APPLICATION NUMBER: 60/064,662
EARLIER FILING DATE: 1997-11-06
EARLIER APPLICATION NUMBER: 60/093,234
EARLIER FILING DATE: 1998-07-17
EARLIER APPLICATION NUMBER: 1240/97
EARLIER FILING DATE: 1997-10-30
EARLIER APPLICATION NUMBER: PA 1998 00936
EARLIER FILING DATE: 1998-07-14
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 5
LENGTH: 480
TYPE: PRT
ORGANISM: Bacillus amyloliquefaciens
US-09-183-412-5

Query Match 100.0%; Score 2624; DB 3; Length 480;
Best Local Similarity 100.0%; Pred. No. 3,8e-230;
Matches 480; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAWIIPRAYKGLSDSDNGYGPYDLY 60
DB 1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAWIIPRAYKGLSDSDNGYGPYDLY 60
QY 61 DLGFEQOKGIVRTKYGTGKSELQDAIGLSHRNQQYGVVNLNKAQADATEDVTAVERN 120
DB 61 DLGFEQOKGIVRTKYGTGKSELQDAIGLSHRNQQYGVVNLNKAQADATEDVTAVERN 120
QY 121 ANRNOETSEBYQIKAWTDFRPPGRGNTYSDFKWHTHFGADWDESRKISRIKFERGEGK 180
DB 121 ANRNOETSEBYQIKAWTDFRPPGRGNTYSDFKWHTHFGADWDESRKISRIKFERGEGK 180
QY 181 AMWWEVSENGNDYLMYADVDDHPDVVAETKKMGITWANEISLDGFRIDAKHIKFSF 240
DB 181 AMWWEVSENGNDYLMYADVDDHPDVVAETKKMGITWANEISLDGFRIDAKHIKFSF 240
QY 241 LRDMVAVRQATGKEMFTVAEYQNNAGKLENTLNTSFNQSVEFVPLHFNLOAASSQGG 300
DB 241 LRDMVAVRQATGKEMFTVAEYQNNAGKLENTLNTSFNQSVEFVPLHFNLOAASSQGG 300
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DB 301 GYMRRLDGTIVSRHEKAVTVEVNDHTOPGQSLSTVQTWKPLAFAFILLRESGYPO 360
QY 361 VFYGDWYGTGKTSPEKIPSLKDNIEPLIKARKEVAYGPOHDYIDHPDIVIGMTREGSSAA 420
DB 361 VFYGDWYGTGKTSPEKIPSLKDNIEPLIKARKEVAYGPOHDYIDHPDIVIGMTREGSSAA 420
QY 421 KSGIALITDGPQSGSKMYAGLKNAGETWYDITGNRSYTYKISDGGGEHFVNDGSYSIY 480
DB 421 KSGIALITDGPQSGSKMYAGLKNAGETWYDITGNRSYTYKISDGGGEHFVNDGSYSIY 480

RESULT 5
US-09-290-734-5
Sequence 5, Application US/09290734
Patent No. 6361989
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Borchert, Torben Vedel
APPLICANT: Bisgaard-Frantzen Henrik
APPLICANT: Oulstrup, Heile
APPLICANT: Nielsen, Bjarne Ronfeldt
APPLICANT: Nielsen, Vibeke Skovgaard
APPLICANT: Hoeck, Lisbeth Hedegaard
TITLE OF INVENTION: No. 6361989e1 -Amylase And -Amylase Mutants
FILE REFERENCE: 5276.400-US
CURRENT APPLICATION NUMBER: US/09/290,734
CURRENT FILING DATE: 1999-04-13
NUMBER OF SEQ ID NOS: 35

SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 5
LENGTH: 480
TYPE: PRT
ORGANISM: B. amyloliquefaciens
US-09-290-734-5

Query Match 100.0%; Score 2624; DB 4; Length 480;
Best Local Similarity 100.0%; Pred. No. 3,8e-230;
Matches 480; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAWIIPRAYKGLSDSDNGYGPYDLY 60
DB 1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAWIIPRAYKGLSDSDNGYGPYDLY 60
QY 61 DLGFEQOKGIVRTKYGTGKSELQDAIGLSHRNQQYGVVNLNKAQADATEDVTAVERN 120
DB 61 DLGFEQOKGIVRTKYGTGKSELQDAIGLSHRNQQYGVVNLNKAQADATEDVTAVERN 120
QY 121 ANRNOETSEBYQIKAWTDFRPPGRGNTYSDFKWHTHFGADWDESRKISRIKFERGEGK 180
DB 121 ANRNOETSEBYQIKAWTDFRPPGRGNTYSDFKWHTHFGADWDESRKISRIKFERGEGK 180
QY 181 AMWWEVSENGNDYLMYADVDDHPDVVAETKKMGITWANEISLDGFRIDAKHIKFSF 240
DB 181 AMWWEVSENGNDYLMYADVDDHPDVVAETKKMGITWANEISLDGFRIDAKHIKFSF 240
QY 241 LRDMVAVRQATGKEMFTVAEYQNNAGKLENTLNTSFNQSVEFVPLHFNLOAASSQGG 300
DB 241 LRDMVAVRQATGKEMFTVAEYQNNAGKLENTLNTSFNQSVEFVPLHFNLOAASSQGG 300
QY 301 GYMRRLDGTIVSRHEKAVTVEVNDHTOPGQSLSTVQTWKPLAFAFILLRESGYPO 360
DB 301 GYMRRLDGTIVSRHEKAVTVEVNDHTOPGQSLSTVQTWKPLAFAFILLRESGYPO 360
QY 361 VFYGDWYGTGKTSPEKIPSLKDNIEPLIKARKEVAYGPOHDYIDHPDIVIGMTREGSSAA 420
DB 361 VFYGDWYGTGKTSPEKIPSLKDNIEPLIKARKEVAYGPOHDYIDHPDIVIGMTREGSSAA 420
QY 421 KSGIALITDGPQSGSKMYAGLKNAGETWYDITGNRSYTYKISDGGGEHFVNDGSYSIY 480
DB 421 KSGIALITDGPQSGSKMYAGLKNAGETWYDITGNRSYTYKISDGGGEHFVNDGSYSIY 480

RESULT 5
US-09-672-459-4
Sequence 4, Application US/09672459
Patent No. 6436888
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Borchert, Torben Vedel
APPLICANT: Bisgaard-Frantzen Henrik
APPLICANT: Oulstrup, Heile
APPLICANT: Nielsen, Bjarne Ronfeldt
APPLICANT: Nielsen, Vibeke Skovgaard
APPLICANT: Hoeck, Lisbeth Hedegaard
TITLE OF INVENTION: Alpha-Amylase Mutants
FILE REFERENCE: 4796.204-US
CURRENT APPLICATION NUMBER: US/09/672,459
CURRENT FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: 09/182,859
PRIOR FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: 0515/96
PRIOR FILING DATE: 1996-04-30
PRIOR APPLICATION NUMBER: 0712/96
PRIOR FILING DATE: 1996-06-28
PRIOR APPLICATION NUMBER: 0775/96
PRIOR FILING DATE: 1996-07-11
PRIOR APPLICATION NUMBER: 1263/96
PRIOR FILING DATE: 1996-11-08
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 480
TYPE: PRT
ORGANISM: Bacillus amyloliquefaciens
US-09-672-459-4

Query Match 100.0%; Score 2624; DB 4; Length 480;
Best Local Similarity 100.0%; Pred. No. 3.8e-230; Indels 0; Gaps 0;
Matches 480; Conservative 0; Mismatches 0;

QY 1 VNGTLMQYFEWYTPNDQGMKRLQNDABHLSDIGITAWIPPAKGLSGSDNGYGYDLY 60
DB 1 VNGTLMQYFEWYTPNDQGMKRLQNDABHLSDIGITAWIPPAKGLSGSDNGYGYDLY 60

QY 61 DLGEFOQKGVTRTKYGTSELODAIGLSHRNVQYGVVLTNKAQADATEDVTAVEVNP 120
DB 61 DLGEFOQKGVTRTKYGTSELODAIGLSHRNVQYGVVLTNKAQADATEDVTAVEVNP 120

QY 121 ANRNOETSEBYQIKAWTDFRFRGNTYSDPKMWHYHDGADWDESRKISRIFKFRGEK 180
DB 121 ANRNOETSEBYQIKAWTDFRFRGNTYSDPKMWHYHDGADWDESRKISRIFKFRGEK 180

QY 181 AMDWEVSSNGNYDYLMTADVDYDHPDVAETKKGWIYANELSLDGRIDAACHIKFSF 240
DB 181 AMDWEVSSNGNYDYLMTADVDYDHPDVAETKKGWIYANELSLDGRIDAACHIKFSF 240

QY 241 LRDWVOAARQATGKEMFTVAEYWNNAKLENYLNKTSFNOSVDPVPHNLQAASSQGG 300
DB 241 LRDWVOAARQATGKEMFTVAEYWNNAKLENYLNKTSFNOSVDPVPHNLQAASSQGG 300

QY 301 GYDMRRLDGTIVSSHPEKAVTFVENHDTOPQOSLESTVQTFKELAYAFILITRESGYPQ 360
DB 301 GYDMRRLDGTIVSSHPEKAVTFVENHDTOPQOSLESTVQTFKELAYAFILITRESGYPQ 360

QY 361 VFYGDMYGTGKTSPEILSKNIEPILKAREYAYGQOHYIDHPDVIQWTRREGDSAA 420
DB 361 VFYGDMYGTGKTSPEILSKNIEPILKAREYAYGQOHYIDHPDVIQWTRREGDSAA 420

QY 421 KSGLAALITDGGSGSKRYAGLKNAGETWYDITGNRSDTVKIGSDGWEFFHNDGSVSIY 480
DB 421 KSGLAALITDGGSGSKRYAGLKNAGETWYDITGNRSDTVKIGSDGWEFFHNDGSVSIY 480

RESULT 7
US-09-545-586-5
Sequence 5; Application US/09545586
Patent No. 6528298
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Borchert, Torben Vedel
APPLICANT: Bisgaard-Frantzen Henrik
APPLICANT: Cuistrup, Heile
APPLICANT: Nielsen, Bjarne Ronfeldt
APPLICANT: Nielsen, Vibeke Skovgaard
APPLICANT: Hoeck, Lisbeth Hedegaard
TITLE OF INVENTION: No. 6528298e1 -Amylase And -Amylase Mutants
FILE REFERENCE: 5276.400-US
CURRENT APPLICATION NUMBER: US/09/545,586
CURRENT FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: US/09/290,734
PRIOR FILING DATE: 1999-04-13
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO: 5
LENGTH: 480
TYPE: PRT
ORGANISM: B. amyloliquefaciens
US-09-545-586-5

Query Match 100.0%; Score 2624; DB 4; Length 480;
Best Local Similarity 100.0%; Pred. No. 3.8e-230; Indels 0; Gaps 0;
Matches 480; Conservative 0; Mismatches 0;

QY 1 VNGTLMQYFEWYTPNDQGMKRLQNDABHLSDIGITAWIPPAKGLSGSDNGYGYDLY 60
DB 1 VNGTLMQYFEWYTPNDQGMKRLQNDABHLSDIGITAWIPPAKGLSGSDNGYGYDLY 60

QY 61 DLGEFOQKGVTRTKYGTSELODAIGLSHRNVQYGVVLTNKAQADATEDVTAVEVNP 120
DB 61 DLGEFOQKGVTRTKYGTSELODAIGLSHRNVQYGVVLTNKAQADATEDVTAVEVNP 120

QY 121 ANRNOETSEBYQIKAWTDFRFRGNTYSDPKMWHYHDGADWDESRKISRIFKFRGEK 180
DB 121 ANRNOETSEBYQIKAWTDFRFRGNTYSDPKMWHYHDGADWDESRKISRIFKFRGEK 180

QY 181 AMDWEVSSNGNYDYLMTADVDYDHPDVAETKKGWIYANELSLDGRIDAACHIKFSF 240
DB 181 AMDWEVSSNGNYDYLMTADVDYDHPDVAETKKGWIYANELSLDGRIDAACHIKFSF 240

QY 241 LRDWVOAARQATGKEMFTVAEYWNNAKLENYLNKTSFNOSVDPVPHNLQAASSQGG 300
DB 241 LRDWVOAARQATGKEMFTVAEYWNNAKLENYLNKTSFNOSVDPVPHNLQAASSQGG 300

QY 301 GYDMRRLDGTIVSSHPEKAVTFVENHDTOPQOSLESTVQTFKELAYAFILITRESGYPQ 360
DB 301 GYDMRRLDGTIVSSHPEKAVTFVENHDTOPQOSLESTVQTFKELAYAFILITRESGYPQ 360

QY 361 VFYGDMYGTGKTSPEILSKNIEPILKAREYAYGQOHYIDHPDVIQWTRREGDSAA 420
DB 361 VFYGDMYGTGKTSPEILSKNIEPILKAREYAYGQOHYIDHPDVIQWTRREGDSAA 420

QY 421 KSGLAALITDGGSGSKRYAGLKNAGETWYDITGNRSDTVKIGSDGWEFFHNDGSVSIY 480
DB 421 KSGLAALITDGGSGSKRYAGLKNAGETWYDITGNRSDTVKIGSDGWEFFHNDGSVSIY 480

RESULT 8
US-10-186-042-4
Sequence 4; Application US/10186042
Patent No. 6642044
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Borchert, Torben
APPLICANT: Bisgaard-Frantzen, Henrik
TITLE OF INVENTION: Alpha-Amylase Mutants
FILE REFERENCE: 4796.204-US
CURRENT APPLICATION NUMBER: US/10/186,042
CURRENT FILING DATE: 2002-06-28
PRIOR APPLICATION NUMBER: US/09/672,459
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: 09/182,859
PRIOR FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: 0515/96
PRIOR FILING DATE: 1996-04-30
PRIOR APPLICATION NUMBER: 0712/96
PRIOR FILING DATE: 1996-06-28
PRIOR APPLICATION NUMBER: 0775/96
PRIOR FILING DATE: 1996-07-11
PRIOR APPLICATION NUMBER: 1263/96
PRIOR FILING DATE: 1996-11-08
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO: 4
LENGTH: 480
TYPE: PRT
ORGANISM: Bacillus amyloliquefaciens
US-10-186-042-4

Query Match 100.0%; Score 2624; DB 4; Length 480;
Best Local Similarity 100.0%; Pred. No. 3.8e-230; Indels 0; Gaps 0;
Matches 480; Conservative 0; Mismatches 0;

QY 1 VNGTLMQYFEWYTPNDQGMKRLQNDABHLSDIGITAWIPPAKGLSGSDNGYGYDLY 60
DB 1 VNGTLMQYFEWYTPNDQGMKRLQNDABHLSDIGITAWIPPAKGLSGSDNGYGYDLY 60

QY 61 DLGEFOQKGVTRTKYGTSELODAIGLSHRNVQYGVVLTNKAQADATEDVTAVEVNP 120
DB 61 DLGEFOQKGVTRTKYGTSELODAIGLSHRNVQYGVVLTNKAQADATEDVTAVEVNP 120

QY 121 ANRNOETSEBYQIKAWTDFRFRGNTYSDPKMWHYHDGADWDESRKISRIFKFRGEK 180
DB 121 ANRNOETSEBYQIKAWTDFRFRGNTYSDPKMWHYHDGADWDESRKISRIFKFRGEK 180

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Db 121 ANRNETSEBYOIKAMTDFRPGKNTYSDFKMHHYHDGADWDSRKSIRLFRKRGSGK 180
Qy 181 AMDWEVSSSENGNDYLYMADVDYDHPDVVAETKKGIWANELSLDGRIDAAXIKFSF 240
Db 181 AMDWEVSSSENGNDYLYMADVDYDHPDVVAETKKGIWANELSLDGRIDAAXIKFSF 240
Qy 241 LRDWVOAVQATGKEMFTVAEYQNNAGKLENTLNTSFNOSVFDPVLFHNLQAASSQGG 300
Db 241 LRDWVOAVQATGKEMFTVAEYQNNAGKLENTLNTSFNOSVFDPVLFHNLQAASSQGG 300
Qy 301 GYDMRLLDGTIVSSRHPKAVTFVENHDTOPGQSLSESTVQWTFKPLAVAFILITRESGPQ 360
Db 301 GYDMRLLDGTIVSSRHPKAVTFVENHDTOPGQSLSESTVQWTFKPLAVAFILITRESGPQ 360
Qy 361 VFYGDWYGTGTSPEKIPSLKDNIEPIILKARKEVAYGPQHDYIDHPDVIQWTRREGSSAA 420
Db 361 VFYGDWYGTGTSPEKIPSLKDNIEPIILKARKEVAYGPQHDYIDHPDVIQWTRREGSSAA 420
Qy 421 KSGLAALITDGPQSGSKMYAGLKNAGETWYDITGNRSDTVKIGSDGWEFFHNDGSVSIY 480
Db 421 KSGLAALITDGPQSGSKMYAGLKNAGETWYDITGNRSDTVKIGSDGWEFFHNDGSVSIY 480

RESULT 9
US-09-769-864-5
; Sequence 5, Application US/09769864
; Patent No. 6673589
; GENERAL INFORMATION:
; APPLICANT: Borchert, Torben V.
; APPLICANT: Andersen, Allan
; APPLICANT: Andersen, Carsten
; APPLICANT: Nielsen, Bjarne
; APPLICANT: Nielsen, Torben L.
; APPLICANT: Kjaerulf, Soren
; TITLE OF INVENTION: Alpha-Amulase Mutants
; FILE REFERENCE: 5368.200-US
; CURRENT APPLICATION NUMBER: US/09/769,864
; CURRENT FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/183,412
; PRIOR FILING DATE: 1998-10-30
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Bacillus amyloliquifaciens
US-09-769-864-5

Query Match 100.0%; Score 2624; DB 4; Length 480;
Best Local Similarity 100.0%; Pred. No. 3,8e-230;
Matches 480; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VNGTLMQYFEMWYTPNDGQHWKRLQNDAEHLSDIGITAWIIPRAYKGLSGSDNGYGPYDLY 60
Db 1 VNGTLMQYFEMWYTPNDGQHWKRLQNDAEHLSDIGITAWIIPRAYKGLSGSDNGYGPYDLY 60
Qy 61 DLGEFOOKGTIVRTKYGTGKSELQDAIGLSHRNVQYGVVNLHKGADATEDEVTAVERNVP 120
Db 61 DLGEFOOKGTIVRTKYGTGKSELQDAIGLSHRNVQYGVVNLHKGADATEDEVTAVERNVP 120
Qy 121 ANRNETSEBYOIKAMTDFRPGKNTYSDFKMHHYHDGADWDSRKSIRLFRKRGSGK 180
Db 121 ANRNETSEBYOIKAMTDFRPGKNTYSDFKMHHYHDGADWDSRKSIRLFRKRGSGK 180
Qy 181 AMDWEVSSSENGNDYLYMADVDYDHPDVVAETKKGIWANELSLDGRIDAAXIKFSF 240
Db 181 AMDWEVSSSENGNDYLYMADVDYDHPDVVAETKKGIWANELSLDGRIDAAXIKFSF 240
Qy 241 LRDWVOAVQATGKEMFTVAEYQNNAGKLENTLNTSFNOSVFDPVLFHNLQAASSQGG 300
Db 241 LRDWVOAVQATGKEMFTVAEYQNNAGKLENTLNTSFNOSVFDPVLFHNLQAASSQGG 300
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Qy 301 GYDMRLLDGTIVSSRHPKAVTFVENHDTOPGQSLSESTVQWTFKPLAVAFILITRESGPQ 360
Db 301 GYDMRLLDGTIVSSRHPKAVTFVENHDTOPGQSLSESTVQWTFKPLAVAFILITRESGPQ 360
Qy 361 VFYGDWYGTGTSPEKIPSLKDNIEPIILKARKEVAYGPQHDYIDHPDVIQWTRREGSSAA 420
Db 361 VFYGDWYGTGTSPEKIPSLKDNIEPIILKARKEVAYGPQHDYIDHPDVIQWTRREGSSAA 420
Qy 421 KSGLAALITDGPQSGSKMYAGLKNAGETWYDITGNRSDTVKIGSDGWEFFHNDGSVSIY 480
Db 421 KSGLAALITDGPQSGSKMYAGLKNAGETWYDITGNRSDTVKIGSDGWEFFHNDGSVSIY 480

RESULT 10
US-09-291-023A-16
; Sequence 16, Application US/09291023A
; Patent No. 6303871
; GENERAL INFORMATION:
; APPLICANT: Ouettrup, Helle
; APPLICANT: Borchert, Torben
; APPLICANT: Nielsen, Bjarne
; APPLICANT: Nielsen, Vibeke
; APPLICANT: Hoeck, Lisbeth
; TITLE OF INVENTION: Polypeptides Having Alkaline Alpha-amylase Activity And Nucleic A
; FILE REFERENCE: 5821.010-US
; CURRENT APPLICATION NUMBER: US/09/291,023A
; CURRENT FILING DATE: 1999-04-13
; PRIOR APPLICATION NUMBER: DK 1999 00438
; PRIOR FILING DATE: 1999-03-31
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 16
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Bacillus
US-09-291-023A-16

Query Match 100.0%; Score 2624; DB 4; Length 483;
Best Local Similarity 100.0%; Pred. No. 3,8e-230;
Matches 480; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VNGTLMQYFEMWYTPNDGQHWKRLQNDAEHLSDIGITAWIIPRAYKGLSGSDNGYGPYDLY 60
Db 1 VNGTLMQYFEMWYTPNDGQHWKRLQNDAEHLSDIGITAWIIPRAYKGLSGSDNGYGPYDLY 60
Qy 61 DLGEFOOKGTIVRTKYGTGKSELQDAIGLSHRNVQYGVVNLHKGADATEDEVTAVERNVP 120
Db 61 DLGEFOOKGTIVRTKYGTGKSELQDAIGLSHRNVQYGVVNLHKGADATEDEVTAVERNVP 120
Qy 121 ANRNETSEBYOIKAMTDFRPGKNTYSDFKMHHYHDGADWDSRKSIRLFRKRGSGK 180
Db 121 ANRNETSEBYOIKAMTDFRPGKNTYSDFKMHHYHDGADWDSRKSIRLFRKRGSGK 180
Qy 181 AMDWEVSSSENGNDYLYMADVDYDHPDVVAETKKGIWANELSLDGRIDAAXIKFSF 240
Db 181 AMDWEVSSSENGNDYLYMADVDYDHPDVVAETKKGIWANELSLDGRIDAAXIKFSF 240
Qy 241 LRDWVOAVQATGKEMFTVAEYQNNAGKLENTLNTSFNOSVFDPVLFHNLQAASSQGG 300
Db 241 LRDWVOAVQATGKEMFTVAEYQNNAGKLENTLNTSFNOSVFDPVLFHNLQAASSQGG 300
Qy 301 GYDMRLLDGTIVSSRHPKAVTFVENHDTOPGQSLSESTVQWTFKPLAVAFILITRESGPQ 360
Db 301 GYDMRLLDGTIVSSRHPKAVTFVENHDTOPGQSLSESTVQWTFKPLAVAFILITRESGPQ 360
Qy 361 VFYGDWYGTGTSPEKIPSLKDNIEPIILKARKEVAYGPQHDYIDHPDVIQWTRREGSSAA 420
Db 361 VFYGDWYGTGTSPEKIPSLKDNIEPIILKARKEVAYGPQHDYIDHPDVIQWTRREGSSAA 420
Qy 421 KSGLAALITDGPQSGSKMYAGLKNAGETWYDITGNRSDTVKIGSDGWEFFHNDGSVSIY 480
Db 421 KSGLAALITDGPQSGSKMYAGLKNAGETWYDITGNRSDTVKIGSDGWEFFHNDGSVSIY 480
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RESULT 11
US-09-537-168-6
; Sequence 6, Application US/09537168
; Patent No. 6410295
; GENERAL INFORMATION:
; APPLICANT: Andersen, Carsten
; APPLICANT: Jorgensen, Christel T.
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Svendsen, Allan
; APPLICANT: Kjaerulff, Soren
; TITLE OF INVENTION: Alpha-Amylase Variants
; FILE REFERENCE: 5886.200-US
; CURRENT APPLICATION NUMBER: US/09/537,168
; CURRENT FILING DATE: 2000-03-29
; EARLIER APPLICATION NUMBER: PA 1999 00437
; EARLIER FILING DATE: 1999-03-30
; EARLIER APPLICATION NUMBER: 60/127,427
; EARLIER FILING DATE: 1999-04-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 6
; LENGTH: 483
; TYPE: PRF
; ORGANISM: Bacillus amyloliquefaciens
US-09-537-168-6

Query Match      100.0%; Score 2624; DB 4; Length 483;
Best Local Similarity 100.0%; Pred. No. 3.8e-230;
Matches 480; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNGTLMQYFEMWTPNDGQHMKRLQNDAEHLSDIGITAWIPPAYKGLSQSDNGYGPYDLY 60
DB 1 VNGTLMQYFEMWTPNDGQHMKRLQNDAEHLSDIGITAWIPPAYKGLSQSDNGYGPYDLY 60
QY 61 DLGEFOQKGTVRTKTKGTSKSELQDAIGSLHSRNQYGVYVNLHKKAGADATEDVTAVEVNP 120
DB 61 DLGEFOQKGTVRTKTKGTSKSELQDAIGSLHSRNQYGVYVNLHKKAGADATEDVTAVEVNP 120
QY 121 ANRNOETSEHYQIKAMTDRFPGRGNTYSDFKMWHYHFGADWDSRKISRIFKRGEGK 180
DB 121 ANRNOETSEHYQIKAMTDRFPGRGNTYSDFKMWHYHFGADWDSRKISRIFKRGEGK 180
QY 181 AMDWEVSSENGNDYLMYADVDPDVAETKMGWIYANELSLDGFRIIDAKKIKFSF 240
DB 181 AMDWEVSSENGNDYLMYADVDPDVAETKMGWIYANELSLDGFRIIDAKKIKFSF 240
QY 241 LRDWQAVRQATGKEMFTVAEYQNNAGKLENTSNQSVFDPVPLHFNLOAASQGG 300
DB 241 LRDWQAVRQATGKEMFTVAEYQNNAGKLENTSNQSVFDPVPLHFNLOAASQGG 300
QY 301 GYDMRRLDGTIVSRPEKAVTFVENHDTQPGSLESTVQTFWKPLAVAFILTRSGYPQ 360
DB 301 GYDMRRLDGTIVSRPEKAVTFVENHDTQPGSLESTVQTFWKPLAVAFILTRSGYPQ 360
QY 361 VFYGDWYGTGTSPEKIPSLKDNIEPILKARKKYAAGPHDYIDHEDVIGWTRGDSAA 420
DB 361 VFYGDWYGTGTSPEKIPSLKDNIEPILKARKKYAAGPHDYIDHEDVIGWTRGDSAA 420
QY 421 KSGIALITDGPQGSKRMVAGLKNAGEETWYDITGNRSDTVKIGSDMGGEFHVNDGSVSIY 480
DB 421 KSGIALITDGPQGSKRMVAGLKNAGEETWYDITGNRSDTVKIGSDMGGEFHVNDGSVSIY 480

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; APPLICANT: IGARASHI, Kazuaki
; APPLICANT: HAGIHARA, Hiroshi
; APPLICANT: HAYASHI, Yasunori
; APPLICANT: ARAKI, Hiroyuki
; APPLICANT: OZAKI, Katsuya
; TITLE OF INVENTION: MUTANT ALPHA-AMYLASES
; FILE REFERENCE: 2173-0115P
; CURRENT APPLICATION NUMBER: US/09/381,687
; CURRENT FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 6
; LENGTH: 483
; TYPE: PRF
; ORGANISM: B. amyloliquefaciens
US-09-381-687-6

Query Match      100.0%; Score 2624; DB 4; Length 483;
Best Local Similarity 100.0%; Pred. No. 3.8e-230;
Matches 480; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNGTLMQYFEMWTPNDGQHMKRLQNDAEHLSDIGITAWIPPAYKGLSQSDNGYGPYDLY 60
DB 1 VNGTLMQYFEMWTPNDGQHMKRLQNDAEHLSDIGITAWIPPAYKGLSQSDNGYGPYDLY 60
QY 61 DLGEFOQKGTVRTKTKGTSKSELQDAIGSLHSRNQYGVYVNLHKKAGADATEDVTAVEVNP 120
DB 61 DLGEFOQKGTVRTKTKGTSKSELQDAIGSLHSRNQYGVYVNLHKKAGADATEDVTAVEVNP 120
QY 121 ANRNOETSEHYQIKAMTDRFPGRGNTYSDFKMWHYHFGADWDSRKISRIFKRGEGK 180
DB 121 ANRNOETSEHYQIKAMTDRFPGRGNTYSDFKMWHYHFGADWDSRKISRIFKRGEGK 180
QY 181 AMDWEVSSENGNDYLMYADVDPDVAETKMGWIYANELSLDGFRIIDAKKIKFSF 240
DB 181 AMDWEVSSENGNDYLMYADVDPDVAETKMGWIYANELSLDGFRIIDAKKIKFSF 240
QY 241 LRDWQAVRQATGKEMFTVAEYQNNAGKLENTSNQSVFDPVPLHFNLOAASQGG 300
DB 241 LRDWQAVRQATGKEMFTVAEYQNNAGKLENTSNQSVFDPVPLHFNLOAASQGG 300
QY 301 GYDMRRLDGTIVSRPEKAVTFVENHDTQPGSLESTVQTFWKPLAVAFILTRSGYPQ 360
DB 301 GYDMRRLDGTIVSRPEKAVTFVENHDTQPGSLESTVQTFWKPLAVAFILTRSGYPQ 360
QY 361 VFYGDWYGTGTSPEKIPSLKDNIEPILKARKKYAAGPHDYIDHEDVIGWTRGDSAA 420
DB 361 VFYGDWYGTGTSPEKIPSLKDNIEPILKARKKYAAGPHDYIDHEDVIGWTRGDSAA 420
QY 421 KSGIALITDGPQGSKRMVAGLKNAGEETWYDITGNRSDTVKIGSDMGGEFHVNDGSVSIY 480
DB 421 KSGIALITDGPQGSKRMVAGLKNAGEETWYDITGNRSDTVKIGSDMGGEFHVNDGSVSIY 480

RESULT 13
US-09-540-715A-16
; Sequence 16, Application US/09540715A
; Patent No. 6623948
; GENERAL INFORMATION:
; APPLICANT: Outtrup, Helle
; APPLICANT: Borchert, Torben
; APPLICANT: Nielsen, Bjarne
; APPLICANT: Nielsen, Videke
; APPLICANT: Hoeck, Lisbeth
; TITLE OF INVENTION: Polypeptides Having Alkaline Alpha-amylase Activity And Nucleic Ac
; FILE REFERENCE: 5821.010-US
; CURRENT APPLICATION NUMBER: US/09/540,715A
; CURRENT FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/291,023
; PRIOR FILING DATE: 2001-08-14
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0

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Tue May 4 14:34:46 2004

us-10-644-187-4.rail

Page 7

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; SEQ ID NO 16
; LENGTH: 483
; TYPE: prt
; ORGANISM: Bacillus
US-09-540-715A-16

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Query Match	100.0%;	Score 2624;	DB 4;	Length 483;
Best Local Similarity	100.0%;	Pred. No. 3,8e-230;		
Matches 480;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

Qy	1	VNGTLMQYFEMTYFPNPGQHWKRLQNDAEHLSDIGITAWIPPAKXGJLSQSNNGEPDLY	60
Db	1	VNGTLMQYFEMTYFPNPGQHWKRLQNDAEHLSDIGITAWIPPAKXGJLSQSNNGEPDLY	60
Qy	61	DLGEFOQKGTVRKTKYGTGKSELDAIGLSLSRVQYGSVYLNHKAQADAEPTYAVNVP	120
Db	61	DLGEFOQKGTVRKTKYGTGKSELDAIGLSLSRVQYGSVYLNHKAQADAEPTYAVNVP	120
Qy	121	ANRQOETSESEYQIKAMTDPRFPGRGNTYSDPFKMHYHFDGADWDSESKISRIFPKRGEGK	180
Db	121	ANRQOETSESEYQIKAMTDPRFPGRGNTYSDPFKMHYHFDGADWDSESKISRIFPKRGEGK	180
Qy	181	AMDWEVSSSENGNDYLTMYADVDYDHPDVPVAETKKGIMYANELSJDGFRIDAAGHIFSF	240
Db	181	AMDWEVSSSENGNDYLTMYADVDYDHPDVPVAETKKGIMYANELSJDGFRIDAAGHIFSF	240
Qy	241	LRDVQVAVRQATGKEMFTVAEYQWQNNAGKLENYLAKTSPNOSVFVPLPHFPLQAASSQGG	300
Db	241	LRDVQVAVRQATGKEMFTVAEYQWQNNAGKLENYLAKTSPNOSVFVPLPHFPLQAASSQGG	300
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Db	301	GYDWRRLLDGTIVVSRHEKAVTFVENHDPQPGSLESITQVTFKFLAYAFILTRESGYPQ	360
Qy	361	VFYGDWYGTGKTSPEKIPSLKDNIEPLTKAREYAYGPOHDYIDHPDYIGMTRBGDSAA	420
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RESULT 14
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 : Sequence 4, Application US/0820899
 : Patent No. 5753460
 : GENERAL INFORMATION:
 : APPLICANT: Bisgaard-Frantzen, Henrik
 : APPLICANT: Borchert, Torben Vedel
 : APPLICANT: Svendsen, Allan
 : APPLICANT: Thellersen, Marianne
 : APPLICANT: Van der Zee, Pia
 : TITLE OF INVENTION: AWTBASE VARIANTS
 : NUMBER OF SEQUENCES: 38
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: No. 57534600 No. 57534600isk of No. 57534600h America, Inc
 : STREET: 405 Lexington Avenue, 64th floor
 : CITY: New York
 : STATE: New York
 : COUNTRY: USA
 : ZIP: 10174-6401
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: PatentIn Release #1.0, Version #1.30
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/720,899
 : FILING DATE: 10-OCT-1996
 : CLASSIFICATION: 435
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: US 08/343,804

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? FILING DATE: 22-NOV-1994
? ATTORNEY/AGENT INFORMATION:
?
? NAME: Lowmye Dr., Karen A.
? REGISTRATION NUMBER: 31,274
? REFERENCE/DOCKET NUMBER: 4054.214-US
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 212-867-0123
? TELEFAX: 212-878-9655
? INFORMATION FOR SEQ ID NO: 4:
? SEQUENCE CHARACTERISTICS:
?
? LENGTH: 514 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
?
US-08-720-899-4

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Query Match	100.0%;	Score 2624;	DB 1;	Length 514;
Best Local Similarity	100.0%;	Pred. No. 4.2e-230;		
Matches 480;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

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Db		32 VNGTLMQFFENTPRDGGHMKRLQNDABHSDIGITAWIPRAYKGLSOGSDNGYBPYLY	91
Qy		61 DLGEFOQKGYVTKYKXGKSELQDAIGSLHSRNVQYGVVLNHRKAGADATEDVTAVERN	120
Db		92 DLGEFOQKGYVTKYKXGKSELQDAIGSLHSRNVQYGVVLNHRKAGADATEDVTAVERN	151
Qy		121 ANRNOETSEBYQIKAWTDPFRPPRGENTYSDPFWMHYHDPGDAMDASRKISRIFKRGEGK	180
Db		152 ANRNOETSEBYQIKAWTDPFRPPRGENTYSDPFWMHYHDPGDAMDASRKISRIFKRGEGK	211
Qy		181 AMDWEVSSENGNYDYLMYADVDYDEPPDVAAETKKGIMWANELSLDGERIDAKIKFSF	240
Db		212 AMDWEVSSENGNYDYLMYADVDYDEPPDVAAETKKGIMWANELSLDGERIDAKIKFSF	271
Qy		241 IARDWQAVRQATGKEMFTVAETVWONNAGKLENYLNTKSNOSVDFPPLHFNIOAASSOGG	300
Db		272 IARDWQAVRQATGKEMFTVAETVWONNAGKLENYLNTKSNOSVDFPPLHFNIOAASSOGG	331
Qy		301 GYDMRRLLDGTVSRHPEKAVTFVENHDPQPOQSLESTQTMFKPLAFAFILTBRESGYEQ	360
Db		332 GYDMRRLLDGTVSRHPEKAVTFVENHDPQPOQSLESTQTMFKPLAFAFILTBRESGYEQ	391
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 ; Sequence 4, Application US/08459610
 ; Patent No. 5801043
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 ; GENERAL INFORMATION:
 ; APPLICANT: Bisgaard-Frantzen, Henrik
 ; APPLICANT: Borchert, Torben Vedel
 ; APPLICANT: Svendsen, Allan
 ; APPLICANT: Thelersen, Marianne
 ; APPLICANT: Van der Zee, Pia
 ; TITLE OF INVENTION: AMYLASE VARIANTS
 ; NUMBER OF SEQUENCES: 38
 ; CORRESPONDENCE ADDRESSES:
 ; ADDRESS: No. 58010430 No. 5801043disk of No. 5801043th America, Inc
 ; STREET: 405 Lexington Avenue, 64th Floor
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10174-6401
 ;
 ; COMPUTER READABLE FORM:
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MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,610
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/343,804
FILING DATE: 22-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lowmey Dr., Karen A.
REGISTRATION NUMBER: 31,274
REFERENCE/DOCKET NUMBER: 4054.214-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 514 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-610-4

Query Match 100.0%; Score 2624; DB 1; Length 514;
Best Local Similarity 100.0%; Pred. No. 4.2e-230;
Matches 480; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 61 DLGEFQOKGTVRTKYGTSELQDAIGSLHSRNVQYGVVNLNKAADATEDVTAVEVNP 120
DB 92 DLGEFQOKGTVRTKYGTSELQDAIGSLHSRNVQYGVVNLNKAADATEDVTAVEVNP 151
QY 121 ANRNOETSEYQIKAMTDFRFGNGNTYSDFKMHWYHFGADWDSRKISRIFFKRGK 180
DB 152 ANRNOETSEYQIKAMTDFRFGNGNTYSDFKMHWYHFGADWDSRKISRIFFKRGK 211
QY 181 AMDWEVSSNGNYDYLMDVADVDYDHPDVAETFKWGIWYANELSLDGFRIDAKKIKFSF 240
DB 212 AMDWEVSSNGNYDYLMDVADVDYDHPDVAETFKWGIWYANELSLDGFRIDAKKIKFSF 271
QY 241 LRDWVOAVQATGKEMFTVAETWONNAGLENYLNKTSFNOSVDPVPLHFNLOAASSOGG 300
DB 272 LRDWVOAVQATGKEMFTVAETWONNAGLENYLNKTSFNOSVDPVPLHFNLOAASSOGG 331
QY 301 GYDMRRLDGTAVSRPEKAVTFVENHDTQPGQSLESTVQTFKPLAYAFITRESGYPO 360
DB 332 GYDMRRLDGTAVSRPEKAVTFVENHDTQPGQSLESTVQTFKPLAYAFITRESGYPO 391
QY 361 VRYGDMYGTGTSPEKIEPLKDNIEPIILAKREYAYGPOHDYIDHPDVIGMTREGSSAA 420
DB 392 VRYGDMYGTGTSPEKIEPLKDNIEPIILAKREYAYGPOHDYIDHPDVIGMTREGSSAA 451
QY 421 KSGIALITDGPQGSKRWYAGLKNAGETWYDITGNRSDTVKIGSDGMBGFHNDGSVSIY 480
DB 452 KSGIALITDGPQGSKRWYAGLKNAGETWYDITGNRSDTVKIGSDGMBGFHNDGSVSIY 511

Search completed: May 3, 2004, 20:35:56
Job time: 17.2492 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 3, 2004, 20:33:58 ; Search time 37.3731 Seconds

(without alignments)
3560.078 Million cell updates/sec

Title: US-10-644-187-4

Perfect score: 2624

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1138120 seqs, 277189581 residues

Total number of hits satisfying chosen parameters: 1138120

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database:

Listing first 45 summaries

Published Applications AA:*
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2: /cgn2_6/prodata/2/pubppa/PCR_NEW_PUB.pep:*
3: /cgn2_6/prodata/2/pubppa/US06_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2624	100.0	480	12 US-10-665-667-5	Sequence 5, Appl1
3	2624	100.0	480	12 US-10-644-187-4	Sequence 4, Appl1
4	2624	100.0	480	12 US-10-327-837-5	Sequence 5, Appl1
5	2624	100.0	480	14 US-10-186-042-4	Sequence 4, Appl1
6	2624	100.0	483	9 US-09-854-346-10	Sequence 10, Appl1
7	2624	100.0	483	9 US-09-918-543-10	Sequence 10, Appl1
8	2624	100.0	483	9 US-09-925-576C-10	Sequence 10, Appl1
9	2624	100.0	514	14 US-10-146-327-6	Sequence 6, Appl1
10	2624	100.0	514	14 US-10-184-771-4	Sequence 4, Appl1
11	2475	94.3	483	14 US-10-184-771-13	Sequence 13, Appl1
12	2190	83.5	481	14 US-10-146-327-2	Sequence 2, Appl1
13	2182	83.2	512	14 US-10-081-872-114	Sequence 114, App
14	2182	83.2	512	14 US-10-105-733-8	Sequence 8, Appl1
15	2182	83.2	512	14 US-10-081-739A-8	Sequence 8, Appl1

16	2182	83.2	512	15 US-10-385-305-114	Sequence 114, App
17	2176	82.9	512	14 US-10-199-922-2	Sequence 2, Appl1
18	2173	82.8	483	9 US-09-769-864-4	Sequence 4, Appl1
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21	2173	82.8	483	9 US-09-918-543-30	Sequence 30, Appl1
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26	2173	82.8	483	14 US-10-146-327-4	Sequence 2, Appl1
27	2173	82.8	483	14 US-10-186-042-2	Sequence 2, Appl1
28	2173	82.8	512	14 US-10-184-771-2	Sequence 2, Appl1
29	1921	73.2	513	14 US-10-081-872-146	Sequence 146, App
30	1921	73.2	513	15 US-10-385-305-146	Sequence 146, App
31	1919	73.1	513	14 US-10-081-872-70	Sequence 70, Appl1
32	1919	73.1	513	15 US-10-385-305-70	Sequence 70, Appl1
33	1911	72.8	478	14 US-10-081-872-166	Sequence 166, App
34	1911	72.8	478	15 US-10-385-305-166	Sequence 166, App
35	1863	71.0	485	9 US-09-769-864-2	Sequence 2, Appl1
36	1863	71.0	485	9 US-09-769-864-8	Sequence 8, Appl1
37	1863	71.0	485	9 US-09-854-346-4	Sequence 4, Appl1
38	1863	71.0	485	9 US-09-902-188A-2	Sequence 2, Appl1
39	1863	71.0	485	9 US-09-918-543-4	Sequence 4, Appl1
40	1863	71.0	485	9 US-09-795-211-2	Sequence 2, Appl1
41	1863	71.0	485	10 US-09-925-576C-4	Sequence 4, Appl1
42	1863	71.0	485	12 US-10-665-667-2	Sequence 2, Appl1
43	1863	71.0	485	12 US-10-665-667-8	Sequence 8, Appl1
44	1863	71.0	485	12 US-10-025-648-2	Sequence 2, Appl1
45	1863	71.0	485	12 US-10-327-837-2	Sequence 2, Appl1

ALIGNMENTS

RESULT 1
US-09-769-864-5
; Sequence 5, Application US/09769864
; Patent No. US20010039253A1
GENERAL INFORMATION:
; APPLICANT: Borchert, Torben V.
; APPLICANT: Svendsen, Allan
; APPLICANT: Andersen, Carsten
; APPLICANT: Nielsen, Bjarne
; APPLICANT: Nissen, Torben L.
; APPLICANT: Kjaerulff, Soren
; TITLE OF INVENTION: Alpha-Amulase Mutants
; FILE REFERENCE: 5368 200-US
CURRENT APPLICATION NUMBER: US/09/769,864
CURRENT FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: 09/183,412
PRIOR FILING DATE: 1998-10-30
NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Bacillus amyloliquifaciens
US-09-769-864-5
Query Match 100.0%; Score 2624; DB 9; Length 480;
Best Local Similarity 100.0%; Pred. No. 3.6e-237;
Matches 480; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 61 DLGEQOQGTATYKGTGSELDALIGSLHSRNVQGVVLTNKAQADATEDYAVAVNP 120
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Db 301 GYDMRRLDGTIVSRHPEKAVTFVENHDTOPQGSLESTVQTMFKPLAVAFILTRBSGYPO 360
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Db 361 VFYGDWYGTGTSPEIKSLKDNIEPIIKARKEVAYGPHDYIDHPDVIQWTRBGSSAA 420
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RESULT 2

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US-10-665-667-5
; Sequence 5, Application US/10665667
; Publication No. US20040038368A1
; GENERAL INFORMATION:
; APPLICANT: Borchert, Torben V.
; APPLICANT: Svendsen, Allan
; APPLICANT: Andersen, Carsten
; APPLICANT: Nielsen, Bjarne
; APPLICANT: Nielsen, Torben L.
; APPLICANT: Kjaerulff, Soren
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 5368-200-US
; CURRENT APPLICATION NUMBER: US/10/665,667
; CURRENT FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: US/09/769,864
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/183,412
; PRIOR FILING DATE: 1998-10-30
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Bacillus amyloliquefaciens
US-10-665-667-5
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Query Match 100.0%; Score 2624; DB 12; Length 480;

Best Local Similarity 100.0%; Pred. No. 3.6e-237; Indels 0; Gaps 0;

Matches 480; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 121 ANRNOETSEBYQIKAWTDFRFGKNTYSDPKMWHYFDGADWDESRKISIFKFRGEK 180
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Db 181 AMDWEVSSENGNDYLMYADVDYDHPDVVAETKMGWIYANELSLDGRIDAAGHIFSF 240
Qy 241 LRDWQAVRQATGKEMFTVAEYQNNAGKLENYLNTKTSFNOSVDFVPLHFNLOAASSOGG 300
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RESULT 3

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US-10-644-187-4
; Sequence 4, Application US/10644187
; Publication No. US20040048351A1
; GENERAL INFORMATION:
; APPLICANT: Borchert, Torben
; APPLICANT: Svendsen, Allan
; APPLICANT: Bisgard-Frantzen, Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 4796-204-US
; CURRENT APPLICATION NUMBER: US/10/644,187
; CURRENT FILING DATE: 2003-08-20
; PRIOR APPLICATION NUMBER: 09/182,859
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: 0515/96
; PRIOR FILING DATE: 1996-04-30
; PRIOR APPLICATION NUMBER: 0712/96
; PRIOR FILING DATE: 1996-06-28
; PRIOR APPLICATION NUMBER: 0775/96
; PRIOR FILING DATE: 1996-07-11
; PRIOR APPLICATION NUMBER: 1263/96
; PRIOR FILING DATE: 1996-11-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 460
; TYPE: PRT
; ORGANISM: Bacillus amyloliquefaciens
US-10-644-187-4
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Query Match 100.0%; Score 2624; DB 12; Length 480;

Best Local Similarity 100.0%; Pred. No. 3.6e-237; Indels 0; Gaps 0;

Matches 480; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 241 LRDWQAVRQATGKEMFTVAEYQNNAGKLENYLNTKTSFNOSVDFVPLHFNLOAASSOGG 300
Db 241 LRDWQAVRQATGKEMFTVAEYQNNAGKLENYLNTKTSFNOSVDFVPLHFNLOAASSOGG 300
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QY 361 VFYGMVGTGKTSPEIKSLKDNIEPIILKARKEAYVGPQHDYIDHPDVIQWTRREGSSAA 420
DB 361 VFYGMVGTGKTSPEIKSLKDNIEPIILKARKEAYVGPQHDYIDHPDVIQWTRREGSSAA 420
QY 421 KSGLAALITDGPSSKRMVAGLKNAGETWYDITGNRSSTVYKISGDGGEFFHVNDGSVSIY 480
DB 421 KSGLAALITDGPSSKRMVAGLKNAGETWYDITGNRSSTVYKISGDGGEFFHVNDGSVSIY 480

RESULT 4

US-10-327-837-5
; Sequence 5, Application US/10327837
; Publication No. US20030211958A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torden Vedel
; APPLICANT: Bisgard-Frantzen Henrik
; APPLICANT: Cuettrup, Heile
; APPLICANT: Nielsen, Bjarne Ronfeldt
; APPLICANT: Nielsen, Vibeke Skovgaard
; APPLICANT: Hoeck, Lisbeth Hedegaard
; TITLE OF INVENTION: Novel Amylase And -Amylase Mutants
; FILE REFERENCE: 52/6.400-US
; CURRENT APPLICATION NUMBER: US/10/327,837
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: US/09/290,734
; PRIOR FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 480
; TYPE: PRT
; ORGANISM: B. amyloliquefaciens
US-10-327-837-5

Query Match 100.0%; Score 2624; DB 12; Length 480;
Best Local Similarity 100.0%; Pred. No. 3.6e-237; Indels 0; Gaps 0;
Matches 480; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNGTLMQYFEMTYPNDQGMKRLQNDAEHLSDIGITAWIPRAYKGLSGSDNGYGPYDLY 60
DB 1 VNGTLMQYFEMTYPNDQGMKRLQNDAEHLSDIGITAWIPRAYKGLSGSDNGYGPYDLY 60
QY 61 DLGEFOQKGTVRITKYGKSELQDAIGSLHSRNVOYGVYVNLNKAQADATEDVTAVERN 120
DB 61 DLGEFOQKGTVRITKYGKSELQDAIGSLHSRNVOYGVYVNLNKAQADATEDVTAVERN 120
QY 121 ANRNOETSEBYQIKAMTDRFRPGKNTYSDFKMHWHPDQADDESKISRIKFRGECK 180
DB 121 ANRNOETSEBYQIKAMTDRFRPGKNTYSDFKMHWHPDQADDESKISRIKFRGECK 180
QY 181 AMDWEVSSSENGNDYLMYADVDDHPDVAETKMGIWYANELSLDGFRIIDAKHIKFSF 240
DB 181 AMDWEVSSSENGNDYLMYADVDDHPDVAETKMGIWYANELSLDGFRIIDAKHIKFSF 240
QY 241 LRDVQAVRQATGKEMFTVAEYQNNAGKLENTLNTSFNOSVFDVPLHFNLOAASSOGG 300
DB 241 LRDVQAVRQATGKEMFTVAEYQNNAGKLENTLNTSFNOSVFDVPLHFNLOAASSOGG 300
QY 301 GYDMRRLDGTIVSRHPEKAVTFVENHDTQPGSLSESTVQTWFKPLAYAFILTRREGYPQ 360
DB 301 GYDMRRLDGTIVSRHPEKAVTFVENHDTQPGSLSESTVQTWFKPLAYAFILTRREGYPQ 360
QY 361 VFYGMVGTGKTSPEIKSLKDNIEPIILKARKEAYVGPQHDYIDHPDVIQWTRREGSSAA 420
DB 361 VFYGMVGTGKTSPEIKSLKDNIEPIILKARKEAYVGPQHDYIDHPDVIQWTRREGSSAA 420
QY 421 KSGLAALITDGPSSKRMVAGLKNAGETWYDITGNRSSTVYKISGDGGEFFHVNDGSVSIY 480
DB 421 KSGLAALITDGPSSKRMVAGLKNAGETWYDITGNRSSTVYKISGDGGEFFHVNDGSVSIY 480

RESULT 5

US-10-186-042-4
; Sequence 4, Application US/10186042
; Publication No. US20030171236A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torden
; APPLICANT: Bisgard-Frantzen, Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 4796.204-US
; CURRENT APPLICATION NUMBER: US/10/186,042
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US/09/672,459
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 09/182,859
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: 0515/96
; PRIOR FILING DATE: 1996-04-30
; PRIOR APPLICATION NUMBER: 0712/96
; PRIOR FILING DATE: 1996-06-28
; PRIOR APPLICATION NUMBER: 0775/96
; PRIOR FILING DATE: 1996-07-11
; PRIOR APPLICATION NUMBER: 1263/96
; PRIOR FILING DATE: 1996-11-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Bacillus amyloliquefaciens
US-10-186-042-4

Query Match 100.0%; Score 2624; DB 14; Length 480;
Best Local Similarity 100.0%; Pred. No. 3.6e-237; Indels 0; Gaps 0;
Matches 480; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNGTLMQYFEMTYPNDQGMKRLQNDAEHLSDIGITAWIPRAYKGLSGSDNGYGPYDLY 60
DB 1 VNGTLMQYFEMTYPNDQGMKRLQNDAEHLSDIGITAWIPRAYKGLSGSDNGYGPYDLY 60
QY 61 DLGEFOQKGTVRITKYGKSELQDAIGSLHSRNVOYGVYVNLNKAQADATEDVTAVERN 120
DB 61 DLGEFOQKGTVRITKYGKSELQDAIGSLHSRNVOYGVYVNLNKAQADATEDVTAVERN 120
QY 121 ANRNOETSEBYQIKAMTDRFRPGKNTYSDFKMHWHPDQADDESKISRIKFRGECK 180
DB 121 ANRNOETSEBYQIKAMTDRFRPGKNTYSDFKMHWHPDQADDESKISRIKFRGECK 180
QY 181 AMDWEVSSSENGNDYLMYADVDDHPDVAETKMGIWYANELSLDGFRIIDAKHIKFSF 240
DB 181 AMDWEVSSSENGNDYLMYADVDDHPDVAETKMGIWYANELSLDGFRIIDAKHIKFSF 240
QY 241 LRDVQAVRQATGKEMFTVAEYQNNAGKLENTLNTSFNOSVFDVPLHFNLOAASSOGG 300
DB 241 LRDVQAVRQATGKEMFTVAEYQNNAGKLENTLNTSFNOSVFDVPLHFNLOAASSOGG 300
QY 301 GYDMRRLDGTIVSRHPEKAVTFVENHDTQPGSLSESTVQTWFKPLAYAFILTRREGYPQ 360
DB 301 GYDMRRLDGTIVSRHPEKAVTFVENHDTQPGSLSESTVQTWFKPLAYAFILTRREGYPQ 360
QY 361 VFYGMVGTGKTSPEIKSLKDNIEPIILKARKEAYVGPQHDYIDHPDVIQWTRREGSSAA 420
DB 361 VFYGMVGTGKTSPEIKSLKDNIEPIILKARKEAYVGPQHDYIDHPDVIQWTRREGSSAA 420
QY 421 KSGLAALITDGPSSKRMVAGLKNAGETWYDITGNRSSTVYKISGDGGEFFHVNDGSVSIY 480
DB 421 KSGLAALITDGPSSKRMVAGLKNAGETWYDITGNRSSTVYKISGDGGEFFHVNDGSVSIY 480

RESULT 6
US-09-854-346-10
; Sequence 10, Application US/09854346
; Patent No. US20020068352A1
; GENERAL INFORMATION:

APPLICANT: No. US20020068352A1ozymes A/S
APPLICANT: Svendsen, Allan
APPLICANT: Jorgensen, Christel Thea
APPLICANT: Nielsen, Bjarne Ronfeldt
TITLE OF INVENTION: Alpha-amylase variants with altered 1,6 activity
FILE REFERENCE: 6140-200-US
CURRENT APPLICATION NUMBER: US/09/854,346
CURRENT FILING DATE: 2001-05-11
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.1
SEQ ID NO 10
LENGTH: 483
TYPE: PRT
ORGANISM: *Bacillus amyloliquefaciens*
US-09-854-346-10

Query Match 100.0%; Score 2624; DB 9; Length 483;
Best Local Similarity 100.0%; Pred. No. 3.6e-237;
Matches 480; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAWMIPPAKGLSGSDNGYGYDLY 60
DB 1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAWMIPPAKGLSGSDNGYGYDLY 60
QY 61 DLGEFOQKGTIVRTKYGKSELQDAIGSLHSRNQVYGDVVLNKKAGADATEDVTAVERN 120
DB 61 DLGEFOQKGTIVRTKYGKSELQDAIGSLHSRNQVYGDVVLNKKAGADATEDVTAVERN 120
QY 121 ANRQETSEEEYQIKAWTDFRPPGRGNTYSDPKMWHYFDGADWDESKISRIFFRGECK 180
DB 121 ANRQETSEEEYQIKAWTDFRPPGRGNTYSDPKMWHYFDGADWDESKISRIFFRGECK 180
QY 181 AMDWEVSSSENGNYDLYMADVDYDHPDVVAETKKMGIMYANELSLDGFRIDAAGHIFSF 240
DB 181 AMDWEVSSSENGNYDLYMADVDYDHPDVVAETKKMGIMYANELSLDGFRIDAAGHIFSF 240
QY 241 LRDWQAVRQATGKEMFTVAEYQWQNAKLENYLNKTSFNOSVDPVPLHFNLAQASSQGG 300
DB 241 LRDWQAVRQATGKEMFTVAEYQWQNAKLENYLNKTSFNOSVDPVPLHFNLAQASSQGG 300
QY 301 GYDMRRLLDGTVVSRHPEKAVTFVENHDTOPGQSLESTVQTFWPKPLAVALITRESGYPQ 360
DB 301 GYDMRRLLDGTVVSRHPEKAVTFVENHDTOPGQSLESTVQTFWPKPLAVALITRESGYPQ 360
QY 361 VFYGMVGTGKTSPEIISLKNIEPIILKAREYAYGQHDYIDHPDVIQWTRGDSAA 420
DB 361 VFYGMVGTGKTSPEIISLKNIEPIILKAREYAYGQHDYIDHPDVIQWTRGDSAA 420
QY 421 KSGLAALITDGPQSKRYAGLKNAGETWYDITGNRSPTVKIGSDGWEFFHVDGSYIY 480
DB 421 KSGLAALITDGPQSKRYAGLKNAGETWYDITGNRSPTVKIGSDGWEFFHVDGSYIY 480

RESULT 7
US-09-918-543-10
Sequence 10, Application US/09918543
Patent No. US20020155574A1
GENERAL INFORMATION:
APPLICANT: No. US20020155574A1ozymes A/S
APPLICANT: Thisted, Thomas
APPLICANT: Kjaerulf, Soren
APPLICANT: Andersen, Carsten
APPLICANT: Fugleang, Claus Crone
TITLE OF INVENTION: Alpha-amylase mutants with altered properties
FILE REFERENCE: 10062-200-US
CURRENT APPLICATION NUMBER: US/09/918,543
CURRENT FILING DATE: 2001-07-31
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.1
SEQ ID NO 10
LENGTH: 483
TYPE: PRT
ORGANISM: *Bacillus amyloliquefaciens*

US-09-918-543-10

Query Match 100.0%; Score 2624; DB 9; Length 483;
Best Local Similarity 100.0%; Pred. No. 3.6e-237;
Matches 480; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAWMIPPAKGLSGSDNGYGYDLY 60
DB 1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAWMIPPAKGLSGSDNGYGYDLY 60
QY 61 DLGEFOQKGTIVRTKYGKSELQDAIGSLHSRNQVYGDVVLNKKAGADATEDVTAVERN 120
DB 61 DLGEFOQKGTIVRTKYGKSELQDAIGSLHSRNQVYGDVVLNKKAGADATEDVTAVERN 120
QY 121 ANRQETSEEEYQIKAWTDFRPPGRGNTYSDPKMWHYFDGADWDESKISRIFFRGECK 180
DB 121 ANRQETSEEEYQIKAWTDFRPPGRGNTYSDPKMWHYFDGADWDESKISRIFFRGECK 180
QY 181 AMDWEVSSSENGNYDLYMADVDYDHPDVVAETKKMGIMYANELSLDGFRIDAAGHIFSF 240
DB 181 AMDWEVSSSENGNYDLYMADVDYDHPDVVAETKKMGIMYANELSLDGFRIDAAGHIFSF 240
QY 241 LRDWQAVRQATGKEMFTVAEYQWQNAKLENYLNKTSFNOSVDPVPLHFNLAQASSQGG 300
DB 241 LRDWQAVRQATGKEMFTVAEYQWQNAKLENYLNKTSFNOSVDPVPLHFNLAQASSQGG 300
QY 301 GYDMRRLLDGTVVSRHPEKAVTFVENHDTOPGQSLESTVQTFWPKPLAVALITRESGYPQ 360
DB 301 GYDMRRLLDGTVVSRHPEKAVTFVENHDTOPGQSLESTVQTFWPKPLAVALITRESGYPQ 360
QY 361 VFYGMVGTGKTSPEIISLKNIEPIILKAREYAYGQHDYIDHPDVIQWTRGDSAA 420
DB 361 VFYGMVGTGKTSPEIISLKNIEPIILKAREYAYGQHDYIDHPDVIQWTRGDSAA 420
QY 421 KSGLAALITDGPQSKRYAGLKNAGETWYDITGNRSPTVKIGSDGWEFFHVDGSYIY 480
DB 421 KSGLAALITDGPQSKRYAGLKNAGETWYDITGNRSPTVKIGSDGWEFFHVDGSYIY 480

RESULT 8
US-09-925-576C-10
Sequence 10, Application US/09925576C
Publication No. US20030129718A1
GENERAL INFORMATION:
APPLICANT: Andersen, Carsten
APPLICANT: Borchert, Torben Vedel
APPLICANT: Nielsen, Bjarne Ronfeldt
TITLE OF INVENTION: Amylase Variants
FILE REFERENCE: 10004-204-US
CURRENT APPLICATION NUMBER: US/09/925,576C
CURRENT FILING DATE: 2001-08-09
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.1
SEQ ID NO 10
LENGTH: 483
TYPE: PRT
ORGANISM: *Bacillus amyloliquefaciens*
US-09-925-576C-10

Query Match 100.0%; Score 2624; DB 10; Length 483;
Best Local Similarity 100.0%; Pred. No. 3.6e-237;
Matches 480; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAWMIPPAKGLSGSDNGYGYDLY 60
DB 1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAWMIPPAKGLSGSDNGYGYDLY 60
QY 61 DLGEFOQKGTIVRTKYGKSELQDAIGSLHSRNQVYGDVVLNKKAGADATEDVTAVERN 120
DB 61 DLGEFOQKGTIVRTKYGKSELQDAIGSLHSRNQVYGDVVLNKKAGADATEDVTAVERN 120
QY 121 ANRQETSEEEYQIKAWTDFRPPGRGNTYSDPKMWHYFDGADWDESKISRIFFRGECK 180
DB 121 ANRQETSEEEYQIKAWTDFRPPGRGNTYSDPKMWHYFDGADWDESKISRIFFRGECK 180

Db 121 ANRQETSEBYQIKAWMDFFPPGKNTYSDFKMHWHFDGADWDESRKISIFKFGEGK 180
Qy 181 AMDWEVSSENGNDYLMYADVDYDHPDVAETKKGIMYANELSLDGFRIIDAAGHIFSF 240
Db 181 AMDWEVSSENGNDYLMYADVDYDHPDVAETKKGIMYANELSLDGFRIIDAAGHIFSF 240
Qy 241 LRDWQAVROATGKEMFTVAEYWNNAKLENTLNTKTSFNOSVDFVPLHFNLOAASSQGG 300
Db 241 LRDWQAVROATGKEMFTVAEYWNNAKLENTLNTKTSFNOSVDFVPLHFNLOAASSQGG 300
Qy 301 GYDMRRLDGTIVSRRHEKAVTFVENHDTOPGQSLSTVQTMFKPLAFAFLITRESGPQ 360
Db 301 GYDMRRLDGTIVSRRHEKAVTFVENHDTOPGQSLSTVQTMFKPLAFAFLITRESGPQ 360
Qy 361 VFYGDWYGTGKTSPEKIPSLKDNIEPILKARKEVAYGQHDYIDHPDVIQWTRBGSSAA 420
Db 361 VFYGDWYGTGKTSPEKIPSLKDNIEPILKARKEVAYGQHDYIDHPDVIQWTRBGSSAA 420
Qy 421 KSGLAALITDGGGSKRYAGLKNAGETWYDITGNRSPTVKIGSDGGEFFHNDGSVSIY 480
Db 421 KSGLAALITDGGGSKRYAGLKNAGETWYDITGNRSPTVKIGSDGGEFFHNDGSVSIY 480

RESULT 9

US-10-146-327-6
Sequence 6, Application US/10146327
Publication No. US20030044954A1
GENERAL INFORMATION:
APPLICANT: Andersen, Carsten
APPLICANT: Jorgensen, Christel T.
APPLICANT: Bisgard-Frantzen, Henrik
APPLICANT: Svendsen, Allan
APPLICANT: Kjaerulff, Soren
TITLE OF INVENTION: Alpha-Amylase Variants
FILE REFERENCE: 5886.280-US
CURRENT APPLICATION NUMBER: US/10/146,327
CURRENT FILING DATE: 2002-05-15
PRIOR APPLICATION NUMBER: US/09/537,168
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: PA 1999 00437
PRIOR FILING DATE: 1999-03-30
PRIOR APPLICATION NUMBER: 60/127,427
PRIOR FILING DATE: 1999-04-01
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 483
TYPE: PRT
ORGANISM: Bacillus amyloliquefaciens
US-10-146-327-6

Query Match 100.0%; Score 2624; DB 14; Length 483;
Best Local Similarity 100.0%; Pred. No. 3.6e-237;
Matches 480; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VNGTLMQYFEMWTPNDGQHKRLQNDAEHLSDIGITAWIPPAKYGLSOSDNGYGPYDLY 60
Db 1 VNGTLMQYFEMWTPNDGQHKRLQNDAEHLSDIGITAWIPPAKYGLSOSDNGYGPYDLY 60
Qy 61 DLGEFOOKGTVRTKYGKSELQDAIGLSHRNVQYGVVNLHKAAGADATEDVTAVERN 120
Db 61 DLGEFOOKGTVRTKYGKSELQDAIGLSHRNVQYGVVNLHKAAGADATEDVTAVERN 120
Qy 121 ANRQETSEBYQIKAWTDFRPPGKNTYSDFKMHWHFDGADWDESRKISIFKFGEGK 180
Db 121 ANRQETSEBYQIKAWTDFRPPGKNTYSDFKMHWHFDGADWDESRKISIFKFGEGK 180
Qy 181 AMDWEVSSENGNDYLMYADVDYDHPDVAETKKGIMYANELSLDGFRIIDAAGHIFSF 240
Db 181 AMDWEVSSENGNDYLMYADVDYDHPDVAETKKGIMYANELSLDGFRIIDAAGHIFSF 240
Qy 241 LRDWQAVROATGKEMFTVAEYWNNAKLENTLNTKTSFNOSVDFVPLHFNLOAASSQGG 300
Db 241 LRDWQAVROATGKEMFTVAEYWNNAKLENTLNTKTSFNOSVDFVPLHFNLOAASSQGG 300

Db 241 LRDWQAVROATGKEMFTVAEYWNNAKLENTLNTKTSFNOSVDFVPLHFNLOAASSQGG 300
Qy 301 GYDMRRLDGTIVSRRHEKAVTFVENHDTOPGQSLSTVQTMFKPLAFAFLITRESGPQ 360
Db 301 GYDMRRLDGTIVSRRHEKAVTFVENHDTOPGQSLSTVQTMFKPLAFAFLITRESGPQ 360
Qy 361 VFYGDWYGTGKTSPEKIPSLKDNIEPILKARKEVAYGQHDYIDHPDVIQWTRBGSSAA 420
Db 361 VFYGDWYGTGKTSPEKIPSLKDNIEPILKARKEVAYGQHDYIDHPDVIQWTRBGSSAA 420
Qy 421 KSGLAALITDGGGSKRYAGLKNAGETWYDITGNRSPTVKIGSDGGEFFHNDGSVSIY 480
Db 421 KSGLAALITDGGGSKRYAGLKNAGETWYDITGNRSPTVKIGSDGGEFFHNDGSVSIY 480

RESULT 10

US-10-184-771-4
Sequence 4, Application US/10184771
Publication No. US20030170769A1
GENERAL INFORMATION:
APPLICANT: Bisgard-Frantzen, Henrik
APPLICANT: Svendsen, Allan
APPLICANT: Borchert, Torben Vedel
TITLE OF INVENTION: Alpha-Amylase Mutants
FILE REFERENCE: 0776/1P216-US2
CURRENT APPLICATION NUMBER: US/10/184,771
CURRENT FILING DATE: 2002-06-28
PRIOR APPLICATION NUMBER: US/09/636,252
PRIOR FILING DATE: 2000-08-10
PRIOR APPLICATION NUMBER: 08/583,838
PRIOR FILING DATE: 1996-07-18
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 514
TYPE: PRT
ORGANISM: B. amyloliquefaciens
US-10-184-771-4

Query Match 100.0%; Score 2624; DB 14; Length 514;
Best Local Similarity 100.0%; Pred. No. 4e-237;
Matches 480; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VNGTLMQYFEMWTPNDGQHKRLQNDAEHLSDIGITAWIPPAKYGLSOSDNGYGPYDLY 60
Db 1 VNGTLMQYFEMWTPNDGQHKRLQNDAEHLSDIGITAWIPPAKYGLSOSDNGYGPYDLY 91
Qy 61 DLGEFOOKGTVRTKYGKSELQDAIGLSHRNVQYGVVNLHKAAGADATEDVTAVERN 120
Db 61 DLGEFOOKGTVRTKYGKSELQDAIGLSHRNVQYGVVNLHKAAGADATEDVTAVERN 151
Qy 121 ANRQETSEBYQIKAWTDFRPPGKNTYSDFKMHWHFDGADWDESRKISIFKFGEGK 180
Db 121 ANRQETSEBYQIKAWTDFRPPGKNTYSDFKMHWHFDGADWDESRKISIFKFGEGK 211
Qy 181 AMDWEVSSENGNDYLMYADVDYDHPDVAETKKGIMYANELSLDGFRIIDAAGHIFSF 240
Db 181 AMDWEVSSENGNDYLMYADVDYDHPDVAETKKGIMYANELSLDGFRIIDAAGHIFSF 271
Qy 241 LRDWQAVROATGKEMFTVAEYWNNAKLENTLNTKTSFNOSVDFVPLHFNLOAASSQGG 300
Db 241 LRDWQAVROATGKEMFTVAEYWNNAKLENTLNTKTSFNOSVDFVPLHFNLOAASSQGG 331
Qy 301 GYDMRRLDGTIVSRRHEKAVTFVENHDTOPGQSLSTVQTMFKPLAFAFLITRESGPQ 360
Db 301 GYDMRRLDGTIVSRRHEKAVTFVENHDTOPGQSLSTVQTMFKPLAFAFLITRESGPQ 391
Qy 361 VFYGDWYGTGKTSPEKIPSLKDNIEPILKARKEVAYGQHDYIDHPDVIQWTRBGSSAA 420
Db 361 VFYGDWYGTGKTSPEKIPSLKDNIEPILKARKEVAYGQHDYIDHPDVIQWTRBGSSAA 451
Qy 421 KSGLAALITDGGGSKRYAGLKNAGETWYDITGNRSPTVKIGSDGGEFFHNDGSVSIY 480
Db 421 KSGLAALITDGGGSKRYAGLKNAGETWYDITGNRSPTVKIGSDGGEFFHNDGSVSIY 480

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us-10-644-187-4.rapb

Page 6

Db 452 KSGLAALITDGPQSGKRYAGLKNAGETWYDITGNRSPTVKIGSDGMEFFHNDGVSIV 511

RESULT 11

US-10-184-771-13

Sequence 13, Application US/10184771

Publication No. US20030170769A1

GENERAL INFORMATION:

APPLICANT: Svendsen, Allan

APPLICANT: Bisgaard-Frantzen, Henrik

APPLICANT: Borchert, Torben Vedel

TITLE OF INVENTION: Alpha-Amylase Mutants

FILE REFERENCE: 0776/1F216-US2

CURRENT FILING DATE: 2002-06-28

PRIOR FILING DATE: 2000-08-10

PRIOR APPLICATION NUMBER: 08/683,838

PRIOR FILING DATE: 1996-07-18

NUMBER OF SEQ ID NOS: 16

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 13

LENGTH: 483

TYPE: PRT

ORGANISM: Bacillus

US-10-184-771-13

Query Match

Best Local Similarity 94.3%; Score 2475; DB 14; Length 483;

Matches 449; Conservative 15; Mismatches 16; Indels 0; Gaps 0;

1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAKGSQSDNGYGPYDLY 60

1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAKGSQSDNGYGPYDLY 60

1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAKGSQSDNGYGPYDLY 60

1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAKGSQSDNGYGPYDLY 60

1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAKGSQSDNGYGPYDLY 60

1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAKGSQSDNGYGPYDLY 60

1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAKGSQSDNGYGPYDLY 60

1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAKGSQSDNGYGPYDLY 60

1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAKGSQSDNGYGPYDLY 60

1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAKGSQSDNGYGPYDLY 60

1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAKGSQSDNGYGPYDLY 60

1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAKGSQSDNGYGPYDLY 60

1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAKGSQSDNGYGPYDLY 60

1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAKGSQSDNGYGPYDLY 60

1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAKGSQSDNGYGPYDLY 60

1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAKGSQSDNGYGPYDLY 60

1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAKGSQSDNGYGPYDLY 60

1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAKGSQSDNGYGPYDLY 60

1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAKGSQSDNGYGPYDLY 60

1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAKGSQSDNGYGPYDLY 60

1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAKGSQSDNGYGPYDLY 60

1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAKGSQSDNGYGPYDLY 60

1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAKGSQSDNGYGPYDLY 60

1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAKGSQSDNGYGPYDLY 60

1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAKGSQSDNGYGPYDLY 60

1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAKGSQSDNGYGPYDLY 60

1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAKGSQSDNGYGPYDLY 60

1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAKGSQSDNGYGPYDLY 60

1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAKGSQSDNGYGPYDLY 60

1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAKGSQSDNGYGPYDLY 60

1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAKGSQSDNGYGPYDLY 60

1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAKGSQSDNGYGPYDLY 60

1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAKGSQSDNGYGPYDLY 60

1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAKGSQSDNGYGPYDLY 60

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1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAKGSQSDNGYGPYDLY 60

1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAKGSQSDNGYGPYDLY 60

1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAKGSQSDNGYGPYDLY 60

APPLICANT: Kjaerulf, Soren

TITLE OF INVENTION: Alpha-Amylase Variants

FILE REFERENCE: 5886.200-US

CURRENT FILING DATE: 2002-05-15

PRIOR FILING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: US/09/537,168

PRIOR FILING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: PA 1999 00437

PRIOR FILING DATE: 1999-03-30

PRIOR APPLICATION NUMBER: 60/127,427

PRIOR FILING DATE: 1999-04-01

NUMBER OF SEQ ID NOS: 40

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 2

LENGTH: 481

TYPE: PRT

ORGANISM: Bacillus subtilis

US-10-146-327-2

Query Match

Best Local Similarity 83.5%; Score 2190; DB 14; Length 481;

Matches 392; Conservative 37; Mismatches 49; Indels 2; Gaps 1;

1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAKGSQSDNGYGPYDLY 60

1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAKGSQSDNGYGPYDLY 60

1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAKGSQSDNGYGPYDLY 60

1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAKGSQSDNGYGPYDLY 60

1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAKGSQSDNGYGPYDLY 60

1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAKGSQSDNGYGPYDLY 60

1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAKGSQSDNGYGPYDLY 60

1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAKGSQSDNGYGPYDLY 60

1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAKGSQSDNGYGPYDLY 60

1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAKGSQSDNGYGPYDLY 60

1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAKGSQSDNGYGPYDLY 60

1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAKGSQSDNGYGPYDLY 60

1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAKGSQSDNGYGPYDLY 60

1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAKGSQSDNGYGPYDLY 60

1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAKGSQSDNGYGPYDLY 60

1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAKGSQSDNGYGPYDLY 60

1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAKGSQSDNGYGPYDLY 60

1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAKGSQSDNGYGPYDLY 60

1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAKGSQSDNGYGPYDLY 60

1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAKGSQSDNGYGPYDLY 60

1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAKGSQSDNGYGPYDLY 60

1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAKGSQSDNGYGPYDLY 60

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1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAKGSQSDNGYGPYDLY 60

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1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAKGSQSDNGYGPYDLY 60

1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAKGSQSDNGYGPYDLY 60

1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAKGSQSDNGYGPYDLY 60

1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAKGSQSDNGYGPYDLY 60

1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAKGSQSDNGYGPYDLY 60

1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAKGSQSDNGYGPYDLY 60

1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAKGSQSDNGYGPYDLY 60

1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAKGSQSDNGYGPYDLY 60

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1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAKGSQSDNGYGPYDLY 60

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1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAKGSQSDNGYGPYDLY 60

Page 6

Page 7

Query Match	83.2%;	Score 2182;	DB 14;	Length 512;
Best Local Similarity	80.8%;	Pred. No. 1.2e-195;		
Matches 388;	Conservative 42;	Mismatches 48;	Indels 2;	Gaps 1

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PRIORITY APPLICATION NUMBER: 60/270,496
PRIOR FILING DATE: 2001-02-21
PRIOR APPLICATION NUMBER: 60/291,122
PRIOR FILING DATE: 2001-05-14
NUMBER OF SEQ ID NOS: 69
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 512
TYPE: PRT
ORGANISM: Environmental
US-10-105-733-8

Query Match      83.2%; Score 2182; DB 14; Length 512;
Best Local Similarity 80.8%; Pred. No. 1,2e-195;
Matches 388; Conservative 42; Mismatches 48; Indels 2; Gaps 1

QY      1 VAGTLMQYFEEWTPPDGQHWRLQNDLNDMEHLSDIGITAWMIIPRAYKGLSGSDNGYGYDYL 60
DB      32 LAGTLMQYFEEWTPPDGQHWRLQNDLNDMEHLSDIGITAWMIIPRAYKGLSGSDNGYGYDYL 91
QY      61 DLGEFQOKGTVATKYGTGSELQDAIGSLHSNVAQYGDVVLNKAQADATEDVTAVEVP 120
DB      92 DLGEFHQGTATVATKYGTGSELQSAIKSLHSRDIWYGDVVLNKKGADATEDVTAVEVP 151
QY      121 ANRNETSEBYIKATWTFRRPGNGNTYSDPKKMTWYFPDADMDDESKISRIKFKGEQK 180
DB      152 ADRNRYSSEHRIKATWTFHPPGGSTYSDPKMTWYFPDGTDDDESKLRIRIKF--QCK 209
QY      181 AMDWEVSENGVADYDLMAVDYDHPDVLVETKKMGIMVANELSLDGFRIIDAKHIKFSF 240
DB      210 AMDWEVSENGVADYDLMAVDIDYDHPDVAALIKMGWGTWYANELQDGFRIIDAVGHIKFSF 269
QY      241 LRDWQVAVQATGKEMFTVAEYWNNAKLENTLNKTSFPOSVFDPVPLEHNLQAASSQGG 300
DB      270 LRDWVAVHAEKTKEMFTVAEYWNQNDLALENYLNKTNFHSVFDVPLHQTFFPAASTQGG 329
QY      301 GYMERLLDGTVASSHPEKATVFYENHDTPGQSLSESTVQTFWEPLAYAFILTRSGYDQ 360
DB      330 GYMERKLLNGTVYVSKPLKATVFVNDHTDTPGQSLSESTVQTFWEPLAYAFILTRSGYDQ 389
QY      361 VFYGDWYTKGTSPKEIPELKDNIPELILKAREYAYGQCHDYIDHPVYICWTEBGSMAA 420
DB      390 VFYGDWYTKGTSDORSREIPALKKIIPILIKARKQYAYGQCHDYIFPHNDIYCWTEBGSMAA 449
QY      421 KSGIALLITDPPGSGSRWYAGAKNNGETWYDITGRSPTYIGSGDWGEFFHVDGVSIIY 480
DB      450 NSGIALLITDPPGSAKRWYGRKNGGETWYDITGRSEFPVYINSGDWGEFFHVDGVSIIY 509

RESULT 15
US-10-081-739A-8
/ Sequence 8, Application US/10081739A
/ Publication No. US20030170634A1
/ GENERAL INFORMATION:
/ APPLICANT: Callen, Walter
/ APPLICANT: Richardson, Toby
/ APPLICANT: Frey, Gerhard
/ APPLICANT: Muller, Carl
/ APPLICANT: Karzaka, Martin
/ APPLICANT: Short, Uay
/ APPLICANT: Machut, Eric
/ TITLE OF INVENTION: ENZYMES HAVING ALPHA AMYLASE ACTIVITY
/ TITLE OF INVENTION: AND METHODS OF USE THEREOF
/ FILE REFERENCE: 09010-107001
/ CURRENT FILING DATE: 2002-02-21
/ PRIOR FILING DATE: 2001-02-21
/ PRIOR APPLICATION NUMBER: 60/270,495
/ PRIOR FILING DATE: 2001-02-21
/ PRIOR APPLICATION NUMBER: 60/291,122
/ PRIOR FILING DATE: 2001-05-14
/ NUMBER OF SEQ ID NOS: 69

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SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8
LENGTH: 512
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Obtained from an environmental sample
US-10-081-739A-8

Query Match 83.2%; Score 2182; DB 14; Length 512;
Best Local Similarity 80.8%; Pred. No. 1.2e-195;
Matches 388; Conservative 42; Mismatches 46; Indels 2; Gaps 1;

```
QY 1 VNGTLMQYFEMWTPNDGQHWKRLQNDAEHLSDIGTAVWIPPAYKGLSQSDNGYGYDLY 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 32 LNTGLMQYFEMWTPNDGQHWKRLQNDASAYLAHGITAVWIPPAYKGLSQADVGAYDLY 91
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 61 DLGEFQKGTVTKYKTSSELDALGSIHSRNVQYGVVNLNKAADATEDVTAWEVP 120
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 92 DLGEFHQKGTVTKYKTSSELDALGSIHSRDNVYGVVNLNKAADATEDVTAWEVP 151
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 121 ANRNOETSEHYQIKAMTDFRFPGRNTYSDFKWHYHFDGADWDESRKISRIKFRGEGK 180
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 152 ADRNRVIGSEHRIKAMTHHFPGRGSTYSDFKWHYHFDGADWDESRKLNRIYKF--QK 209
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 181 AMDMEVSSNGNYDYLMTADVVDYDHPDYVAETKKGITWYANELSLDGPRIDAAKHKFSF 240
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 210 AMDMEVSSNGNYDYLMTADIDYDHPDYVAETKKGITWYANELSLDGPRIDAAKHKFSF 269
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 241 LEDWQAVQATGKEMFTVAEYWNAGKLENYLNKTSFNOSVPEVPLHFNLOAASQGG 300
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 270 LEDWVNHAREKTKGEMFTVAEYWNAGKLENYLNKTSFNOSVPEVPLHFNLOAASQGG 329
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 301 GYDMRRLDGTIVVSRHPEKAVTFVENHDTQPGQSLESTVQTFKPLAYAFILITRESGYPQ 360
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 330 GYDMRRLDGTIVVSRHPEKAVTFVENHDTQPGQSLESTVQTFKPLAYAFILITRESGYPQ 389
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 361 VFYGDWYGTGKTSPEKIEPILKDNIEPILKARKEVAYGQHDYIDHPDVIQWTRGESSAA 420
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 390 VFYGDWYGTGKTSPEKIEPILKDNIEPILKARKEVAYGQHDYIDHPDVIQWTRGESSAA 449
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 421 KSGLAALITDGPQSGKMTAGLKNAGETVYDITGNRSDTVKIGSDQWGEFHNQDSVSIY 480
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 450 KSGLAALITDGPQSGKMTAGLKNAGETVYDITGNRSDTVKIGSDQWGEFHNQDSVSIY 509
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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Search completed: May 3, 2004, 20:47:46
JDB time : 38.3731 sec

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 3, 2004, 20:29:27 ; Search time 16.3507 Seconds
(without alignments)
1525.031 Million cell updates/sec

Title: US-10-644-187-2
Perfect score: 2666
Sequence: 1 ANLNGTLMQFEWMPNDGQ.....SEGWGEFHNQGSVSIVQR 483
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep.*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep.*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep.*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep.*
5: /cgn2_6/ptodata/2/1aa/PCCTS.COMB.pep.*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2666	100.0	483	3	US-09-182-859-2 Sequence 2, Appli
2	2666	100.0	483	3	US-09-170-670-4 Sequence 4, Appli
3	2666	100.0	483	3	US-09-193-068-4 Sequence 4, Appli
4	2666	100.0	483	3	US-09-183-412-4 Sequence 2, Appli
5	2666	100.0	483	3	US-09-264-097-2 Sequence 2, Appli
6	2666	100.0	483	4	US-09-291-023A-21 Sequence 21, Appli
7	2666	100.0	483	4	US-09-290-734-4 Sequence 4, Appli
8	2666	100.0	483	4	US-09-537-168-4 Sequence 2, Appli
9	2666	100.0	483	4	US-09-672-459-2 Sequence 4, Appli
10	2666	100.0	483	4	US-09-545-586-4 Sequence 4, Appli
11	2666	100.0	483	4	US-09-540-715A-21 Sequence 21, Appli
12	2666	100.0	483	4	US-10-186-042-2 Sequence 2, Appli
13	2666	100.0	483	4	US-09-769-864-4 Sequence 4, Appli
14	2666	100.0	512	1	US-08-720-899-2 Sequence 2, Appli
15	2666	100.0	512	1	US-08-459-610-2 Sequence 2, Appli
16	2666	100.0	512	2	US-08-343-804-2 Sequence 2, Appli
17	2666	100.0	512	2	US-08-687-399-2 Sequence 2, Appli
18	2666	100.0	512	2	US-08-600-908A-2 Sequence 2, Appli
19	2666	100.0	512	4	US-08-683-838A-2 Sequence 2, Appli
20	2666	100.0	512	4	US-09-636-252A-2 Sequence 2, Appli
21	2666	100.0	631	3	US-08-814-052-8 Sequence 8, Appli
22	2666	100.0	631	3	US-08-812-829-8 Sequence 8, Appli
23	2663	99.9	483	1	US-08-468-700-34 Sequence 34, Appli
24	2663	99.9	483	2	US-08-468-220-32 Sequence 32, Appli
25	2663	99.9	483	2	US-08-468-698-32 Sequence 32, Appli
26	2663	99.9	483	2	US-08-704-706A-34 Sequence 34, Appli
27	2663	99.9	483	3	US-08-890-383-3 Sequence 3, Appli

28	2663	99.9	483	3	US-08-914-679A-3 Sequence 3, Appli
29	2663	99.9	483	3	US-08-985-659-35 Sequence 35, Appli
30	2663	99.9	483	3	US-08-194-664A-32 Sequence 32, Appli
31	2663	99.9	483	5	PCT-US94-01553A-32 Sequence 32, Appli
32	2663	99.9	483	5	PCT-US95-10426-32 Sequence 32, Appli
33	2663	99.9	487	2	US-08-468-220-37 Sequence 37, Appli
34	2663	99.9	487	2	US-08-468-698-37 Sequence 37, Appli
35	2663	99.9	487	2	US-08-194-664A-37 Sequence 37, Appli
36	2663	99.9	487	5	PCT-US94-01553A-37 Sequence 37, Appli
37	2663	99.9	487	5	PCT-US95-10426-37 Sequence 37, Appli
38	2663	99.9	512	1	US-07-623-983-3 Sequence 3, Appli
39	2663	99.9	512	1	US-07-623-983-3 Sequence 3, Appli
40	2663	99.9	512	3	US-08-985-659-34 Sequence 34, Appli
41	2657	99.7	483	2	US-08-468-220-36 Sequence 36, Appli
42	2657	99.7	483	2	US-08-468-698-36 Sequence 36, Appli
43	2657	99.7	483	3	US-08-194-664A-36 Sequence 36, Appli
44	2657	99.7	483	5	PCT-US94-01553A-36 Sequence 36, Appli
45	2657	99.7	483	5	PCT-US95-10426-36 Sequence 36, Appli

ALIGNMENTS

RESULT 1
US-09-182-859-2
Sequence 2, Application US/09182859
Patent No. 6143708
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Borcherdt, Torben
APPLICANT: Bisgaard-Frantzen, Henrik
TITLE OF INVENTION: Alpha-Amylase Mutants
FILE REFERENCE: 4796.204-US
CURRENT APPLICATION NUMBER: US/09/182, 859
EARLIER FILING DATE: 1998-10-29
EARLIER APPLICATION NUMBER: 0515/96
EARLIER FILING DATE: 1996-04-30
EARLIER APPLICATION NUMBER: 0712/96
EARLIER FILING DATE: 1996-06-28/96
EARLIER APPLICATION NUMBER: 0775/96
EARLIER FILING DATE: 1996-07-11
EARLIER APPLICATION NUMBER: 1263/96
EARLIER FILING DATE: 1996-11-08
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 483
TYPE: PRT
ORGANISM: Bacillus licheniformis
US-09-182-859-2
Query Match 100.0%; Score 2666; DB 3; Length 483;
Best Local Similarity 100.0%; Pred No. 2.9e-240; Indels 0; Gaps 0;
Matches 483; Conservative 0; Mismatches 0;
QY 1 ANLNGTLMQFEWMPNDGQMRRLQNSAYLAHSGITAWIIPAYKGSQADVGYAYD 60
Db 1 ANLNGTLMQFEWMPNDGQMRRLQNSAYLAHSGITAWIIPAYKGSQADVGYAYD 60
QY 61 LYDGEFHQGTGRTKYGKGLQSAIKLSHSDIIVYGVVNHGADATEDYATAVY 120
Db 61 LYDGEFHQGTGRTKYGKGLQSAIKLSHSDIIVYGVVNHGADATEDYATAVY 120
QY 121 DPADRNVIISGEHLIKATHTFHPGRGSTYSDPKMWHYFDGTDMDSKRLNIYFOGK 180
Db 121 DPADRNVIISGEHLIKATHTFHPGRGSTYSDPKMWHYFDGTDMDSKRLNIYFOGK 180
QY 181 AMDEVENENGNVDYLMYADIDYDHPDYAAEIRKMGITWYANELQDGFRLDAYKHKFSF 240
Db 181 AMDEVENENGNVDYLMYADIDYDHPDYAAEIRKMGITWYANELQDGFRLDAYKHKFSF 240
QY 241 LRDVNVREKTKGEMFTVAEYQNDLQALENYLNKTNFHSVFDVPLHYQFHAATGQGG 300
Db 241 LRDVNVREKTKGEMFTVAEYQNDLQALENYLNKTNFHSVFDVPLHYQFHAATGQGG 300

Tue May 4 14:34:43 2004

us-10-644-187-2.ra1

Page 2

Db 241 LRDVNVHREKIGKEMFTVAEYONDGLALENYLNKTNFNSVFDVPLHYGFHAASGOG 300
QY 301 GYDMRKILNGTVVSKPKLSVTFVDNHDTPQGOSLESTVQTFKFLAFAFILTRESGYPQ 360
Db 301 GYDMRKILNGTVVSKPKLSVTFVDNHDTPQGOSLESTVQTFKFLAFAFILTRESGYPQ 360
QY 361 VFYGDWYGTGKDSQREIPALKEKIEPILAKQYAGACHDYFDHDIWGTREDSVA 420
Db 361 VFYGDWYGTGKDSQREIPALKEKIEPILAKQYAGACHDYFDHDIWGTREDSVA 420
QY 421 NSGLAALITDGPAGAKRMVYGRONAGETWHDITGNRSEPVINSKGGEFHVNGGSVSIY 480
Db 421 NSGLAALITDGPAGAKRMVYGRONAGETWHDITGNRSEPVINSKGGEFHVNGGSVSIY 480
QY 481 VOR 483
Db 481 VOR 483

RESULT 2

US-09-170-670-4
Sequence 4, Application US/09170670
Patent No. 6187576
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Borchert, Torben
APPLICANT: Bisgaard-Frantzen, Henrik
TITLE OF INVENTION: Alpha-Amylase Mutants
FILE REFERENCE: 5276,200-US
CURRENT APPLICATION NUMBER: US/09/170,670
EARLIER FILING DATE: 1998-10-13
EARLIER APPLICATION NUMBER: 1172/97
EARLIER FILING DATE: 1997-10-13
EARLIER APPLICATION NUMBER: 60/063,306
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 483
TYPE: PRT
ORGANISM: B. licheniformis
US-09-170-670-4

Query Match 100.0%; Score 2666; DB 3; Length 483;
Best Local Similarity 100.0%; Pred. No. 2,9e-240;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANNLGTLMOYFEMYMNDGQHRRLONDSAYLAEGITAWIPPAKYGTSGADVGYGAYD 60
Db 1 ANNLGTLMOYFEMYMNDGQHRRLONDSAYLAEGITAWIPPAKYGTSGADVGYGAYD 60
QY 61 LVDLGEFHQKGTVRTKYGTKGELQSAIKSLHSRDINVGDVVINKGADATEDVTAVEY 120
Db 61 LVDLGEFHQKGTVRTKYGTKGELQSAIKSLHSRDINVGDVVINKGADATEDVTAVEY 120
QY 121 DPADNRVYSGEHLIKAMTHHFPFGSGTSDFKMHWYHFDGTDWDSRKLNIYKFOGK 180
Db 121 DPADNRVYSGEHLIKAMTHHFPFGSGTSDFKMHWYHFDGTDWDSRKLNIYKFOGK 180
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Db 181 AMDWEVSNENGVYDLYMADIDYDHPVAAEIKRWGTWVANELQDGFRLDAVXHKFSF 240
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Db 241 LRDVNVHREKIGKEMFTVAEYONDGLALENYLNKTNFNSVFDVPLHYGFHAASGOG 300
QY 301 GYDMRKILNGTVVSKPKLSVTFVDNHDTPQGOSLESTVQTFKFLAFAFILTRESGYPQ 360
Db 301 GYDMRKILNGTVVSKPKLSVTFVDNHDTPQGOSLESTVQTFKFLAFAFILTRESGYPQ 360
QY 361 VFYGDWYGTGKDSQREIPALKEKIEPILAKQYAGACHDYFDHDIWGTREDSVA 420

Db 361 VFYGDWYGTGKDSQREIPALKEKIEPILAKQYAGACHDYFDHDIWGTREDSVA 420
QY 421 NSGLAALITDGPAGAKRMVYGRONAGETWHDITGNRSEPVINSKGGEFHVNGGSVSIY 480
Db 421 NSGLAALITDGPAGAKRMVYGRONAGETWHDITGNRSEPVINSKGGEFHVNGGSVSIY 480
QY 481 VOR 483
Db 481 VOR 483

RESULT 3

US-09-193-068-4
Sequence 4, Application US/09193068
Patent No. 6197565
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Kjulf, S ren
APPLICANT: Bisgaard-Frantzen, Henrik
APPLICANT: Andersen, Carsten
TITLE OF INVENTION: -Amylase Variants
FILE REFERENCE: 5709,000-US
CURRENT APPLICATION NUMBER: US/09/193,068
CURRENT FILING DATE: 1998-11-16
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 483
TYPE: PRT
ORGANISM: B. licheniformis
US-09-193-068-4

Query Match 100.0%; Score 2666; DB 3; Length 483;
Best Local Similarity 100.0%; Pred. No. 2,9e-240;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANNLGTLMOYFEMYMNDGQHRRLONDSAYLAEGITAWIPPAKYGTSGADVGYGAYD 60
Db 1 ANNLGTLMOYFEMYMNDGQHRRLONDSAYLAEGITAWIPPAKYGTSGADVGYGAYD 60
QY 61 LVDLGEFHQKGTVRTKYGTKGELQSAIKSLHSRDINVGDVVINKGADATEDVTAVEY 120
Db 61 LVDLGEFHQKGTVRTKYGTKGELQSAIKSLHSRDINVGDVVINKGADATEDVTAVEY 120
QY 121 DPADNRVYSGEHLIKAMTHHFPFGSGTSDFKMHWYHFDGTDWDSRKLNIYKFOGK 180
Db 121 DPADNRVYSGEHLIKAMTHHFPFGSGTSDFKMHWYHFDGTDWDSRKLNIYKFOGK 180
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Db 181 AMDWEVSNENGVYDLYMADIDYDHPVAAEIKRWGTWVANELQDGFRLDAVXHKFSF 240
QY 241 LRDVNVHREKIGKEMFTVAEYONDGLALENYLNKTNFNSVFDVPLHYGFHAASGOG 300
Db 241 LRDVNVHREKIGKEMFTVAEYONDGLALENYLNKTNFNSVFDVPLHYGFHAASGOG 300
QY 301 GYDMRKILNGTVVSKPKLSVTFVDNHDTPQGOSLESTVQTFKFLAFAFILTRESGYPQ 360
Db 301 GYDMRKILNGTVVSKPKLSVTFVDNHDTPQGOSLESTVQTFKFLAFAFILTRESGYPQ 360
QY 361 VFYGDWYGTGKDSQREIPALKEKIEPILAKQYAGACHDYFDHDIWGTREDSVA 420
Db 361 VFYGDWYGTGKDSQREIPALKEKIEPILAKQYAGACHDYFDHDIWGTREDSVA 420
QY 421 NSGLAALITDGPAGAKRMVYGRONAGETWHDITGNRSEPVINSKGGEFHVNGGSVSIY 480
Db 421 NSGLAALITDGPAGAKRMVYGRONAGETWHDITGNRSEPVINSKGGEFHVNGGSVSIY 480
QY 481 VOR 483
Db 481 VOR 483

RESULT 4
US-09-183-412-4
Sequence 4, Application US/09183412
Patent No. 6204232
GENERAL INFORMATION:
APPLICANT: Borchert, Torben V.
APPLICANT: Svendsen, Allan
APPLICANT: Andersen, Carsten
APPLICANT: Nielsen, Bjarne
APPLICANT: Nielsen, Torben L.
APPLICANT: Kjærulff, Søren
TITLE OF INVENTION: Alpha-Amulase Mutants
FILE REFERENCE: 5368.200-US
CURRENT APPLICATION NUMBER: US/09/183,412
EARLIER FILING DATE: 1998-10-30
EARLIER APPLICATION NUMBER: 60/064,662
EARLIER FILING DATE: 1997-11-06
EARLIER APPLICATION NUMBER: 60/093,234
EARLIER FILING DATE: 1998-07-17
EARLIER APPLICATION NUMBER: 1240/97
EARLIER FILING DATE: 1997-10-30
EARLIER APPLICATION NUMBER: PA 1998 00936
EARLIER FILING DATE: 1998-07-14
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 483
TYPE: PRT
ORGANISM: Bacillus licheniformis
US-09-183-412-4

Query Match 100.0%; Score 2666; DB 3; Length 483;
Best Local Similarity 100.0%; Pred. No. 2.9e-240; Indels 0; Gaps 0;
Matches 483; Conservative 0; Mismatches 0

QY 1 ANINGTLMQYFEMWYMPNDGQHWRLQNDASAYLAHSGITAWIPPAKGTSGADVGAYD 60
1 ANINGTLMQYFEMWYMPNDGQHWRLQNDASAYLAHSGITAWIPPAKGTSGADVGAYD 60
DB 1 ANINGTLMQYFEMWYMPNDGQHWRLQNDASAYLAHSGITAWIPPAKGTSGADVGAYD 60
QY 61 LYDLGEFHQKGTATKGTGTGELQSAIKSLHSRDINVGVDVNNHKGADATEDVTAVEY 120
61 LYDLGEFHQKGTATKGTGTGELQSAIKSLHSRDINVGVDVNNHKGADATEDVTAVEY 120
DB 61 LYDLGEFHQKGTATKGTGTGELQSAIKSLHSRDINVGVDVNNHKGADATEDVTAVEY 120
QY 121 DPADNRNVISEHILIKMTWTFHFPGRGSTYSDFKMWYHFDGTDWDSRKLNIYKFGOK 180
121 DPADNRNVISEHILIKMTWTFHFPGRGSTYSDFKMWYHFDGTDWDSRKLNIYKFGOK 180
DB 121 DPADNRNVISEHILIKMTWTFHFPGRGSTYSDFKMWYHFDGTDWDSRKLNIYKFGOK 180
QY 181 AMDWEVSNEGNNDYLYMADIDYDHPVAAEIKRWGTWYANELODGFRLDAVKHKFSF 240
181 AMDWEVSNEGNNDYLYMADIDYDHPVAAEIKRWGTWYANELODGFRLDAVKHKFSF 240
DB 181 AMDWEVSNEGNNDYLYMADIDYDHPVAAEIKRWGTWYANELODGFRLDAVKHKFSF 240
QY 241 LRDVNNHREKTKGEMFTVAEYMONDGLALENYLNTKTNFHSVFDVPLHYQFHAASFOG 300
241 LRDVNNHREKTKGEMFTVAEYMONDGLALENYLNTKTNFHSVFDVPLHYQFHAASFOG 300
DB 241 LRDVNNHREKTKGEMFTVAEYMONDGLALENYLNTKTNFHSVFDVPLHYQFHAASFOG 300
QY 301 GYDMRKLNGTIVSKHPLKSVTFVDNHDTPGQSLSTVQTFWFPPLAFAFLITRESGYPQ 360
301 GYDMRKLNGTIVSKHPLKSVTFVDNHDTPGQSLSTVQTFWFPPLAFAFLITRESGYPQ 360
DB 301 GYDMRKLNGTIVSKHPLKSVTFVDNHDTPGQSLSTVQTFWFPPLAFAFLITRESGYPQ 360
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361 VFYGDWYGTGKDSOREIPALHKIEPIILKAKQAYAGQHDYFPHHDIVGWTREGDSSVA 420
DB 361 VFYGDWYGTGKDSOREIPALHKIEPIILKAKQAYAGQHDYFPHHDIVGWTREGDSSVA 420
QY 421 NSGLAALITDGPAGAKMYVGRQNAGETWHDITGNRSEPVVINSGEWGFHVNGGSVSIY 480
421 NSGLAALITDGPAGAKMYVGRQNAGETWHDITGNRSEPVVINSGEWGFHVNGGSVSIY 480
DB 421 NSGLAALITDGPAGAKMYVGRQNAGETWHDITGNRSEPVVINSGEWGFHVNGGSVSIY 480
QY 481 VOR 483
481 VOR 483
DB 481 VOR 483

US-09-264-097-2
Sequence 2, Application US/09264097
Patent No. 6287826
GENERAL INFORMATION:
APPLICANT: No. 6287826man, Barry Edmund
APPLICANT: Hendriksen, Hanne Vang
TITLE OF INVENTION: Enzymatic Preparation of Glucose Syrup
FILE REFERENCE: 5278.200-US
CURRENT APPLICATION NUMBER: US/09/264,097
EARLIER FILING DATE: 1999-03-08
EARLIER APPLICATION NUMBER: PA 0321/98
EARLIER FILING DATE: 1998-03-09
EARLIER APPLICATION NUMBER: 60/079,209
EARLIER FILING DATE: 1998-03-24
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 483
TYPE: PRT
ORGANISM: Bacillus licheniformis
US-09-264-097-2

Query Match 100.0%; Score 2666; DB 3; Length 483;
Best Local Similarity 100.0%; Pred. No. 2.9e-240; Indels 0; Gaps 0;
Matches 483; Conservative 0; Mismatches 0

QY 1 ANINGTLMQYFEMWYMPNDGQHWRLQNDASAYLAHSGITAWIPPAKGTSGADVGAYD 60
1 ANINGTLMQYFEMWYMPNDGQHWRLQNDASAYLAHSGITAWIPPAKGTSGADVGAYD 60
DB 1 ANINGTLMQYFEMWYMPNDGQHWRLQNDASAYLAHSGITAWIPPAKGTSGADVGAYD 60
QY 61 LYDLGEFHQKGTATKGTGTGELQSAIKSLHSRDINVGVDVNNHKGADATEDVTAVEY 120
61 LYDLGEFHQKGTATKGTGTGELQSAIKSLHSRDINVGVDVNNHKGADATEDVTAVEY 120
DB 61 LYDLGEFHQKGTATKGTGTGELQSAIKSLHSRDINVGVDVNNHKGADATEDVTAVEY 120
QY 121 DPADNRNVISEHILIKMTWTFHFPGRGSTYSDFKMWYHFDGTDWDSRKLNIYKFGOK 180
121 DPADNRNVISEHILIKMTWTFHFPGRGSTYSDFKMWYHFDGTDWDSRKLNIYKFGOK 180
DB 121 DPADNRNVISEHILIKMTWTFHFPGRGSTYSDFKMWYHFDGTDWDSRKLNIYKFGOK 180
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181 AMDWEVSNEGNNDYLYMADIDYDHPVAAEIKRWGTWYANELODGFRLDAVKHKFSF 240
DB 181 AMDWEVSNEGNNDYLYMADIDYDHPVAAEIKRWGTWYANELODGFRLDAVKHKFSF 240
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241 LRDVNNHREKTKGEMFTVAEYMONDGLALENYLNTKTNFHSVFDVPLHYQFHAASFOG 300
DB 241 LRDVNNHREKTKGEMFTVAEYMONDGLALENYLNTKTNFHSVFDVPLHYQFHAASFOG 300
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301 GYDMRKLNGTIVSKHPLKSVTFVDNHDTPGQSLSTVQTFWFPPLAFAFLITRESGYPQ 360
DB 301 GYDMRKLNGTIVSKHPLKSVTFVDNHDTPGQSLSTVQTFWFPPLAFAFLITRESGYPQ 360
QY 361 VFYGDWYGTGKDSOREIPALHKIEPIILKAKQAYAGQHDYFPHHDIVGWTREGDSSVA 420
361 VFYGDWYGTGKDSOREIPALHKIEPIILKAKQAYAGQHDYFPHHDIVGWTREGDSSVA 420
DB 361 VFYGDWYGTGKDSOREIPALHKIEPIILKAKQAYAGQHDYFPHHDIVGWTREGDSSVA 420
QY 421 NSGLAALITDGPAGAKMYVGRQNAGETWHDITGNRSEPVVINSGEWGFHVNGGSVSIY 480
421 NSGLAALITDGPAGAKMYVGRQNAGETWHDITGNRSEPVVINSGEWGFHVNGGSVSIY 480
DB 421 NSGLAALITDGPAGAKMYVGRQNAGETWHDITGNRSEPVVINSGEWGFHVNGGSVSIY 480
QY 481 VOR 483
481 VOR 483
DB 481 VOR 483

RESULT 6
US-09-291-023A-21
Sequence 21, Application US/09291023A
Patent No. 6309871
GENERAL INFORMATION:
APPLICANT: Outtrup, Helle
APPLICANT: Borchert, Torben
APPLICANT: Nielsen, Bjarne
APPLICANT: Nielsen, Vibeke

Tue May 4 14:34:43 2004

us-10-644-187-2.ra1

Page 4

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; APPLICANT: Hoeck, Lisbeth
; TITLE OF INVENTION: Polypeptides Having Alkaline Alpha-amylase Activity And Nucleic A
; FILE REFERENCE: 5821.010-US
; CURRENT APPLICATION NUMBER: US/09/291.023A
; PRIOR FILING DATE: 1999-04-13
; PRIOR APPLICATION NUMBER: DK 1999 00438
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 21
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Bacillus
US-09-291-023A-21

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Query Match          100.0%; Score 2666; DB 4; Length 483;
Best Local Similarity 100.0%; Pred. No. 2,9e-240;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ANLNGTLNQYFPEWYMPNDGQHRRLQNDSAVLAHGITAAMIIPAYKGTSGADVGYGAYD 60
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QY 61 LVDLGEFHQKGTVRTKYGTKGELQSAIKLSHRDINVGDVVNHKGADATEVTAVEV 120
DB 61 LVDLGEFHQKGTVRTKYGTKGELQSAIKLSHRDINVGDVVNHKGADATEVTAVEV 120
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DB 121 DPADNRNRYISGSHLIKAWTHFFPGRGSTYSDPKMWHFPGDTMDESRKLNRIYKQOK 180
QY 181 AMDWEVSNGNNGYDLYMTADIDYHPVAAEIKRWGTWYANELQDGFRLDAVNHKIFSF 240
DB 181 AMDWEVSNGNNGYDLYMTADIDYHPVAAEIKRWGTWYANELQDGFRLDAVNHKIFSF 240
QY 241 LRDVNVHREKTKGEMFTVAEYQNDLGALENYLNKTNFNSVDFVPLHYQFHAASQOG 300
DB 241 LRDVNVHREKTKGEMFTVAEYQNDLGALENYLNKTNFNSVDFVPLHYQFHAASQOG 300
QY 301 GYDMRKLNGTVASGHPKLSVTFVNDHDTQPGQSLSTVQTFKPLAFAFLITRESGYPQ 360
DB 301 GYDMRKLNGTVASGHPKLSVTFVNDHDTQPGQSLSTVQTFKPLAFAFLITRESGYPQ 360
QY 361 VFYGDWYGTGKDSQREIPALKEIPILKARQVAYGAQHDYFDHHDIVGWTREDDSSVA 420
DB 361 VFYGDWYGTGKDSQREIPALKEIPILKARQVAYGAQHDYFDHHDIVGWTREDDSSVA 420
QY 421 NSGLAALLITDGPQAKRMVYGRQNGETWHDITGNRSEPVVINSBGWGEFHVNGGSVSIY 480
DB 421 NSGLAALLITDGPQAKRMVYGRQNGETWHDITGNRSEPVVINSBGWGEFHVNGGSVSIY 480
QY 481 VQR 483
DB 481 VQR 483

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RESULT 7
US-09-290-734-4
; Sequence 4, Application US/09290734
; Patent No. 6361989
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borcherdt, Torben Vedel
; APPLICANT: Bisgaard-Frantzen Henrik
; APPLICANT: Oulttrup, Helle
; APPLICANT: Nielsen, Bjarne Ronfeldt
; APPLICANT: Nielsen, Vibeke Skovgaard
; APPLICANT: Hoeck, Lisbeth Hedegaard
; TITLE OF INVENTION: No 6361989el -Amylase And -Amylase Mutants
; FILE REFERENCE: 5276.400-US
; CURRENT APPLICATION NUMBER: US/09/290,734
; CURRENT FILING DATE: 1999-04-13

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; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 483
; TYPE: PRT
; ORGANISM: B. licheniformis
US-09-290-734-4

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Query Match          100.0%; Score 2666; DB 4; Length 483;
Best Local Similarity 100.0%; Pred. No. 2,9e-240;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ANLNGTLNQYFPEWYMPNDGQHRRLQNDSAVLAHGITAAMIIPAYKGTSGADVGYGAYD 60
DB 1 ANLNGTLNQYFPEWYMPNDGQHRRLQNDSAVLAHGITAAMIIPAYKGTSGADVGYGAYD 60
QY 61 LVDLGEFHQKGTVRTKYGTKGELQSAIKLSHRDINVGDVVNHKGADATEVTAVEV 120
DB 61 LVDLGEFHQKGTVRTKYGTKGELQSAIKLSHRDINVGDVVNHKGADATEVTAVEV 120
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DB 121 DPADNRNRYISGSHLIKAWTHFFPGRGSTYSDPKMWHFPGDTMDESRKLNRIYKQOK 180
QY 181 AMDWEVSNGNNGYDLYMTADIDYHPVAAEIKRWGTWYANELQDGFRLDAVNHKIFSF 240
DB 181 AMDWEVSNGNNGYDLYMTADIDYHPVAAEIKRWGTWYANELQDGFRLDAVNHKIFSF 240
QY 241 LRDVNVHREKTKGEMFTVAEYQNDLGALENYLNKTNFNSVDFVPLHYQFHAASQOG 300
DB 241 LRDVNVHREKTKGEMFTVAEYQNDLGALENYLNKTNFNSVDFVPLHYQFHAASQOG 300
QY 301 GYDMRKLNGTVASGHPKLSVTFVNDHDTQPGQSLSTVQTFKPLAFAFLITRESGYPQ 360
DB 301 GYDMRKLNGTVASGHPKLSVTFVNDHDTQPGQSLSTVQTFKPLAFAFLITRESGYPQ 360
QY 361 VFYGDWYGTGKDSQREIPALKEIPILKARQVAYGAQHDYFDHHDIVGWTREDDSSVA 420
DB 361 VFYGDWYGTGKDSQREIPALKEIPILKARQVAYGAQHDYFDHHDIVGWTREDDSSVA 420
QY 421 NSGLAALLITDGPQAKRMVYGRQNGETWHDITGNRSEPVVINSBGWGEFHVNGGSVSIY 480
DB 421 NSGLAALLITDGPQAKRMVYGRQNGETWHDITGNRSEPVVINSBGWGEFHVNGGSVSIY 480
QY 481 VQR 483
DB 481 VQR 483

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RESULT 8
US-09-537-168-4
; Sequence 4, Application US/09537168
; Patent No. 6410295
; GENERAL INFORMATION:
; APPLICANT: Andersen, Carsten
; APPLICANT: Jorgensen, Christel T.
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Svendsen, Allan
; APPLICANT: Kjaerulf, Soren
; TITLE OF INVENTION: Alpha-Amylase Variants
; FILE REFERENCE: 5886.200-US
; CURRENT APPLICATION NUMBER: US/09/537,168
; PRIOR FILING DATE: 2000-03-29
; EARLIER APPLICATION NUMBER: PA 1999 00437
; EARLIER FILING DATE: 1999-03-30
; EARLIER APPLICATION NUMBER: 60/127,427
; EARLIER FILING DATE: 1999-04-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Bacillus licheniformis

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US-09-537-168-4

Query Match 100.0%; Score 2666; DB 4; Length 483;
Best Local Similarity 100.0%; Pred. No. 2.9e-240;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ANINGTLMQYFEMWMPNDGQHWRLQNDASVLAHEGITAAMIIPPAKGTSGADVGAYD 60
DB 1 ANINGTLMQYFEMWMPNDGQHWRLQNDASVLAHEGITAAMIIPPAKGTSGADVGAYD 60
QY 61 LYDLGEFHQKGYRTKTYGTGKGLQSAIKSLHSRDINVGDVVINKGADATEDVTAVEY 120
DB 61 LYDLGEFHQKGYRTKTYGTGKGLQSAIKSLHSRDINVGDVVINKGADATEDVTAVEY 120
QY 121 DPADNRNVIISGEHLIKAMTHFFHPGRGSTYSDPKMWHYFDGTDWDESKLRIRYKFOGK 180
DB 121 DPADNRNVIISGEHLIKAMTHFFHPGRGSTYSDPKMWHYFDGTDWDESKLRIRYKFOGK 180
QY 181 AMDWEVSNENGNVDYLMYADIDYDHPVAAEIKRWGTWANELQDGFRLDAVKHIKFSF 240
DB 181 AMDWEVSNENGNVDYLMYADIDYDHPVAAEIKRWGTWANELQDGFRLDAVKHIKFSF 240
QY 241 LRDMVNHVREKTKEMFTVAEYQNDLGALENTLNKTNFHSVFDVPLHYQFHAASGQGG 300
DB 241 LRDMVNHVREKTKEMFTVAEYQNDLGALENTLNKTNFHSVFDVPLHYQFHAASGQGG 300
QY 301 GYDMRKLLNGTVSKHPLKSVTFVDNHDTPQGSLSTVQTFWKPLAFAFILTRSGYPO 360
DB 301 GYDMRKLLNGTVSKHPLKSVTFVDNHDTPQGSLSTVQTFWKPLAFAFILTRSGYPO 360
QY 361 VFYGDYMTGKGDSDREIPALKHKIEPIILKARKOYAAGQHDYDHDHDYGMTRREGSSVA 420
DB 361 VFYGDYMTGKGDSDREIPALKHKIEPIILKARKOYAAGQHDYDHDHDYGMTRREGSSVA 420
QY 421 NSGLAALITDGGPGAKMYVGRONAGETWHDITGNSEPVVINSSEGGEFHVNGSVSIT 480
DB 421 NSGLAALITDGGPGAKMYVGRONAGETWHDITGNSEPVVINSSEGGEFHVNGSVSIT 480
QY 481 VOR 483
DB 481 VOR 483
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RESULT 9

US-09-672-459-2
Sequence 2, Application US/09672459
Patent No. 643688

GENERAL INFORMATION:

APPLICANT: Svendsen, Allan

APPLICANT: Borchert, Torben

APPLICANT: Bisgard-Frantzen, Henrik

TITLE OF INVENTION: Alpha-Amylase Mutants

FILE REFERENCE: 4796.204-US

CURRENT APPLICATION NUMBER: US/09/672,459

CURRENT FILING DATE: 2000-09-28

PRIOR APPLICATION NUMBER: 09/182,859

PRIOR FILING DATE: 1998-10-29

PRIOR APPLICATION NUMBER: 0515/96

PRIOR FILING DATE: 1996-04-30

PRIOR APPLICATION NUMBER: 0712/96

PRIOR FILING DATE: 1996-06-28

PRIOR APPLICATION NUMBER: 0775/96

PRIOR FILING DATE: 1996-07-11

PRIOR APPLICATION NUMBER: 1263/96

PRIOR FILING DATE: 1996-11-08

NUMBER OF SEQ ID NOS: 37

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 2

LENGTH: 483

TYPE: PRT

ORGANISM: Bacillus licheniformis

US-09-672-459-2

Query Match 100.0%; Score 2666; DB 4; Length 483;
Best Local Similarity 100.0%; Pred. No. 2.9e-240;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ANINGTLMQYFEMWMPNDGQHWRLQNDASVLAHEGITAAMIIPPAKGTSGADVGAYD 60
DB 1 ANINGTLMQYFEMWMPNDGQHWRLQNDASVLAHEGITAAMIIPPAKGTSGADVGAYD 60
QY 61 LYDLGEFHQKGYRTKTYGTGKGLQSAIKSLHSRDINVGDVVINKGADATEDVTAVEY 120
DB 61 LYDLGEFHQKGYRTKTYGTGKGLQSAIKSLHSRDINVGDVVINKGADATEDVTAVEY 120
QY 121 DPADNRNVIISGEHLIKAMTHFFHPGRGSTYSDPKMWHYFDGTDWDESKLRIRYKFOGK 180
DB 121 DPADNRNVIISGEHLIKAMTHFFHPGRGSTYSDPKMWHYFDGTDWDESKLRIRYKFOGK 180
QY 181 AMDWEVSNENGNVDYLMYADIDYDHPVAAEIKRWGTWANELQDGFRLDAVKHIKFSF 240
DB 181 AMDWEVSNENGNVDYLMYADIDYDHPVAAEIKRWGTWANELQDGFRLDAVKHIKFSF 240
QY 241 LRDMVNHVREKTKEMFTVAEYQNDLGALENTLNKTNFHSVFDVPLHYQFHAASGQGG 300
DB 241 LRDMVNHVREKTKEMFTVAEYQNDLGALENTLNKTNFHSVFDVPLHYQFHAASGQGG 300
QY 301 GYDMRKLLNGTVSKHPLKSVTFVDNHDTPQGSLSTVQTFWKPLAFAFILTRSGYPO 360
DB 301 GYDMRKLLNGTVSKHPLKSVTFVDNHDTPQGSLSTVQTFWKPLAFAFILTRSGYPO 360
QY 361 VFYGDYMTGKGDSDREIPALKHKIEPIILKARKOYAAGQHDYDHDHDYGMTRREGSSVA 420
DB 361 VFYGDYMTGKGDSDREIPALKHKIEPIILKARKOYAAGQHDYDHDHDYGMTRREGSSVA 420
QY 421 NSGLAALITDGGPGAKMYVGRONAGETWHDITGNSEPVVINSSEGGEFHVNGSVSIT 480
DB 421 NSGLAALITDGGPGAKMYVGRONAGETWHDITGNSEPVVINSSEGGEFHVNGSVSIT 480
QY 481 VOR 483
DB 481 VOR 483
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RESULT 10

US-09-545-586-4
Sequence 4, Application US/09545586
Patent No. 6528298

GENERAL INFORMATION:

APPLICANT: Svendsen, Allan

APPLICANT: Borchert, Torben Vedel

APPLICANT: Bisgard-Frantzen, Henrik

APPLICANT: Outtrup, Helle

APPLICANT: Nielsen, Bjarne Ronfeldt

APPLICANT: Nielsen, Vibeke Skovgaard

APPLICANT: Hoeck, Lisbeth Hedegaard

TITLE OF INVENTION: No. 6528298-1 -Amylase And -Amylase Mutants

FILE REFERENCE: 5276.400-US

CURRENT APPLICATION NUMBER: US/09/545,586

CURRENT FILING DATE: 2000-04-07

PRIOR APPLICATION NUMBER: US/09/290,734

PRIOR FILING DATE: 1999-04-13

NUMBER OF SEQ ID NOS: 35

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 4

LENGTH: 483

TYPE: PRT

ORGANISM: B. licheniformis

US-09-545-586-4

Query Match 100.0%; Score 2666; DB 4; Length 483;
Best Local Similarity 100.0%; Pred. No. 2.9e-240;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ANINGTLMQYFEMWMPNDGQHWRLQNDASVLAHEGITAAMIIPPAKGTSGADVGAYD 60
DB 1 ANINGTLMQYFEMWMPNDGQHWRLQNDASVLAHEGITAAMIIPPAKGTSGADVGAYD 60
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Db 1 ANINGTLMQYFEWMPNDGQWRLQNDASAYLAHEGITAIVMIPPAKGTSGADVGAYD 60
QY 61 LYDGEFHQKGTATKTKGTGELQSAIKSLHSRDINVGDVVNHKGADATEDVTAVEV 120
Db 61 LYDGEFHQKGTATKTKGTGELQSAIKSLHSRDINVGDVVNHKGADATEDVTAVEV 120
QY 121 DPADRNVIISGEHLIKAMTHFHPGSGSTYSDFKMHYHFDGTDWDSRKLNR1YFQOK 180
Db 121 DPADRNVIISGEHLIKAMTHFHPGSGSTYSDFKMHYHFDGTDWDSRKLNR1YFQOK 180
QY 181 AMDWVSNNENNYLYMADIDYHPVAAEIKRWGTWYANELODGFRLDAYKH1KFSF 240
Db 181 AMDWVSNNENNYLYMADIDYHPVAAEIKRWGTWYANELODGFRLDAYKH1KFSF 240
QY 241 LRDWNVHREKTKGEMFTVAEYWNQDGALENYLNKTNFHSYFVDPVLAHYQFHAAS1QOG 300
Db 241 LRDWNVHREKTKGEMFTVAEYWNQDGALENYLNKTNFHSYFVDPVLAHYQFHAAS1QOG 300
QY 301 GYDMRKLINGTVSKHPLKSTYFVNDNDTPQGSLSTVQTFWFKPLAYAFIL1TRESGYPQ 360
Db 301 GYDMRKLINGTVSKHPLKSTYFVNDNDTPQGSLSTVQTFWFKPLAYAFIL1TRESGYPQ 360
QY 361 VFYGDWYGTKDSOREIPALKHKIEPIIKAKQYAYGAQHDYFPDHD1VGTREGDSSVA 420
Db 361 VFYGDWYGTKDSOREIPALKHKIEPIIKAKQYAYGAQHDYFPDHD1VGTREGDSSVA 420
QY 421 NSGLAALITDGPQAKMYVGRQNAGETWHDITGNRSEPVVINSBGGEFFHNGGSV1Y 480
Db 421 NSGLAALITDGPQAKMYVGRQNAGETWHDITGNRSEPVVINSBGGEFFHNGGSV1Y 480
QY 481 VQR 483
Db 481 VQR 483

RESULT 11
US-09-540-715A-21
Sequence 21, Application US/09540715A

Patent No. 6623948
GENERAL INFORMATION:
APPLICANT: Outtrup, Helle
APPLICANT: Borchert, Torben
APPLICANT: Nielsen, Bjarne
APPLICANT: Nielsen, Bjarne
APPLICANT: Hoeck, Lisbeth
TITLE OF INVENTION: Polypeptides Having Alkaline Alpha-amylase Activity And Nucleic A
FILE REFERENCE: 5821.010-US
CURRENT APPLICATION NUMBER: US/09/540,715A
CURRENT FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/291,023
PRIOR FILING DATE: 2001-08-14
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PatentIn version 3.0
SEQ ID NO 21
LENGTH: 483
TYPE: PRT
ORGANISM: Bacillus
US-09-540-715A-21

Query Match 100.0%; Score 2666; DB 4; Length 483;
Best Local Similarity 100.0%; Pred. No. 2,9e-240;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANINGTLMQYFEWMPNDGQWRLQNDASAYLAHEGITAIVMIPPAKGTSGADVGAYD 60
Db 1 ANINGTLMQYFEWMPNDGQWRLQNDASAYLAHEGITAIVMIPPAKGTSGADVGAYD 60
QY 61 LYDGEFHQKGTATKTKGTGELQSAIKSLHSRDINVGDVVNHKGADATEDVTAVEV 120
Db 61 LYDGEFHQKGTATKTKGTGELQSAIKSLHSRDINVGDVVNHKGADATEDVTAVEV 120
QY 121 DPADRNVIISGEHLIKAMTHFHPGSGSTYSDFKMHYHFDGTDWDSRKLNR1YFQOK 180

Db 121 DPADRNVIISGEHLIKAMTHFHPGSGSTYSDFKMHYHFDGTDWDSRKLNR1YFQOK 180
QY 181 AMDWVSNNENNYLYMADIDYHPVAAEIKRWGTWYANELODGFRLDAYKH1KFSF 240
Db 181 AMDWVSNNENNYLYMADIDYHPVAAEIKRWGTWYANELODGFRLDAYKH1KFSF 240
QY 241 LRDWNVHREKTKGEMFTVAEYWNQDGALENYLNKTNFHSYFVDPVLAHYQFHAAS1QOG 300
Db 241 LRDWNVHREKTKGEMFTVAEYWNQDGALENYLNKTNFHSYFVDPVLAHYQFHAAS1QOG 300
QY 301 GYDMRKLINGTVSKHPLKSTYFVNDNDTPQGSLSTVQTFWFKPLAYAFIL1TRESGYPQ 360
Db 301 GYDMRKLINGTVSKHPLKSTYFVNDNDTPQGSLSTVQTFWFKPLAYAFIL1TRESGYPQ 360
QY 361 VFYGDWYGTKDSOREIPALKHKIEPIIKAKQYAYGAQHDYFPDHD1VGTREGDSSVA 420
Db 361 VFYGDWYGTKDSOREIPALKHKIEPIIKAKQYAYGAQHDYFPDHD1VGTREGDSSVA 420
QY 421 NSGLAALITDGPQAKMYVGRQNAGETWHDITGNRSEPVVINSBGGEFFHNGGSV1Y 480
Db 421 NSGLAALITDGPQAKMYVGRQNAGETWHDITGNRSEPVVINSBGGEFFHNGGSV1Y 480
QY 481 VQR 483
Db 481 VQR 483

RESULT 12
US-10-186-042-2
Sequence 2, Application US/10186042

Patent No. 6642044
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Borchert, Torben
APPLICANT: Bisgaard-Frantzen, Henrik
TITLE OF INVENTION: Alpha-Amylase Mutants
FILE REFERENCE: 4796.204-US
CURRENT APPLICATION NUMBER: US/10/186,042
CURRENT FILING DATE: 2002-06-28
PRIOR APPLICATION NUMBER: US/09/672,459
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: 09/182,859
PRIOR FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: 0515/96
PRIOR FILING DATE: 1996-04-30
PRIOR APPLICATION NUMBER: 0712/96
PRIOR FILING DATE: 1996-06-28
PRIOR APPLICATION NUMBER: 0775/96
PRIOR FILING DATE: 1996-07-11
PRIOR APPLICATION NUMBER: 1263/96
PRIOR FILING DATE: 1996-11-08
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 483
TYPE: PRT
ORGANISM: Bacillus licheniformis
US-10-186-042-2

Query Match 100.0%; Score 2666; DB 4; Length 483;
Best Local Similarity 100.0%; Pred. No. 2,9e-240;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANINGTLMQYFEWMPNDGQWRLQNDASAYLAHEGITAIVMIPPAKGTSGADVGAYD 60
Db 1 ANINGTLMQYFEWMPNDGQWRLQNDASAYLAHEGITAIVMIPPAKGTSGADVGAYD 60
QY 61 LYDGEFHQKGTATKTKGTGELQSAIKSLHSRDINVGDVVNHKGADATEDVTAVEV 120
Db 61 LYDGEFHQKGTATKTKGTGELQSAIKSLHSRDINVGDVVNHKGADATEDVTAVEV 120
QY 121 DPADRNVIISGEHLIKAMTHFHPGSGSTYSDFKMHYHFDGTDWDSRKLNR1YFQOK 180

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Db      121  DPADNRRTISGEHLIKATHTPHFPGRGSTYSDPFKMHVHPFGCTMDSRKLRNLYXQCK 180
Qy      181  AMDWEVSNENGVYDLYMADIDYDHPDVAALIKEMGTWYANELQDGRFLDAVGHKIFSF 240
Db      181  AMDWEVSNENGVYDLYMADIDYDHPDVAALIKEMGTWYANELQDGRFLDAVGHKIFSF 240
Qy      241  LRDWVNHREKTKGEMFTVAEYQNDLGALENYLNKTNFNSVDFVPLHYQFHAASIOGG 300
Db      241  LRDWVNHREKTKGEMFTVAEYQNDLGALENYLNKTNFNSVDFVPLHYQFHAASIOGG 300
Qy      301  GYDMKRLNGTVSGKPLKSVTFVNDHDTOPQOSLESTVQTMFKPLAVALITRESGYPO 360
Db      301  GYDMKRLNGTVSGKPLKSVTFVNDHDTOPQOSLESTVQTMFKPLAVALITRESGYPO 360
Qy      361  VFYGMVGTGKDSQREIPALKHKIEPILKARKQVAYGAQHDYFDHHDIVGWTREGDSSVA 420
Db      361  VFYGMVGTGKDSQREIPALKHKIEPILKARKQVAYGAQHDYFDHHDIVGWTREGDSSVA 420
Qy      421  NSGLAALITDGPQAKRMVYGRQNGETWHDITGNRSEPVVINSBGWGFPHVNGGSVSIY 480
Db      421  NSGLAALITDGPQAKRMVYGRQNGETWHDITGNRSEPVVINSBGWGFPHVNGGSVSIY 480
Qy      481  VQR 483
Db      481  VQR 483

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RESULT 13
US-09-769-864-4
Sequence 4, Application US/09769864
Patent No. 6673589

GENERAL INFORMATION:
APPLICANT: Borchert, Torben V.
APPLICANT: Svendsen, Allan
APPLICANT: Andersen, Carsten
APPLICANT: Nielsen, Bjarne
APPLICANT: Nielsen, Torben L.
APPLICANT: Kjaerulf, Soren
TITLE OF INVENTION: Alpha-Amulase Mutants
FILE REFERENCE: 5368.200-US
CURRENT APPLICATION NUMBER: US/09/769,864
CURRENT FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: 09/183,412
PRIOR FILING DATE: 1998-10-30
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 483
TYPE: PRT
ORGANISM: Bacillus licheniformis
US-09-769-864-4

Query Match 100.0%; Score 2666; DB 4; Length 483;
Best Local Similarity 100.0%; Pred. No. 2,9e-240;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1  ANNGTLMQYFEWYMPNDGQHRRLQNDASVYLAHEGITTAVWIPRAYKTSQADVGYAYD 60
Db      1  ANNGTLMQYFEWYMPNDGQHRRLQNDASVYLAHEGITTAVWIPRAYKTSQADVGYAYD 60
Qy      61  LVDLGEFHQKGTVRTKGTGKELQSAIKSLHSRDINVGDVYVNHKGADATEDVTAVEV 120
Db      61  LVDLGEFHQKGTVRTKGTGKELQSAIKSLHSRDINVGDVYVNHKGADATEDVTAVEV 120
Qy      121  DPADNRRTISGEHLIKATHTPHFPGRGSTYSDPFKMHVHPFGCTMDSRKLRNLYXQCK 180
Db      121  DPADNRRTISGEHLIKATHTPHFPGRGSTYSDPFKMHVHPFGCTMDSRKLRNLYXQCK 180
Qy      181  AMDWEVSNENGVYDLYMADIDYDHPDVAALIKEMGTWYANELQDGRFLDAVGHKIFSF 240
Db      181  AMDWEVSNENGVYDLYMADIDYDHPDVAALIKEMGTWYANELQDGRFLDAVGHKIFSF 240

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Qy      241  LRDWVNHREKTKGEMFTVAEYQNDLGALENYLNKTNFNSVDFVPLHYQFHAASIOGG 300
Db      241  LRDWVNHREKTKGEMFTVAEYQNDLGALENYLNKTNFNSVDFVPLHYQFHAASIOGG 300
Qy      301  GYDMKRLNGTVSGKPLKSVTFVNDHDTOPQOSLESTVQTMFKPLAVALITRESGYPO 360
Db      301  GYDMKRLNGTVSGKPLKSVTFVNDHDTOPQOSLESTVQTMFKPLAVALITRESGYPO 360
Qy      361  VFYGMVGTGKDSQREIPALKHKIEPILKARKQVAYGAQHDYFDHHDIVGWTREGDSSVA 420
Db      361  VFYGMVGTGKDSQREIPALKHKIEPILKARKQVAYGAQHDYFDHHDIVGWTREGDSSVA 420
Qy      421  NSGLAALITDGPQAKRMVYGRQNGETWHDITGNRSEPVVINSBGWGFPHVNGGSVSIY 480
Db      421  NSGLAALITDGPQAKRMVYGRQNGETWHDITGNRSEPVVINSBGWGFPHVNGGSVSIY 480
Qy      481  VQR 483
Db      481  VQR 483

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RESULT 14
US-08-720-899-2
Sequence 2, Application US/08720899
Patent No. 5753460

GENERAL INFORMATION:
APPLICANT: Bisgaard-Frantzen, Henrik
APPLICANT: Borchert, Torben Vedel
APPLICANT: Svendsen, Allan
APPLICANT: Thøgersen, Marianne
APPLICANT: Van der Zee, Pia
TITLE OF INVENTION: AMYLASE VARIANTS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5753460 No. 5753460disk of No. 5753460ch America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/720,899
FILING DATE: 10-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/343,804
FILING DATE: 22-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lowrey Dr., Karen A.
REGISTRATION NUMBER: 31,274
REFERENCE/DOCKET NUMBER: 4054,214-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 512 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-720-899-2

Query Match 100.0%; Score 2666; DB 1; Length 512;
Best Local Similarity 100.0%; Pred. No. 3.2e-240;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Tue May 4 14:34:43 2004

us-10-644-187-2.ral

Page 8

Db 30 ANINGTLMQYFEWYMPNDGQHRRLQNDASAYLAHGIITAWIIPAYKGTQADVGAYD 89
QY 61 LYDLGEFHOKGTVRTKTKGTGKELQSAIKSLHSRDINVGDVYINHGADATEDVTAVEV 120
Db 90 LYDLGEFHOKGTVRTKTKGTGKELQSAIKSLHSRDINVGDVYINHGADATEDVTAVEV 149
QY 121 DPADRRRVISGEHLIKAMTHFFHPGSGTSDPKMWHFPGDITWDSRKLRIYKFGQK 180
Db 150 DPADRRRVISGEHLIKAMTHFFHPGSGTSDPKMWHFPGDITWDSRKLRIYKFGQK 209
QY 181 AMDWEVSNENGVNDYLMYADIDYDHPDVAEIKRMGTWYANELQDGFRLDAVKIKFSF 240
Db 210 AMDWEVSNENGVNDYLMYADIDYDHPDVAEIKRMGTWYANELQDGFRLDAVKIKFSF 269
QY 241 LRDMVNVHREKTKGEMFTVAEYQNDLGALNTNPNHSPVDFVPLHYQFHAASSTQG 300
Db 270 LRDMVNVHREKTKGEMFTVAEYQNDLGALNTNPNHSPVDFVPLHYQFHAASSTQG 329
QY 301 GYDMRKLINGTVVSKPLKSVTFVDNHDTPQGSLSTVQTFKPLAVALITRESGYPQ 360
Db 330 GYDMRKLINGTVVSKPLKSVTFVDNHDTPQGSLSTVQTFKPLAVALITRESGYPQ 389
QY 361 VFYGDWYGTGKDSOREIPALKHKEIPILKARKOYAGAOHYFDHHDIVGWTREGDSSVA 420
Db 390 VFYGDWYGTGKDSOREIPALKHKEIPILKARKOYAGAOHYFDHHDIVGWTREGDSSVA 449
QY 421 NSGLAALITDGPQAKRMVYGRONAGETWHDITGNRSEPVVINSBGGEFHVNGSVSIV 480
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QY 481 VQR 483
Db 510 VQR 512

RESULT 15
US-08-459-610-2
Sequence 2, Application US/08459610
Patent No. 5801043
GENERAL INFORMATION:
APPLICANT: Bisgaard-Frantzen, Henrik
APPLICANT: Borchert, Torben Vedel
APPLICANT: Svendsen, Allan
APPLICANT: Thøgersen, Marianne
APPLICANT: Van der Zee, Pia
TITLE OF INVENTION: AMYLASE VARIANTS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 58010433 of No. 58010433th America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,610
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/343,804
FILING DATE: 22-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lowmey Dr., Karen A.
REGISTRATION NUMBER: 31,274
REFERENCE/DOCKET NUMBER: 4054.214-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 512 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-610-2
Query Match 100.0%; Score 2666; DB 1; Length 512;
Best Local Similarity 100.0%; Pident. No. 3.2e-240;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ANINGTLMQYFEWYMPNDGQHRRLQNDASAYLAHGIITAWIIPAYKGTQADVGAYD 60
Db 30 ANINGTLMQYFEWYMPNDGQHRRLQNDASAYLAHGIITAWIIPAYKGTQADVGAYD 89
QY 61 LYDLGEFHOKGTVRTKTKGTGKELQSAIKSLHSRDINVGDVYINHGADATEDVTAVEV 120
Db 90 LYDLGEFHOKGTVRTKTKGTGKELQSAIKSLHSRDINVGDVYINHGADATEDVTAVEV 149
QY 121 DPADRRRVISGEHLIKAMTHFFHPGSGTSDPKMWHFPGDITWDSRKLRIYKFGQK 180
Db 150 DPADRRRVISGEHLIKAMTHFFHPGSGTSDPKMWHFPGDITWDSRKLRIYKFGQK 209
QY 181 AMDWEVSNENGVNDYLMYADIDYDHPDVAEIKRMGTWYANELQDGFRLDAVKIKFSF 240
Db 210 AMDWEVSNENGVNDYLMYADIDYDHPDVAEIKRMGTWYANELQDGFRLDAVKIKFSF 269
QY 241 LRDMVNVHREKTKGEMFTVAEYQNDLGALNTNPNHSPVDFVPLHYQFHAASSTQG 300
Db 270 LRDMVNVHREKTKGEMFTVAEYQNDLGALNTNPNHSPVDFVPLHYQFHAASSTQG 329
QY 301 GYDMRKLINGTVVSKPLKSVTFVDNHDTPQGSLSTVQTFKPLAVALITRESGYPQ 360
Db 330 GYDMRKLINGTVVSKPLKSVTFVDNHDTPQGSLSTVQTFKPLAVALITRESGYPQ 389
QY 361 VFYGDWYGTGKDSOREIPALKHKEIPILKARKOYAGAOHYFDHHDIVGWTREGDSSVA 420
Db 390 VFYGDWYGTGKDSOREIPALKHKEIPILKARKOYAGAOHYFDHHDIVGWTREGDSSVA 449
QY 421 NSGLAALITDGPQAKRMVYGRONAGETWHDITGNRSEPVVINSBGGEFHVNGSVSIV 480
Db 450 NSGLAALITDGPQAKRMVYGRONAGETWHDITGNRSEPVVINSBGGEFHVNGSVSIV 509
QY 481 VQR 483
Db 510 VQR 512

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Job time: 18.3507 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 3, 2004, 20:33:58 ; Search time 37.6066 Seconds

(without alignments)
3560.078 Million cell updates/sec

Title: US-10-644-187-2

Perfect score: 2666

Sequence: 1 ANLNGTLMQYFWMYMPNDQ.....SEGWGEFHWGSGVSIVYQR 483

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1138120 seqs, 277189581 residues

Total number of hits satisfying chosen parameters: 1138120

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2666	100.0	483	9	US-09-769-864-4
2	2666	100.0	483	9	US-09-854-346-8
3	2666	100.0	483	9	US-09-918-543-8
4	2666	100.0	483	9	US-09-918-543-10
5	2666	100.0	483	9	US-09-925-576C-8
6	2666	100.0	483	12	US-10-665-667-4
7	2666	100.0	483	12	US-10-644-187-2
8	2666	100.0	483	12	US-10-327-837-4
9	2666	100.0	483	14	US-10-146-327-4
10	2666	100.0	483	14	US-10-186-042-2
11	2666	100.0	512	14	US-10-184-771-2
12	2663	99.9	512	14	US-10-189-822-2
13	2654	99.5	512	14	US-10-081-872-114
14	2654	99.5	512	14	US-10-105-733-8
15	2654	99.5	512	14	US-10-081-739A-8

16	2654	99.5	512	15	US-10-385-305-114	Sequence 114, Appl
17	2582	96.8	481	14	US-10-146-327-2	Sequence 2, Appl
18	2338	87.7	483	14	US-10-184-771-13	Sequence 13, Appl
19	2184	81.9	483	9	US-09-854-346-10	Sequence 10, Appl
20	2184	81.9	483	9	US-09-918-543-10	Sequence 10, Appl
21	2184	81.9	483	10	US-09-925-576C-10	Sequence 6, Appl
22	2184	81.9	483	14	US-10-146-327-6	Sequence 4, Appl
23	2184	81.9	514	14	US-10-184-771-4	Sequence 5, Appl
24	2173	81.5	480	12	US-10-665-667-5	Sequence 5, Appl
25	2173	81.5	480	12	US-10-644-187-4	Sequence 4, Appl
26	2173	81.5	480	12	US-10-327-837-5	Sequence 4, Appl
27	2173	81.5	480	14	US-10-186-042-4	Sequence 70, Appl
28	2173	81.5	513	14	US-10-081-872-70	Sequence 70, Appl
29	1999	75.0	513	15	US-10-385-305-70	Sequence 146, App
30	1999	75.0	513	15	US-10-081-872-146	Sequence 146, App
31	1979	74.2	513	14	US-10-385-305-146	Sequence 166, App
32	1979	74.2	513	15	US-10-081-872-166	Sequence 166, App
33	1961	73.6	478	14	US-10-081-872-166	Sequence 166, App
34	1961	73.6	478	15	US-10-385-305-166	Sequence 166, App
35	1950	73.1	485	9	US-09-769-864-8	Sequence 2, Appl
36	1950	73.1	485	9	US-09-769-864-8	Sequence 2, Appl
37	1950	73.1	485	9	US-09-854-346-4	Sequence 2, Appl
38	1950	73.1	485	9	US-09-902-188A-2	Sequence 2, Appl
39	1950	73.1	485	9	US-09-918-543-4	Sequence 2, Appl
40	1950	73.1	485	9	US-09-925-576C-4	Sequence 2, Appl
41	1950	73.1	485	10	US-09-925-576C-4	Sequence 2, Appl
42	1950	73.1	485	12	US-10-665-667-2	Sequence 2, Appl
43	1950	73.1	485	12	US-10-665-667-8	Sequence 2, Appl
44	1950	73.1	485	12	US-10-025-648-2	Sequence 2, Appl
45	1950	73.1	485	12	US-10-327-837-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-09-769-864-4 ; Sequence 4, Application US/09769864
; Patent No. US20010039253A1
; GENERAL INFORMATION:
; APPLICANT: Borchert, Torden V.
; APPLICANT: Svendsen, Allan
; APPLICANT: Andersen, Carsten
; APPLICANT: Nielsen, Bjørne
; APPLICANT: Nissen, Torden L.
; APPLICANT: Kjærulff, Søren
; TITLE OF INVENTION: Alpha-Amulase Mutants
; FILE REFERENCE: 5368.200-US
; CURRENT APPLICATION NUMBER: US/09/769,864
; CURRENT FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/183,412
; PRIOR FILING DATE: 1998-10-30
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 4
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-09-769-864-4
Query Match 100.0%; Score 2666; DB 9; Length 483;
Best Local Similarity 100.0%; Pred. No. 6.9e-239;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ANLNGTLMQYFWMYMPNDQ.....SAIYAEHGITAWTTPPAYKGTSGQADVGAYD 60
DB 1 ANLNGTLMQYFWMYMPNDQ.....SAIYAEHGITAWTTPPAYKGTSGQADVGAYD 60
QY 61 IVDLGFHOKGIVRYKYGKGLQSAIKLSRSDINVGIVYINHGAGADATEDYAVEV 120
DB 61 IVDLGFHOKGIVRYKYGKGLQSAIKLSRSDINVGIVYINHGAGADATEDYAVEV 120
QY 121 DPADRNRVLSGHLIKAWTHFHPGSGTYSDFKMHWHFPGTDWDESRKLNRIYKPGQK 180

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Db 121 DPADNRKVISGEHLIKAMTHFFHPGRGSTYSDFKMWHFPGDTMDESKLRIRYKFGK 180
Qy 181 AMDWEVSNGNNDYLMYADIDYDHPDVAEIKRWGTWYANELQDGFRLDAVKIKRSF 240
Db 181 AMDWEVSNGNNDYLMYADIDYDHPDVAEIKRWGTWYANELQDGFRLDAVKIKRSF 240
Qy 241 LRDWNVHREKTKGEMFTVAEYWMNDLGALENYLNKTNFNHSPVPLHYOFHAASSTGG 300
Db 241 LRDWNVHREKTKGEMFTVAEYWMNDLGALENYLNKTNFNHSPVPLHYOFHAASSTGG 300
Qy 301 GYDMRKLNGTVVSKHPLKSVTFVNDHDTOPQGSLESTVQTFWFKPLAYAFILTRBSGYPO 360
Db 301 GYDMRKLNGTVVSKHPLKSVTFVNDHDTOPQGSLESTVQTFWFKPLAYAFILTRBSGYPO 360
Qy 361 VFYGDWYGTGKDSOREIPALKHKIEPILKARKQYVGAQHDYFDHHDIVGWTREBDSVA 420
Db 361 VFYGDWYGTGKDSOREIPALKHKIEPILKARKQYVGAQHDYFDHHDIVGWTREBDSVA 420
Qy 421 NSGLAALITDGPQAKRMVYGRQNAGETWHDITGNRSEPVVINSBGWGFHNGGSVSIY 480
Db 421 NSGLAALITDGPQAKRMVYGRQNAGETWHDITGNRSEPVVINSBGWGFHNGGSVSIY 480
Qy 481 VQR 483
Db 481 VQR 483
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RESULT 2

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US-09-854-346-8
/ Sequence 8, Application US/09854346
/ Patent No. US20020068352A1
/ GENERAL INFORMATION:
/ APPLICANT: No. US20020068352A1ozymes A/S
/ APPLICANT: Svendsen, Allan
/ APPLICANT: Jorgensen, Christel Thea
/ APPLICANT: Nielsen, Bjarne Ronfeldt
/ TITLE OF INVENTION: Alpha-amylase variants with altered 1,6 activity
/ FILE REFERENCE: 6140.200-US
/ CURRENT APPLICATION NUMBER: US/09/854,346
/ NUMBER OF SEQ ID NOS: 15
/ SOFTWARE: Patentin version 3.1
/ SEQ ID NO 8
/ LENGTH: 483
/ TYPE: PRT
/ ORGANISM: Bacillus licheniformis
US-09-854-346-8
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Query Match 100.0%; Score 2666; DB 9; Length 483;
Best Local Similarity 100.0%; Pred. No. 6.9e-239;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 ANLNGTLMQYFEWYMPNDGQWHRRLONDSAYLAHEGITAWMIPRAYKGTSGADVGYAYD 60
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Db 61 LVLDGEFHQKGTVRTKYGKELQSAIKSLHSRDINVGDVYINHGADATEDVTAVEV 120
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Db 121 DPADNRKVISGEHLIKAMTHFFHPGRGSTYSDFKMWHFPGDTMDESKLRIRYKFGK 180
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Db 181 AMDWEVSNGNNDYLMYADIDYDHPDVAEIKRWGTWYANELQDGFRLDAVKIKRSF 240
Qy 241 LRDWNVHREKTKGEMFTVAEYWMNDLGALENYLNKTNFNHSPVPLHYOFHAASSTGG 300
Db 241 LRDWNVHREKTKGEMFTVAEYWMNDLGALENYLNKTNFNHSPVPLHYOFHAASSTGG 300
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Qy 301 GYDMRKLNGTVVSKHPLKSVTFVNDHDTOPQGSLESTVQTFWFKPLAYAFILTRBSGYPO 360
Db 301 GYDMRKLNGTVVSKHPLKSVTFVNDHDTOPQGSLESTVQTFWFKPLAYAFILTRBSGYPO 360
Qy 361 VFYGDWYGTGKDSOREIPALKHKIEPILKARKQYVGAQHDYFDHHDIVGWTREBDSVA 420
Db 361 VFYGDWYGTGKDSOREIPALKHKIEPILKARKQYVGAQHDYFDHHDIVGWTREBDSVA 420
Qy 421 NSGLAALITDGPQAKRMVYGRQNAGETWHDITGNRSEPVVINSBGWGFHNGGSVSIY 480
Db 421 NSGLAALITDGPQAKRMVYGRQNAGETWHDITGNRSEPVVINSBGWGFHNGGSVSIY 480
Qy 481 VQR 483
Db 481 VQR 483
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RESULT 3

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US-09-918-543-8
/ Sequence 8, Application US/0918543
/ Patent No. US2002015574A1
/ GENERAL INFORMATION:
/ APPLICANT: No. US2002015574A1ozymes A/S
/ APPLICANT: Thisted, Thomas
/ APPLICANT: Kjaeruliff, Soren
/ APPLICANT: Andersen, Carsten
/ APPLICANT: Fuglsang, Claus Crone
/ TITLE OF INVENTION: Alpha-amylase mutants with altered properties
/ FILE REFERENCE: 10062.200-US
/ CURRENT APPLICATION NUMBER: US/09/918,543
/ NUMBER OF SEQ ID NOS: 30
/ SOFTWARE: Patentin version 3.1
/ SEQ ID NO 8
/ LENGTH: 483
/ TYPE: PRT
/ ORGANISM: Bacillus licheniformis
US-09-918-543-8
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Query Match 100.0%; Score 2666; DB 9; Length 483;
Best Local Similarity 100.0%; Pred. No. 6.9e-239;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 ANLNGTLMQYFEWYMPNDGQWHRRLONDSAYLAHEGITAWMIPRAYKGTSGADVGYAYD 60
Db 1 ANLNGTLMQYFEWYMPNDGQWHRRLONDSAYLAHEGITAWMIPRAYKGTSGADVGYAYD 60
Qy 61 LVLDGEFHQKGTVRTKYGKELQSAIKSLHSRDINVGDVYINHGADATEDVTAVEV 120
Db 61 LVLDGEFHQKGTVRTKYGKELQSAIKSLHSRDINVGDVYINHGADATEDVTAVEV 120
Qy 121 DPADNRKVISGEHLIKAMTHFFHPGRGSTYSDFKMWHFPGDTMDESKLRIRYKFGK 180
Db 121 DPADNRKVISGEHLIKAMTHFFHPGRGSTYSDFKMWHFPGDTMDESKLRIRYKFGK 180
Qy 181 AMDWEVSNGNNDYLMYADIDYDHPDVAEIKRWGTWYANELQDGFRLDAVKIKRSF 240
Db 181 AMDWEVSNGNNDYLMYADIDYDHPDVAEIKRWGTWYANELQDGFRLDAVKIKRSF 240
Qy 241 LRDWNVHREKTKGEMFTVAEYWMNDLGALENYLNKTNFNHSPVPLHYOFHAASSTGG 300
Db 241 LRDWNVHREKTKGEMFTVAEYWMNDLGALENYLNKTNFNHSPVPLHYOFHAASSTGG 300
Qy 301 GYDMRKLNGTVVSKHPLKSVTFVNDHDTOPQGSLESTVQTFWFKPLAYAFILTRBSGYPO 360
Db 301 GYDMRKLNGTVVSKHPLKSVTFVNDHDTOPQGSLESTVQTFWFKPLAYAFILTRBSGYPO 360
Qy 361 VFYGDWYGTGKDSOREIPALKHKIEPILKARKQYVGAQHDYFDHHDIVGWTREBDSVA 420
Db 361 VFYGDWYGTGKDSOREIPALKHKIEPILKARKQYVGAQHDYFDHHDIVGWTREBDSVA 420
Qy 421 NSGLAALITDGPQAKRMVYGRQNAGETWHDITGNRSEPVVINSBGWGFHNGGSVSIY 480
Db 421 NSGLAALITDGPQAKRMVYGRQNAGETWHDITGNRSEPVVINSBGWGFHNGGSVSIY 480
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Tue May 4 14:34:43 2004

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Page 3

DB 421 NSGLAALITDGPAGKRMVYGRONAGETWHDITGNRSEPVVINSBGWGEFHVNGGSVSIY 480
QY 481 VOR 483
DB 481 VOR 483

RESULT 4
US-09-918-543-30
; Sequence 30, Application US/09918543
; Patent No. US20020155574A1
; GENERAL INFORMATION:
; APPLICANT: No. US20020155574A1:ozymes A/S
; APPLICANT: Thisted, Thomas
; APPLICANT: Kjaerulf, Soren
; APPLICANT: Andersen, Carsten
; APPLICANT: Egelang, Claus-Crone
; TITLE OF INVENTION: Alpha-amylase mutants with altered properties
; FILE REFERENCE: 10062,200-US
; CURRENT APPLICATION NUMBER: US/09/918,543
; CURRENT FILING DATE: 2001-07-31
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 30
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-09-918-543-30

Query Match 100.0%; Score 2666; DB 9; Length 483;
Best Local Similarity 100.0%; Pred. No. 6,9e-239;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANLNGTLMQYFEMWMPNDGQWRRRLONDSAYLAEGITLWIPPAKGTSGADVGAYD 60
DB 1 ANLNGTLMQYFEMWMPNDGQWRRRLONDSAYLAEGITLWIPPAKGTSGADVGAYD 60
QY 61 LVDLGEFHOGKTVRTKYGKELQSAIKSLHSRDINVGDVYINHGADATEDVTAVEV 120
DB 61 LVDLGEFHOGKTVRTKYGKELQSAIKSLHSRDINVGDVYINHGADATEDVTAVEV 120
QY 121 DPADRNKRVISGEHLIKAMTHFHPGSGSTYSDPKMWHYFDGTDWDESKLNRIYKFOGK 180
DB 121 DPADRNKRVISGEHLIKAMTHFHPGSGSTYSDPKMWHYFDGTDWDESKLNRIYKFOGK 180
QY 181 AMDWESNENGNVDYLMYADIDYDHPDVAEIKRWGTWYANLQDGFRLDAVKIKFSF 240
DB 181 AMDWESNENGNVDYLMYADIDYDHPDVAEIKRWGTWYANLQDGFRLDAVKIKFSF 240
QY 241 LRDVNVHVRKTKGEMFTVAEYQNDLGALENYLNKTNFNHSVFDVPLHYQFHAASGOGG 300
DB 241 LRDVNVHVRKTKGEMFTVAEYQNDLGALENYLNKTNFNHSVFDVPLHYQFHAASGOGG 300
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DB 301 GYDMRKLNGTVVSKPLKSVTFVDNHDTPQGSLSTVQTWKPLAYAFILTRBSGYPO 360
QY 361 VFYGDWYGTGDSQREIPLAKHIEPIILKARKQYAGACHDYFDHDI VGMTEGDSVA 420
DB 361 VFYGDWYGTGDSQREIPLAKHIEPIILKARKQYAGACHDYFDHDI VGMTEGDSVA 420
QY 421 NSGLAALITDGPAGKRMVYGRONAGETWHDITGNRSEPVVINSBGWGEFHVNGGSVSIY 480
DB 421 NSGLAALITDGPAGKRMVYGRONAGETWHDITGNRSEPVVINSBGWGEFHVNGGSVSIY 480
QY 481 VOR 483
DB 481 VOR 483

RESULT 5
US-09-925-576C-8
; Sequence 8, Application US/09925576C

; Publication No. US20030129718A1
; GENERAL INFORMATION:
; APPLICANT: Andersen, Carsten
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Nielsen, Bjarne Ronfeldt
; TITLE OF INVENTION: Amylase Variants
; FILE REFERENCE: 10004,204-US
; CURRENT APPLICATION NUMBER: US/09/925,576C
; CURRENT FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 8
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-09-925-576C-8

Query Match 100.0%; Score 2666; DB 10; Length 483;
Best Local Similarity 100.0%; Pred. No. 6,9e-239;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANLNGTLMQYFEMWMPNDGQWRRRLONDSAYLAEGITLWIPPAKGTSGADVGAYD 60
DB 1 ANLNGTLMQYFEMWMPNDGQWRRRLONDSAYLAEGITLWIPPAKGTSGADVGAYD 60
QY 61 LVDLGEFHOGKTVRTKYGKELQSAIKSLHSRDINVGDVYINHGADATEDVTAVEV 120
DB 61 LVDLGEFHOGKTVRTKYGKELQSAIKSLHSRDINVGDVYINHGADATEDVTAVEV 120
QY 121 DPADRNKRVISGEHLIKAMTHFHPGSGSTYSDPKMWHYFDGTDWDESKLNRIYKFOGK 180
DB 121 DPADRNKRVISGEHLIKAMTHFHPGSGSTYSDPKMWHYFDGTDWDESKLNRIYKFOGK 180
QY 181 AMDWESNENGNVDYLMYADIDYDHPDVAEIKRWGTWYANLQDGFRLDAVKIKFSF 240
DB 181 AMDWESNENGNVDYLMYADIDYDHPDVAEIKRWGTWYANLQDGFRLDAVKIKFSF 240
QY 241 LRDVNVHVRKTKGEMFTVAEYQNDLGALENYLNKTNFNHSVFDVPLHYQFHAASGOGG 300
DB 241 LRDVNVHVRKTKGEMFTVAEYQNDLGALENYLNKTNFNHSVFDVPLHYQFHAASGOGG 300
QY 301 GYDMRKLNGTVVSKPLKSVTFVDNHDTPQGSLSTVQTWKPLAYAFILTRBSGYPO 360
DB 301 GYDMRKLNGTVVSKPLKSVTFVDNHDTPQGSLSTVQTWKPLAYAFILTRBSGYPO 360
QY 361 VFYGDWYGTGDSQREIPLAKHIEPIILKARKQYAGACHDYFDHDI VGMTEGDSVA 420
DB 361 VFYGDWYGTGDSQREIPLAKHIEPIILKARKQYAGACHDYFDHDI VGMTEGDSVA 420
QY 421 NSGLAALITDGPAGKRMVYGRONAGETWHDITGNRSEPVVINSBGWGEFHVNGGSVSIY 480
DB 421 NSGLAALITDGPAGKRMVYGRONAGETWHDITGNRSEPVVINSBGWGEFHVNGGSVSIY 480
QY 481 VOR 483
DB 481 VOR 483

RESULT 6
US-10-665-667-4
; Sequence 4, Application US/10665667
; Publication No. US20040038368A1
; GENERAL INFORMATION:
; APPLICANT: Borchert, Torben V.
; APPLICANT: Svendsen, Allan
; APPLICANT: Andersen, Carsten
; APPLICANT: Nielsen, Bjarne
; APPLICANT: Nielsen, Torben L.
; APPLICANT: Kjaerulf, Soren
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 5368,200-US
; CURRENT APPLICATION NUMBER: US/10/665,667
; CURRENT FILING DATE: 2003-09-19

PRIOR APPLICATION NUMBER: US/09/769,864
PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: 09/183,412
PRIOR FILING DATE: 1998-10-30
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 483
TYPE: PRT
ORGANISM: Bacillus licheniformis
US-10-665-667-4

Query Match 100.0%; Score 2666; DB 12; Length 483;
Best Local Similarity 100.0%; Pred. No. 6.9e-239; Indels 0; Gaps 0;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANLNGTLMQYFEMWPNNDGQHRRLQNDASAYLAHEGITAAMIIPRAYKGTSGADVGAYD 60
DB 1 ANLNGTLMQYFEMWPNNDGQHRRLQNDASAYLAHEGITAAMIIPRAYKGTSGADVGAYD 60
QY 61 LYDLGEFHQKGTVRITKYGKGLQSAIKSLHSRDINVGDVYINHKGGADATEDVTAIEV 120
DB 61 LYDLGEFHQKGTVRITKYGKGLQSAIKSLHSRDINVGDVYINHKGGADATEDVTAIEV 120
QY 121 DPADRRVVISGSHLIKAWTHFHPGRGSTYSDFKMHWYHFDGTDWDESRKLNRIYKFGOK 180
DB 121 DPADRRVVISGSHLIKAWTHFHPGRGSTYSDFKMHWYHFDGTDWDESRKLNRIYKFGOK 180
QY 181 AMDWEVSNENGVNDYLMVADIDYDHPDVAALIKRWGTYANELQDGFRLDAVKIKTSF 240
DB 181 AMDWEVSNENGVNDYLMVADIDYDHPDVAALIKRWGTYANELQDGFRLDAVKIKTSF 240
QY 241 LEDWNVHVEKTKGEMFTVAEYQNDLGALENYLKTNNHNSVFPVPLHYQFHAASIQG 300
DB 241 LEDWNVHVEKTKGEMFTVAEYQNDLGALENYLKTNNHNSVFPVPLHYQFHAASIQG 300
QY 301 GYDMRKILNGTVSSKPLKSVTFVNDHDTQPGQSLESTVQTFKPLAVAFILITRESSGYPQ 360
DB 301 GYDMRKILNGTVSSKPLKSVTFVNDHDTQPGQSLESTVQTFKPLAVAFILITRESSGYPQ 360
QY 361 VFYGMWYGTGDSOREIPALKKIEPIILAKROYAAGAHQDFDHDIVGMRBGDSVA 420
DB 361 VFYGMWYGTGDSOREIPALKKIEPIILAKROYAAGAHQDFDHDIVGMRBGDSVA 420
QY 421 NSGLAALITDGPAGAKMYVGRONAGETWHDITGNRSEPVVINSSEGWGFHVNGSVSIY 480
DB 421 NSGLAALITDGPAGAKMYVGRONAGETWHDITGNRSEPVVINSSEGWGFHVNGSVSIY 480
QY 481 VQR 483
DB 481 VQR 483

RESULT 7
US-10-644-187-2

; Sequence 2, Application US/10644187
; Publication No. US20040048351A1
; GENERAL INFORMATION:

APPLICANT: Svendsen, Allan
APPLICANT: Bisgard-Frantzen, Henrik
TITLE OF INVENTION: Alpha-Amylase Mutants
FILE REFERENCE: 4796,204-US
CURRENT APPLICATION NUMBER: US/10/644,187
CURRENT FILING DATE: 2003-08-20
PRIOR APPLICATION NUMBER: 09/182,859
PRIOR FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: 0515/96
PRIOR FILING DATE: 1996-04-30
PRIOR APPLICATION NUMBER: 0712/96
PRIOR FILING DATE: 1996-06-28
PRIOR APPLICATION NUMBER: 0775/96
PRIOR FILING DATE: 1996-07-11

PRIOR APPLICATION NUMBER: 1263/96
PRIOR FILING DATE: 1996-11-08
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 483
TYPE: PRT
ORGANISM: Bacillus licheniformis
US-10-644-187-2

Query Match 100.0%; Score 2666; DB 12; Length 483;
Best Local Similarity 100.0%; Pred. No. 6.9e-239; Indels 0; Gaps 0;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANLNGTLMQYFEMWPNNDGQHRRLQNDASAYLAHEGITAAMIIPRAYKGTSGADVGAYD 60
DB 1 ANLNGTLMQYFEMWPNNDGQHRRLQNDASAYLAHEGITAAMIIPRAYKGTSGADVGAYD 60
QY 61 LYDLGEFHQKGTVRITKYGKGLQSAIKSLHSRDINVGDVYINHKGGADATEDVTAIEV 120
DB 61 LYDLGEFHQKGTVRITKYGKGLQSAIKSLHSRDINVGDVYINHKGGADATEDVTAIEV 120
QY 121 DPADRRVVISGSHLIKAWTHFHPGRGSTYSDFKMHWYHFDGTDWDESRKLNRIYKFGOK 180
DB 121 DPADRRVVISGSHLIKAWTHFHPGRGSTYSDFKMHWYHFDGTDWDESRKLNRIYKFGOK 180
QY 181 AMDWEVSNENGVNDYLMVADIDYDHPDVAALIKRWGTYANELQDGFRLDAVKIKTSF 240
DB 181 AMDWEVSNENGVNDYLMVADIDYDHPDVAALIKRWGTYANELQDGFRLDAVKIKTSF 240
QY 241 LRWNVHVEKTKGEMFTVAEYQNDLGALENYLKTNNHNSVFPVPLHYQFHAASIQG 300
DB 241 LRWNVHVEKTKGEMFTVAEYQNDLGALENYLKTNNHNSVFPVPLHYQFHAASIQG 300
QY 301 GYDMRKILNGTVSSKPLKSVTFVNDHDTQPGQSLESTVQTFKPLAVAFILITRESSGYPQ 360
DB 301 GYDMRKILNGTVSSKPLKSVTFVNDHDTQPGQSLESTVQTFKPLAVAFILITRESSGYPQ 360
QY 361 VFYGMWYGTGDSOREIPALKKIEPIILAKROYAAGAHQDFDHDIVGMRBGDSVA 420
DB 361 VFYGMWYGTGDSOREIPALKKIEPIILAKROYAAGAHQDFDHDIVGMRBGDSVA 420
QY 421 NSGLAALITDGPAGAKMYVGRONAGETWHDITGNRSEPVVINSSEGWGFHVNGSVSIY 480
DB 421 NSGLAALITDGPAGAKMYVGRONAGETWHDITGNRSEPVVINSSEGWGFHVNGSVSIY 480
QY 481 VQR 483
DB 481 VQR 483

RESULT 8
US-10-327-837-4

; Sequence 4, Application US/10327837
; Publication No. US20030211958A1
; GENERAL INFORMATION:

APPLICANT: Svendsen, Allan
APPLICANT: Bisgard-Frantzen Henrik
APPLICANT: Outtrup, Helle
APPLICANT: Nielsen, Bjarne Ronfeldt
APPLICANT: Nielsen, Vibeke Skovgaard
TITLE OF INVENTION: Novel -Amylase And -Amylase Mutants
FILE REFERENCE: 5276,400-US
CURRENT APPLICATION NUMBER: US/10/327,837
CURRENT FILING DATE: 2002-12-23
PRIOR APPLICATION NUMBER: US/09/290,734
PRIOR FILING DATE: 1999-04-13
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 483

```

; TYPE: PRT
; ORGANISM: B. licheniformis
US-10-327-837-4

Query Match      100.0%; Score 2666; DB 12; Length 483;
Best Local Similarity 100.0%; Pred. No. 6.9e-239;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANNGTLMQYFEWYMPNDGQWRLQNDASVLAHEGTTAWIPPAKYGTSQADVYGAYD 60
DB 1 ANNGTLMQYFEWYMPNDGQWRLQNDASVLAHEGTTAWIPPAKYGTSQADVYGAYD 60
QY 61 LYLGEFHOKGTATKTKGTGKELQSAIKSLHSRDINVGDVVINKGADATEDVTAVEV 120
DB 61 LYLGEFHOKGTATKTKGTGKELQSAIKSLHSRDINVGDVVINKGADATEDVTAVEV 120
QY 121 DPADNRNVISGEHLIKAMTHFHPGSGTYSDFKMWYHFDGTDWDSRKLNRITYEQGK 180
DB 121 DPADNRNVISGEHLIKAMTHFHPGSGTYSDFKMWYHFDGTDWDSRKLNRITYEQGK 180
QY 181 AMDWEVSNNENGVYLMYADIDYDHPVAAEIKRWGTWYANELQDGFRLDAYKHIFSF 240
DB 181 AMDWEVSNNENGVYLMYADIDYDHPVAAEIKRWGTWYANELQDGFRLDAYKHIFSF 240
QY 241 LRDWVNHVREKTKGEMFTVAEYQNDLGALENYLNKTNFHSVFDVPLHYQFHAASTQG 300
DB 241 LRDWVNHVREKTKGEMFTVAEYQNDLGALENYLNKTNFHSVFDVPLHYQFHAASTQG 300
QY 301 GYDWRKLLNGTVVSKHPLKSVTFVNDHNDTPGQSLSTVQTWFKPLAYAFILTRREGSYQ 360
DB 301 GYDWRKLLNGTVVSKHPLKSVTFVNDHNDTPGQSLSTVQTWFKPLAYAFILTRREGSYQ 360
QY 361 VFYGDMYGTGKDSQREIPALKHKIEPILKARKQYAGACHDYPDHDIVGWTREGDSVA 420
DB 361 VFYGDMYGTGKDSQREIPALKHKIEPILKARKQYAGACHDYPDHDIVGWTREGDSVA 420
QY 421 NSGLAALITDPPGAKRMVYGRQNAGETWHDITGNRSEPVYINSEGGEFHVGGSVSIV 480
DB 421 NSGLAALITDPPGAKRMVYGRQNAGETWHDITGNRSEPVYINSEGGEFHVGGSVSIV 480
QY 481 VQR 483
DB 481 VQR 483

RESULT 9
US-10-146-327-4
; Sequence 4, Application US/10146327
; Publication No. US20030044954A1
; GENERAL INFORMATION:
; APPLICANT: Andersen, Carsten
; APPLICANT: Jorgensen, Christel T.
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Svendsen, Allan
; APPLICANT: Kjaerulff, Soren
; TITLE OF INVENTION: Alpha-Amylase Variants
; FILE REFERENCE: 5886.200-US
; CURRENT APPLICATION NUMBER: US/10/146,327
; CURRENT FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: US/09/537,168
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: PA 1999 00437
; PRIOR FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: 60/127,427
; PRIOR FILING DATE: 1999-04-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-10-146-327-4

```

```

Query Match      100.0%; Score 2666; DB 14; Length 483;
Best Local Similarity 100.0%; Pred. No. 6.9e-239;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANNGTLMQYFEWYMPNDGQWRLQNDASVLAHEGTTAWIPPAKYGTSQADVYGAYD 60
DB 1 ANNGTLMQYFEWYMPNDGQWRLQNDASVLAHEGTTAWIPPAKYGTSQADVYGAYD 60
QY 61 LYLGEFHOKGTATKTKGTGKELQSAIKSLHSRDINVGDVVINKGADATEDVTAVEV 120
DB 61 LYLGEFHOKGTATKTKGTGKELQSAIKSLHSRDINVGDVVINKGADATEDVTAVEV 120
QY 121 DPADNRNVISGEHLIKAMTHFHPGSGTYSDFKMWYHFDGTDWDSRKLNRITYEQGK 180
DB 121 DPADNRNVISGEHLIKAMTHFHPGSGTYSDFKMWYHFDGTDWDSRKLNRITYEQGK 180
QY 181 AMDWEVSNNENGVYLMYADIDYDHPVAAEIKRWGTWYANELQDGFRLDAYKHIFSF 240
DB 181 AMDWEVSNNENGVYLMYADIDYDHPVAAEIKRWGTWYANELQDGFRLDAYKHIFSF 240
QY 241 LRDWVNHVREKTKGEMFTVAEYQNDLGALENYLNKTNFHSVFDVPLHYQFHAASTQG 300
DB 241 LRDWVNHVREKTKGEMFTVAEYQNDLGALENYLNKTNFHSVFDVPLHYQFHAASTQG 300
QY 301 GYDWRKLLNGTVVSKHPLKSVTFVNDHNDTPGQSLSTVQTWFKPLAYAFILTRREGSYQ 360
DB 301 GYDWRKLLNGTVVSKHPLKSVTFVNDHNDTPGQSLSTVQTWFKPLAYAFILTRREGSYQ 360
QY 361 VFYGDMYGTGKDSQREIPALKHKIEPILKARKQYAGACHDYPDHDIVGWTREGDSVA 420
DB 361 VFYGDMYGTGKDSQREIPALKHKIEPILKARKQYAGACHDYPDHDIVGWTREGDSVA 420
QY 421 NSGLAALITDPPGAKRMVYGRQNAGETWHDITGNRSEPVYINSEGGEFHVGGSVSIV 480
DB 421 NSGLAALITDPPGAKRMVYGRQNAGETWHDITGNRSEPVYINSEGGEFHVGGSVSIV 480
QY 481 VQR 483
DB 481 VQR 483

RESULT 10
US-10-186-042-2
; Sequence 2, Application US/10186042
; Publication No. US20030171236A1
; GENERAL INFORMATION:
; APPLICANT: Borchert, Allan
; APPLICANT: Svendsen, Allan
; APPLICANT: Bisgaard-Frantzen, Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 4796.204-US
; CURRENT APPLICATION NUMBER: US/10/186,042
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US/09/672,459
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 09/182,859
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: 0515/96
; PRIOR FILING DATE: 1996-04-30
; PRIOR APPLICATION NUMBER: 0712/96
; PRIOR FILING DATE: 1996-06-28
; PRIOR APPLICATION NUMBER: 0775/96
; PRIOR FILING DATE: 1996-07-11
; PRIOR APPLICATION NUMBER: 1263/96
; PRIOR FILING DATE: 1996-11-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-10-186-042-2

```

Query Match 100.0%; Score 2666; DB 14; Length 483;
 Best Local Similarity 100.0%; Pred. No. 6.9e-239;
 Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANLNGTLMQYFEWYMPNDGQHRRLQNDASAYLAHGTITAVWIPPAKGTSGADVGAYD 60
 DB 1 ANLNGTLMQYFEWYMPNDGQHRRLQNDASAYLAHGTITAVWIPPAKGTSGADVGAYD 60
 QY 61 LVDLGEFHOKGTVRTKTYGTGKELQSAIKSLHSRDLINVGDVYINHGADATEDVTAVEV 120
 DB 61 LVDLGEFHOKGTVRTKTYGTGKELQSAIKSLHSRDLINVGDVYINHGADATEDVTAVEV 120
 QY 121 DPADRNRVLSGHEHLIKAWTHFHPFGSGTYSDFPKMWHYFDDTWDDESKLNRIYKFGQK 180
 DB 121 DPADRNRVLSGHEHLIKAWTHFHPFGSGTYSDFPKMWHYFDDTWDDESKLNRIYKFGQK 180
 QY 121 DPADRNRVLSGHEHLIKAWTHFHPFGSGTYSDFPKMWHYFDDTWDDESKLNRIYKFGQK 180
 DB 121 DPADRNRVLSGHEHLIKAWTHFHPFGSGTYSDFPKMWHYFDDTWDDESKLNRIYKFGQK 180
 QY 181 AMDMEVSNENGVNDYLMYADIDYDHPDVAEIKRWGTWYANELQDGFRLDAVKIKRSF 240
 DB 181 AMDMEVSNENGVNDYLMYADIDYDHPDVAEIKRWGTWYANELQDGFRLDAVKIKRSF 240
 QY 241 LRDMVNHVREKTKENFTVAEYQNDLGLNENYLNKTNFNHVSFVPLHYQFHAASGCG 300
 DB 241 LRDMVNHVREKTKENFTVAEYQNDLGLNENYLNKTNFNHVSFVPLHYQFHAASGCG 300
 QY 301 GYDMRKLLNGTVVSKAPLSVTFVDNHDTPQGSLESTVQTFKPLAYAFILTRBSGYPO 360
 DB 301 GYDMRKLLNGTVVSKAPLSVTFVDNHDTPQGSLESTVQTFKPLAYAFILTRBSGYPO 360
 QY 361 VFYGDWYGTGDSQREIPALKKIEPILKARKQYAGAOHDYFDHHDIVGWTREBSSVA 420
 DB 361 VFYGDWYGTGDSQREIPALKKIEPILKARKQYAGAOHDYFDHHDIVGWTREBSSVA 420
 QY 421 NSGLAALLTDGPGAGARMYVGRONAGETWHDITGNRSEBVVINSBGMGEFHNNGSVSIY 480
 DB 421 NSGLAALLTDGPGAGARMYVGRONAGETWHDITGNRSEBVVINSBGMGEFHNNGSVSIY 480
 QY 481 VOR 483
 DB 481 VOR 483

RESULT 11
 US-10-184-771-2
 ; Sequence 2, Application US/10184771
 ; Publication No. US20030170769A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Svendsen, Allan
 ; APPLICANT: Bisgaard-Frantzen, Henrik
 ; APPLICANT: Borchert, Torben Vedel
 ; TITLE OF INVENTION: Alpha-Amylase Mutants
 ; FILE REFERENCE: 0776/1P216-US2
 ; CURRENT APPLICATION NUMBER: US/10/184,771
 ; PRIOR FILING DATE: 2002-06-28
 ; PRIOR APPLICATION NUMBER: US/09/636,252
 ; PRIOR FILING DATE: 2000-08-10
 ; PRIOR APPLICATION NUMBER: 08/683,838
 ; PRIOR FILING DATE: 1996-07-18
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 2
 ; LENGTH: 512
 ; TYPE: PRT
 ; ORGANISM: B. licheniformis
 ; US-10-184-771-2

Query Match 100.0%; Score 2666; DB 14; Length 512;
 Best Local Similarity 100.0%; Pred. No. 7.5e-239;
 Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANLNGTLMQYFEWYMPNDGQHRRLQNDASAYLAHGTITAVWIPPAKGTSGADVGAYD 60
 DB 30 ANLNGTLMQYFEWYMPNDGQHRRLQNDASAYLAHGTITAVWIPPAKGTSGADVGAYD 89

QY 61 LVDLGEFHOKGTVRTKTYGTGKELQSAIKSLHSRDLINVGDVYINHGADATEDVTAVEV 120
 DB 90 LVDLGEFHOKGTVRTKTYGTGKELQSAIKSLHSRDLINVGDVYINHGADATEDVTAVEV 149
 QY 121 DPADRNRVLSGHEHLIKAWTHFHPFGSGTYSDFPKMWHYFDDTWDDESKLNRIYKFGQK 180
 DB 150 DPADRNRVLSGHEHLIKAWTHFHPFGSGTYSDFPKMWHYFDDTWDDESKLNRIYKFGQK 209
 QY 181 AMDMEVSNENGVNDYLMYADIDYDHPDVAEIKRWGTWYANELQDGFRLDAVKIKRSF 240
 DB 210 AMDMEVSNENGVNDYLMYADIDYDHPDVAEIKRWGTWYANELQDGFRLDAVKIKRSF 269
 QY 241 LRDMVNHVREKTKENFTVAEYQNDLGLNENYLNKTNFNHVSFVPLHYQFHAASGCG 300
 DB 270 LRDMVNHVREKTKENFTVAEYQNDLGLNENYLNKTNFNHVSFVPLHYQFHAASGCG 329
 QY 301 GYDMRKLLNGTVVSKAPLSVTFVDNHDTPQGSLESTVQTFKPLAYAFILTRBSGYPO 360
 DB 330 GYDMRKLLNGTVVSKAPLSVTFVDNHDTPQGSLESTVQTFKPLAYAFILTRBSGYPO 389
 QY 361 VFYGDWYGTGDSQREIPALKKIEPILKARKQYAGAOHDYFDHHDIVGWTREBSSVA 420
 DB 390 VFYGDWYGTGDSQREIPALKKIEPILKARKQYAGAOHDYFDHHDIVGWTREBSSVA 449
 QY 421 NSGLAALLTDGPGAGARMYVGRONAGETWHDITGNRSEBVVINSBGMGEFHNNGSVSIY 480
 DB 450 NSGLAALLTDGPGAGARMYVGRONAGETWHDITGNRSEBVVINSBGMGEFHNNGSVSIY 509
 QY 481 VOR 483
 DB 510 VOR 512

RESULT 12
 US-10-199-922-2
 ; Sequence 2, Application US/10199922
 ; Publication No. US20030022346A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gist-brocades B.V.
 ; TITLE OF INVENTION: Alpha-amylase mutants
 ; NUMBER OF SEQUENCES: 2
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Gist-brocades B.V.
 ; STREET: Wateringseweg 1
 ; CITY: Delft
 ; COUNTRY: The Netherlands
 ; ZIP: 2611 XT
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/199,922
 ; FILING DATE: 18-Jul-2002
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 512 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 ; US-10-199-922-2

Query Match 99.9%; Score 2663; DB 14; Length 512;
 Best Local Similarity 99.8%; Pred. No. 1.4e-238;
 Matches 482; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANLNGTLMQYFEWYMPNDGQHRRLQNDASAYLAHGTITAVWIPPAKGTSGADVGAYD 60
 DB 30 ANLNGTLMQYFEWYMPNDGQHRRLQNDASAYLAHGTITAVWIPPAKGTSGADVGAYD 89
 QY 61 LVDLGEFHOKGTVRTKTYGTGKELQSAIKSLHSRDLINVGDVYINHGADATEDVTAVEV 120

Db 90 LYLDFEHPQKGVTRTKYCTKGBELQSAIKSLHSRDINVTGDDVINHKGADATEDVTAVEV 149

Qy 121 DPADRRNRVISEGHEILIKAMTHFHPGRGSTYSDFKWMWYHPDGTWDBSRKLNRIYKFGK 180

Db 150 DPADRRNRVISEGHEILIKAMTHFHPGRGSTYSDFKWMWYHPDGTWDBSRKLNRIYKFGK 209

Qy 181 AMWEVSNENGNDYDLYMTADIDYDEHDVAELKRMGTVAANELQDGRDLAVGHITFSF 240

Db 210 AMWEVSNENGNDYDLYMTADIDYDEHDVAELKRMGTVAANELQDGRDLAVGHITFSF 268

Qy 241 LRDMVNVHREKTKEMFTVAEYQNDLGALENYLKTNPNSVFPDVPJHYQFHAASQGG 300

Db 270 LRDMVNVHREKTKEMFTVAEYQNDLGALENYLKTNPNSVFPDVPJHYQFHAASQGG 328

Qy 301 GYDMRKLLNLTVWSKHPKLSVTFVNDHNDPOQGSLESTVQTFKFLAFAFLLTRESGPQC 360

Db 330 GYDMRKLLNLTVWSKHPKLSVTFVNDHNDPOQGSLESTVQTFKFLAFAFLLTRESGPQC 389

Qy 361 VFYGDWYGTYSQDSREIPALPKHIEIILKARQVAYGAQHDYFDHHDIVGMTREGDSSVA 420

Db 390 VFYGDWYGTYSQDSREIPALPKHIEIILKARQVAYGAQHDYFDHHDIVGMTREGDSSVA 449

Qy 421 NSGLAALITGPGGAKRMVYGRNMAETWHDITGNRSEPVVINSGWEEFHNNGSVISY 480

Db 450 NSGLAALITGPGGAKRMVYGRNMAETWHDITGNRSEPVVINSGWEEFHNNGSVISY 509

Qy 481 VOR 483

Db 510 VOR 512

```

RESULT 13
US-10-081-872-114
; Sequence 114, Application US/10081872,
; Publication No. US20030125534A1
; GENERAL INFORMATION:
; APPLICANT: Callen, Walter
; APPLICANT: Richardson, Toby
; APPLICANT: Frey, Gerhard
; APPLICANT: Short, Jay M.
; APPLICANT: Machut, Eric J.
; APPLICANT: Gray, Kevin A.
; APPLICANT: Kervov, Janne S.
; APPLICANT: Slupska, Malgorzata
; TITLE OF INVENTION: ENZYMES HAVING ALPHA AMYLASE ACTIVITY
; TITLE OF INVENTION: AND METHODS OF USE THEREOF
; FILE REFERENCE: 098010-108001
; CURRENT APPLICATION NUMBER: US/10/081, 872
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/270,495
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: US 60/270,496
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: US 60/291,122
; PRIOR FILING DATE: 2001-05-14
; NUMBER OF SEQ ID NOS: 321
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 114
; LENGTH: 512
; TYPE: prt
; ORGANISM: Environmental
US-10-081-872-114

```

Query Match	99.5%	Score	2654	DB	14	Length	512
Best Local Similarity	99.4%	Score	No. 8e-238				
Matches	480	Conservative	2	Mismatches	1	Indels	0
Gaps							0

QY	1	AALNTGIMKYPFMYMNDSCDHPRLONDSBAYLAHGTITVMVPPAKTGSQADVYGAGD	60
Dd	30	AALNTGLIMVFEMINPDQDHMLGNDSDAIALEHGITAVMPAPAKTGSQADVIGAGD	89
QY	61	LYDGEFHOKGVTRIKYTGKBLQSAIKLSHDINDIVNGDVVINHKGADATEDVTAVEV	120

Db 149 LYLDFHFKGKVRFKYGTKELOSAIKSLSRDINYYGCVJINHKGADATEDVAAVEY 149

QY 121 DPADRRNRVISEHLLIKAMTHHFHFGSGSTYDFPKMWHYHFDGTWDSRKLNRILYKFOGK 180

Db 150 DPAADRNRVISEGRRJKAMTHHFHFGSGSTYDFPKMWHYHFDGTWDSRKLNRILYKFOGK 209

QY 181 AMWMEVSNNGVADYLAADIDYDHPDVAABIKRMGTWYANELDLPDRLDAYVHKIFSF 240

Db 210 AMWMEVSNNGVADYLAADIDYDHPDVAABIKRMGTWYANELDLPDRLDAYVHKIFSF 269

QY 241 LRDPMVHVEEKTGKEMFTVAEYQNDLGALENYLNKTNFNHVPDELYHQFAASTOGG 300

Db 270 LRDPMVHVEEKTGKEMFTVAEYQNDLGALENYLNKTNFNHVPDELYHQFAASTOGG 329

QY 301 GYDMRKLLNGTVVSKHPLKSYTFVNDHDTQPOQSIESTVQTFWEPFLAATLITRESGYPO 360

Db 330 GYDMRKLLNGTVVSKHPLAATFVNDHDTQPOQSIESTVQTFWEPFLAATLITRESGYPO 389

QY 361 VFFGDMYTGKGSQRPILPKKIEPIILAKKQVAYGQHDYFPHHPIVMTRESGSVA 420

Db 390 VFFGDMYTGKGSQRPILPKKIEPIILAKKQVAYGQHDYFPHHPIVMTRESGSVA 449

QY 421 NSGLAALLTDGPGAGAMTVGRONAGETWHDITGNRSEFPVINSNGGEFFHNVGGSYIY 480

Db 450 NSGLAALLTDGPGAGAMTVGRONAGETWHDITGNRSEFPVINSNGGEFFHNVGGSYIY 509

QY 481 VQR 483

Db 510 VQR 512

```

1      RESULT 14
2      US-10-105-733-8
3      ; Sequence 8, Application US/10105733
4      ; Publication No. US20030138786A1
5      ;
6      ; GENERAL INFORMATION:
7      ;
8      ; APPLICANT: Callen, Walter
9      ; APPLICANT: Richardson, Toby
10     ; APPLICANT: Frey, Gerhard
11     ; APPLICANT: Miller, Carl
12     ; APPLICANT: Kazaoka, Martin
13     ; APPLICANT: Short, Jay
14     ; APPLICANT: Mathur, Eric
15     ; TITLE OF INVENTION: ENZYMES HAVING ALPHA AMYLASE ACTIVITY
16     ; TITLE OF INVENTION: AND METHODS OF USE THEREOF
17     ;
18     ; FILE REFERENCE: 09010-107002
19     ; CURRENT APPLICATION NUMBER: US/10/105,733
20     ; CURRENT FILING DATE: 2002-03-22
21     ; PRIOR APPLICATION NUMBER: 10/081,739
22     ; PRIOR FILING DATE: 2002-02-21
23     ; PRIOR APPLICATION NUMBER: 60/270,495
24     ; PRIOR FILING DATE: 2001-02-21
25     ; PRIOR APPLICATION NUMBER: 60/270,496
26     ; PRIOR FILING DATE: 2001-02-21
27     ; PRIOR APPLICATION NUMBER: 60/291,122
28     ; PRIOR FILING DATE: 2001-05-14
29     ; NUMBER OF SEQ ID NOS: 69
30     ; SOFTWARE: FASTSEQ for Windows Version 4.0
31     ; SEQ ID NO 8
32     ; LENGTH: 512
33     ;
34     ; TYPE: PRT
35     ; ORGANISM: Environmental
36     ;
37     ; US-10-105-733-8

```

```

Query Match 99.5% Score 2654; DB 14; Length 512;
Best Local Similarity 99.4% Pred. No. 9.8e-236;
Matches 480; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 ANNTNTLWGYEMWPNNGCHMRRLONDSATLAHGHTAVNIIPRYKSTQADYGYKAYD 60
DB 30 ANNTNTLWGYEMWPNNGCHMRRLONDSATLAHGHTAVNIIPRYKSTQADYGYKAYD 89

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QY 61 LYDGEFHOKGTVRTKYGTKGELQSAIKSLHSRDINYYGDDVINHKGGADATEDVTAVEV 120
DB 90 LYDGEFHOKGTVRTKYGTKGELQSAIKSLHSRDINYYGDDVINHKGGADATEDVTAVEV 149
QY 121 DPADNRVYISGEHLIKAWTHFHPFGSGTYSDFKWHYHFDGTDWDSRKLNRIFYEQGK 180
DB 150 DPADNRVYISGEHLIKAWTHFHPFGSGTYSDFKWHYHFDGTDWDSRKLNRIFYEQGK 209
QY 181 AMDWEVSNENGNYYDYLMAADIDYDHPDVAAEIKKMGTYANELQDGFRLDAVGHIFSF 240
DB 210 AMDWEVSNENGNYYDYLMAADIDYDHPDVAAEIKKMGTYANELQDGFRLDAVGHIFSF 269
QY 241 LRDWVNHVREKTKGEMFTVAEYMONDGLALENYLNKTNFNSVDFVPLHYQFHAASIQGG 300
DB 270 LRDWVNHVREKTKGEMFTVAEYMONDGLALENYLNKTNFNSVDFVPLHYQFHAASIQGG 329
QY 301 GYDMRKLNGTVVSKHPLKSVTFVNDHDTOPGQSLESTVQTFKPLAYAFILITRESGYPQ 360
DB 330 GYDMRKLNGTVVSKHPLKAVTFVNDHDTOPGQSLESTVQTFKPLAYAFILITRESGYPQ 389
QY 361 VFYGDWYGTGKDSQREIPALKHKLEPILKARKQYAYGAQHDYFDHDI VGMTREGDSSVA 420
DB 390 VFYGDWYGTGKDSQREIPALKHKLEPILKARKQYAYGAQHDYFDHDI VGMTREGDSSVA 449
QY 421 NSGLAALITDGPQAKRMVYGRQNGETWHDITGNRSEPVYINSEGWGEFHVNGGSVSIY 480
DB 450 NSGLAALITDGPQAKRMVYGRQNGETWHDITGNRSEPVYINSEGWGEFHVNGGSVSIY 509
QY 481 VQR 483
DB 510 VQR 512

```

RESULT 15

```

US-10-081-739A-8
/ Sequence 8, Application US/10081739A
/ Publication No. US20030170634A1
/ GENERAL INFORMATION:
/ APPLICANT: Callen, Walter
/ APPLICANT: Richardson, Toby
/ APPLICANT: Frey, Gerhard
/ APPLICANT: Miller, Carl
/ APPLICANT: Kazaoka, Martin
/ APPLICANT: Short, Jay
/ APPLICANT: Mathur, Eric
/ TITLE OF INVENTION: ENZYMES HAVING ALPHA AMYLASE ACTIVITY
/ FILE REFERENCE: 09010-107001
/ CURRENT APPLICATION NUMBER: US/10/081,739A
/ CURRENT FILING DATE: 2002-02-21
/ PRIOR APPLICATION NUMBER: 60/270,495
/ PRIOR FILING DATE: 2001-02-21
/ PRIOR APPLICATION NUMBER: 60/270,496
/ PRIOR FILING DATE: 2001-02-21
/ PRIOR FILING DATE: 2001-05-14
/ NUMBER OF SEQ ID NOS: 69
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 8
/ LENGTH: 512
/ TYPE: PRT
/ ORGANISM: Unknown
/ FEATURE:
/ OTHER INFORMATION: Obtained from an environmental sample
US-10-081-739A-8

```

```

Query Match 99.5%; Score 2654; DB 14; Length 512;
Best local similarity 99.4%; Pred. No. 9, 8e-238;
Matches 480; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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```

QY 1 ANINGTLMQYFEWYMNDSQHRRLQNDASNYLAERGITAVWIPRAYKTSQADVGAYD 60
DB 30 ANINGTLMQYFEWYMNDSQHRRLQNDASNYLAERGITAVWIPRAYKTSQADVGAYD 89

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```

QY 61 LYDGEFHOKGTVRTKYGTKGELQSAIKSLHSRDINYYGDDVINHKGGADATEDVTAVEV 120
DB 90 LYDGEFHOKGTVRTKYGTKGELQSAIKSLHSRDINYYGDDVINHKGGADATEDVTAVEV 149
QY 121 DPADNRVYISGEHLIKAWTHFHPFGSGTYSDFKWHYHFDGTDWDSRKLNRIFYEQGK 180
DB 150 DPADNRVYISGEHLIKAWTHFHPFGSGTYSDFKWHYHFDGTDWDSRKLNRIFYEQGK 209
QY 181 AMDWEVSNENGNYYDYLMAADIDYDHPDVAAEIKKMGTYANELQDGFRLDAVGHIFSF 240
DB 210 AMDWEVSNENGNYYDYLMAADIDYDHPDVAAEIKKMGTYANELQDGFRLDAVGHIFSF 269
QY 241 LRDWVNHVREKTKGEMFTVAEYMONDGLALENYLNKTNFNSVDFVPLHYQFHAASIQGG 300
DB 270 LRDWVNHVREKTKGEMFTVAEYMONDGLALENYLNKTNFNSVDFVPLHYQFHAASIQGG 329
QY 301 GYDMRKLNGTVVSKHPLKSVTFVNDHDTOPGQSLESTVQTFKPLAYAFILITRESGYPQ 360
DB 330 GYDMRKLNGTVVSKHPLKAVTFVNDHDTOPGQSLESTVQTFKPLAYAFILITRESGYPQ 389
QY 361 VFYGDWYGTGKDSQREIPALKHKLEPILKARKQYAYGAQHDYFDHDI VGMTREGDSSVA 420
DB 390 VFYGDWYGTGKDSQREIPALKHKLEPILKARKQYAYGAQHDYFDHDI VGMTREGDSSVA 449
QY 421 NSGLAALITDGPQAKRMVYGRQNGETWHDITGNRSEPVYINSEGWGEFHVNGGSVSIY 480
DB 450 NSGLAALITDGPQAKRMVYGRQNGETWHDITGNRSEPVYINSEGWGEFHVNGGSVSIY 509
QY 481 VQR 483
DB 510 VQR 512

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Search completed: May 3, 2004, 20:47:45
Job time : 39.6066 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 3, 2004, 20:44:58 ; Search time 34.365 Seconds
(without alignments)
4438.289 Million cell updates/sec

Title: US-10-644-187-2

Perfect score: 2666
Sequence: 1 AALNTLMQYFEMWMDNDQ.....SEGWGEFHYNGSVSYVQR 483

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SP archaea:*
2: SP bacteria:*
3: SP fungi:*
4: SP human:*
5: SP invertebrate:*
6: SP mammal:*
7: SP_mhc:*
8: SP_organella:*
9: SP_phage:*
10: SP_plant:*
11: SP_rodent:*
12: SP_virus:*
13: SP_vertebrate:*
14: SP_unclassified:*
15: SP_virus:*
16: SP_bacteriap:*
17: SP_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2025	76.0	513	16	Q81AS4 bacillus ce
2	2021	75.8	519	2	Q9RQ78 cytophaga s
3	2021	75.8	533	2	Q9AQ54 bacillus me
4	1991	74.7	513	16	Q81YJ4 bacillus an
5	1909	71.6	516	2	Q82839 bacillus sp
6	1789.5	67.1	549	2	Q31193 bacillus st
7	1784.5	66.9	521	2	P71034 bacillus sp
8	1784.5	66.8	549	2	Q9KXV6 bacillus st
9	1783.5	65.8	613	2	Q59222 bacillus sp
10	1753.5	64.6	501	2	Q93148 bacillus sp
11	1502.5	56.4	507	16	Q87H66 vibrio para
12	1336	50.1	481	16	Q89YPI bacteroides
13	1262	47.3	493	2	Q03657 bacillus ci
14	1244	46.7	492	16	Q8YU21 anabaena sp
15	1233	46.2	484	16	Q97049 streptococc
16	1230.5	46.2	484	2	Q50583 streptococc

17	1228	46.1	484	16	Q8DPC8	Q8DPC8 streptococc
18	1197.5	44.9	488	16	Q8E696	Q8E696 streptococc
19	1186.5	44.9	488	16	Q8E0M2	Q8E0M2 streptococc
20	1185.5	44.8	486	16	Q8DT08	Q8DT08 streptococc
21	1182.5	44.4	485	2	Q53786	Q53786 streptococc
22	1156.5	43.4	486	2	Q68875	Q68875 streptococc
23	1108	41.6	491	16	Q9C959	Q9C959 lactococcus
24	1091.5	40.9	506	16	Q8U916	Q8U916 agrobacteri
25	1053	39.5	484	16	Q8E555	Q8E555 salmonella
26	1048	39.3	485	16	Q8E6L8	Q8E6L8 escherichia
27	1047	39.3	495	16	Q8XBB6	Q8XBB6 escherichia
28	1037	38.9	495	16	Q7UAB0	Q7UAB0 shigella fl
29	1035	38.8	495	16	Q83R40	Q83R40 shigella fl
30	1018.5	38.2	529	3	Q877B1	Q877B1 aspergillus
31	1018.5	38.2	460	1	Q9P9L0	Q9P9L0 pyrococcus
32	1018.5	38.2	460	1	Q08452	Q08452 pyrococcus
33	1018.5	38.2	460	1	Q08452	Q08452 pyrococcus
34	1018.5	38.2	460	1	Q08452	Q08452 pyrococcus
35	1018.5	38.2	460	1	Q08452	Q08452 pyrococcus
36	1018.5	38.2	460	1	Q08452	Q08452 pyrococcus
37	1018.5	38.2	460	1	Q08452	Q08452 pyrococcus
38	1018.5	38.2	460	1	Q08452	Q08452 pyrococcus
39	1018.5	38.2	460	1	Q08452	Q08452 pyrococcus
40	1018.5	38.2	460	1	Q08452	Q08452 pyrococcus
41	1018.5	38.2	460	1	Q08452	Q08452 pyrococcus
42	1018.5	38.2	460	1	Q08452	Q08452 pyrococcus
43	1018.5	38.2	460	1	Q08452	Q08452 pyrococcus
44	1018.5	38.2	460	1	Q08452	Q08452 pyrococcus
45	1018.5	38.2	460	1	Q08452	Q08452 pyrococcus

ALIGNMENTS

RESULT 1	Q81AS4	PRELIMINARY:	PRT:	513 AA.
ID	Q81AS4			
AC	Q81AS4			
DT	01-JUN-2003 (TREMBLrel. 24, Created)			
DI	01-JUN-2003 (TREMBLrel. 24, Last sequence update)			
DE	01-OCT-2003 (TREMBLrel. 25, Last annotation update)			
GN	Glucan 1,4-alpha-maltohexosidase (EC 3.2.1.98)			
OC	Bacillus cereus (strain ATCC 14579 / DSM 31)			
OX	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.			
NCBI_TaxID	226900;			
SEQUENCE FROM N.A.				
MD	MEDLINE:22608415; PubMed:12721630;			
RA	Ivanova N., Sorokin A., Anderson I., Galleron N., Candelson B.,			
RA	Kapitel V., Bhattacharya A., Reznik G., Mikhailova N., Lapidis A.,			
RA	Chu L., Mazur M., Goltzman E., Larsen N., D'Souza M., Malinas T.,			
RA	Greckin Y., Pusch G., Haselkorn R., Forstein K., Ehrlich S.D.,			
RT	Overbeek R., Kyrpides N.,			
RT	"Genome sequence of Bacillus cereus and comparative analysis with			
RT	Bacillus anthracis",			
RT	Nature 423:87-91(2003).			
EMBL	AE017009; AAP10417.1;			
GO	GO:0004556; F:alpha-amyase activity; IEA.			
GO	GO:0016786; F:hydrolase activity; acting on glycosyl bonds; IEA.			
GO	GO:0005975; P:carbohydrate metabolism; IEA.			
DR	InterPro; IPR006047; Alpha_ami1_cat.			
DR	InterPro; IPR006589; Alp_ami1_cat_sub.			
DR	Pfam; PF00128; alpha-amyase; 1.			
DR	SMART; SM00642; Aamy; 1			
KW	Glycosidase; Hydrolase; Complete proteome.			
SEQUENCE	513 AA; 58306 MW; 05C4611CBFF9F6 CRC64;			
Query Match	76.0%; Score 2025; DB 16; Length 513;			
Best Local Similarity	74.5%; Pred. No. 2,4e-140;			
Matches	359; Conservative 49; Mismatches 72; Indels 2; Gaps 1;			
QY	4 NOTLMQYFEMWMDNDQ...RLNDSDAYLAHGHTAVWIPAYKGTSGADVGAYADLYD 63			

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Db 32 NGTLMQFEMVAPRDGQHMNRRLTDVNLAEKQISWIPPAVKGTITNDVGAYDLYD 91
QY 64 LGDFHQKGTAVRTKTKGTGELQSAIKSLHSRDINVDVYINHRGADATEDYTAVEV 123
Db 92 LGDFHQKGTAVRTKTKGTGELQSAIKSLHSRDINVDVYINHRGADATEDYTAVEV 151
QY 124 DRNVIQGEHLIKAWTHFHPGSGTSDPKMTHYFDGTDMPESKLNRIYKFO--CKA 181
Db 152 NRNEVSGSDYEISAMTGFNPGKSDTSNFKMTHYFDGTDMPESKLNRIYKFOCKA 211
QY 182 MDWVSNENGVYDLYMADIDYDHPDVAAEIKKMGWYANLQDGPRLDAVKHIF 241
Db 212 MDWVSNENGVYDLYMADIDYDHPDVAEMKMGWYANLQDGPRLDAVKHIDHBYL 271
QY 242 RDWYVNRREKTKGEMFTVAEYWMQDGLALENYLNKTNFNHSDVDPVLAHYQFHAATQGG 301
Db 272 RDWYVNRREKTKGEMFTVAEYWMQDGLALENYLNKTNFNHSDVDPVLAHYQFHAATQGG 331
QY 302 YDMRKLNGTVYVSKPLKSVTFVNDHDTQPGSLSTVQTPKPLAYAFILTRBSGY 361
Db 332 YDMRKLNGTVYVSKPLKSVTFVNDHDTQPGSLSTVQTPKPLAYAFILTRBSGY 391
QY 362 FYGDMYGTGKDSOREIPALKXIEPIILKAKROYAGQHDYFDHDIQVMTRESGS 421
Db 392 FYGDMYGTGKDSOREIPALKXIEPIILKAKROYAGQHDYFDHDIQVMTRESGS 451
QY 422 SGLAALITDGPCKAKMYVGRONAGETWHDITGNRESEPVYINSEGEHFNHNGS 481
Db 452 SGLAALITDGPCKAKMYVGRONAGETWHDITGNRESEPVYINSEGEHFNHNGS 511
QY 482 QY 483
Db 512 QY 513

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RESULT 2

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QY 09ROT8 PRELIMINARY; PRT; 519 AA.
AC 09ROT8;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Raw starch digesting amylase precursor.
OS Cytophaga sp.
OC Bacteria; Bacteroidetes; Sphingobacteria; Sphingobacteriales;
OC Flexibacteraceae; Cytophaga.
RN NCBI_TaxID=29535;
RP SEQUENCE FROM N.A.
RA Jeung C.L., Chen L.S., Chen M.Y.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF067653; AF060567.1; -
DR HSSP; P06278; IYTS.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0005975; F:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amyl_cat.
DR InterPro; IPR006589; Alp_amyl_cat_sub.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; alpha-amylase; 1.
DR PRINTS; PRC0110; alpha-amylase.
DR SMART; SMO0642; Amy; 1.
KW Signal.
FT SIGNAL.
FT CHAIN 58 519 POTENTIAL.
SEQUENCE 519 AA; 58337 MW; 36888ADP98B163 CRC64;

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Query Match 75.8%; Score 2021; DB 2; Length 519;
 Best Local Similarity 73.4%; Pred. No. 4,9e-140;
 Matches 356; Conservative 60; Mismatches 67; Indels 2; Gaps 1;

1 ANLNGTLMQFEMVAPRDGQHMNRRLQDSDAYLAHSGITAVMTIPPAVKGTSDADVGYAYD 60

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Db 35 AATNGTLMQFEMVAPRDGQHMNRRLQDSDAYLAHSGITAVMTIPPAVKGTSDADVGYAYD 94
QY 61 LYDGEFHQKGTAVRTKTKGTGELQSAIKSLHSRDINVDVYINHRGADATEDYTAVEV 120
Db 95 LYDGEFHQKGTAVRTKTKGTGELQSAIKSLHSRDINVDVYINHRGADATEDYTAVEV 154
QY 121 DPADNRVTSGEHLIKAWTHFHPGSGTSDPKMTHYFDGTDMPESKLNRIYKFO-- 178
Db 155 NPSNRNQTSESEITQMTGENPFGRTTSNFKMTHYFDGTDMPESKLNRIYKFOCKA 214
QY 179 GRAMDVSNENGVYDLYMADIDYDHPDVAAEIKKMGWYANLQDGPRLDAVKHIF 238
Db 215 GRAMDVSNENGVYDLYMADIDYDHPDVAEMKMGWYANLQDGPRLDAVKHIDHBYL 274
QY 239 SFLRDMVNRREKTKGEMFTVAEYWMQDGLALENYLNKTNFNHSDVDPVLAHYQFHAATQGG 298
Db 275 SFLRDMVNRREKTKGEMFTVAEYWMQDGLALENYLNKTNFNHSDVDPVLAHYQFHAATQGG 334
QY 299 GGYDMRKLNGTVYVSKPLKSVTFVNDHDTQPGSLSTVQTPKPLAYAFILTRBSGY 358
Db 335 GGYDMRKLNGTVYVSKPLKSVTFVNDHDTQPGSLSTVQTPKPLAYAFILTRBSGY 394
QY 359 PCVIFYGDMYGTGKDSOREIPALKXIEPIILKAKROYAGQHDYFDHDIQVMTRESGS 418
Db 395 PCVIFYGDMYGTGKDSOREIPALKXIEPIILKAKROYAGQHDYFDHDIQVMTRESGS 454
QY 419 VANSGLAALITDGPCKAKMYVGRONAGETWHDITGNRESEPVYINSEGEHFNHNGS 478
Db 455 KKSGLAALITDGPCKAKMYVGRONAGETWHDITGNRESEPVYINSEGEHFNHNGS 514
QY 479 IYVQR 483
Db 515 VVWQ 519

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RESULT 3

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QY 09A054 PRELIMINARY; PRT; 533 AA.
AC 09A054;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Alpha-amylase.
OS Bacillus megaterium.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
RN NCBI_TaxID=1404;
RP SEQUENCE FROM N.A.
RA Kim Y.B., Lee B.N., Son H.C., Lee J.W., Kim B.J., Kim Y.-W.,
RA Park K.-H.;
RL "Cloning of maltopentase-producing amylase from Bacillus megaterium
RT KSM-B-404."
DR EMBL; AR220440; AAK0058.1; -
DR HSSP; P06278; IYTS.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0005975; F:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amyl_cat.
DR InterPro; IPR006589; Alp_amyl_cat_sub.
DR Pfam; PF00128; alpha-amylase; 1.
DR SMART; SMO0642; Amy; 1.
SEQUENCE 533 AA; 60557 MW; 7899CECD6A19C7DDE CRC64;

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Query Match 75.8%; Score 2021; DB 2; Length 533;
 Best Local Similarity 74.3%; Pred. No. 4,9e-140;
 Matches 358; Conservative 49; Mismatches 73; Indels 2; Gaps 1;

4 NGTLMQFEMVAPRDGQHMNRRLQDSDAYLAHSGITAVMTIPPAVKGTSDADVGYAYD 63
 Db 52 NGTLMQFEMVAPRDGQHMNRRLQDSDAYLAHSGITAVMTIPPAVKGTSDADVGYAYD 111
 QY 64 LGDFHQKGTAVRTKTKGTGELQSAIKSLHSRDINVDVYINHRGADATEDYTAVEV 123

Db 112 LGFENQKGTVRTKYGKKAQKSAIDALHKKNIDYGVVNMHKGADYETVTAVERDPS 171
 QY 124 DNRNVIISGEHLIKAMTHFHPGRGSTYSDPKMWHYFDGTDWDESKLRIRYKFO--GKA 181
 Db 172 NRVNVEGSDYELISANTGFEPGRGDSYSFKKMKHHPDGTDMDEGRKLRIRYKFGIGKA 231
 QY 182 WMEVSNENGNNDYLMYADIDYDHPVAALIKRMGTWIANEQLDGFRLDAVKHIFKESFL 241
 Db 233 WMEVSNENGNNDYLMYADIDYDHPVAALIKRMGTWIANEQLDGFRLDAVKHIDHEYL 291
 QY 242 RDMVNHVREKTKEMFTVAEYWMNDLGALENTYLNKTENHSVFDVPLHYOFHAASQGGG 301
 Db 292 RDMVNHVREKTKEMFTVAEYWMNDLGALENTYLNKTENHSVFDVPLHYOFHAASQGGG 351
 QY 302 YDMRKLNGTVYSKHEPLKSVTFVDNHDTPGQSLESTVQWTKPLAYAFILTRREGYPOV 361
 Db 352 YDMRKLNGTVYSKHEPLKSVTFVDNHDTPGQSLESTVQWTKPLAYAFILTRREGYPOV 411
 QY 362 FYGDMYGTGDSQREIPALKKHIEPILKARKQYAGAHQDFDHDHIVGWTREGSSVAN 421
 Db 412 FYGDMYGTGDSQREIPALKKHIEPILKARKQYAGAHQDFDHDHIVGWTREGSSVAN 471
 QY 422 SGLAALITDGPQAKMYVGRONAGETWHDITGNRSEPVINSSENGEFTVNGSSVSIVY 481
 Db 472 SGLAALITDGPQAKMYVGRONAGETWHDITGNRSEPVINSSENGEFTVNGSSVSIVY 531
 QY 482 QR 483
 Db 532 QR 533

RESULT 4
 ID 081Y04 PRELIMINARY; PRT; 513 AA.
 AC 081Y04;
 DT 01-JUN-2003 (TREMBlrel. 24, Created)
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Alpha-amylose.
 GN AMYS OR BA3551.
 OS Bacillus anthracis (strain Ames).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 CX NCBI_TaxID=198094;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=2608414; PubMed=12721629;
 RA Read T.D., Peterson S.N., Tourasse N., Baillie L.W., Paulsen I.T.,
 RA Nelson K.E., Tetrelin H., Fouts D.E., Eisen J.A., Gill S.R.,
 RA Holtzapple E.K., Ostad O.A., Helgeson E., Ralston J., Wu M.,
 RA Kolonay J.F., Beaman W.J., Dodson R.J., Brinkac L.M., Galin K.,
 RA Deboy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,
 RA Nelson M.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
 RA Barton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,
 RA Berry K.J., Plant R.D., Wolf A.M., Watkins K.L., Niemeyer W.C.,
 RA Haren A.J., Cline R., Redmond C., Thwaiter J.E., White O., Salzberg S.L.,
 RA Thomsen B., Friedlander A.M., Koehler T.M., Hanna P.C., Kolsto A.-B.,
 RA Fraser C.M.;
 RT "The genome sequence of Bacillus anthracis Ames and comparison to
 RT closely related bacteria.";
 RL Nature 423:81-86(2003).
 DR EMBL; AB017035; AAP27311.1; -
 DR TIGR; BA3551.1; -
 DR GO; GO:0004556; F:alpha-amylose activity; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro; IPR006047; Alpha_amy1_cat.
 DR InterPro; IPR006589; Alp_amy1_cat_sub.
 DR Pfam; PF00128; alpha-amy1_cat_sub.
 DR SMART; SM00642; Amy; 1.
 DR Complete proteome.
 SQ SEQUENCE 513 AA; 58445 MW; 558D6EF282FD159B CRC64;

Query Match 74.7%; Score 1991; DB 16; Length 513;
 Best Local Similarity 73.0%; Pred. No. 7,5e-138;

Matches 352; Conservative 51; Mismatches 77; Indels 2; Gaps 1;
 QY 4 NGTLMQYFEWYAPSDNNHNRJLTDAENLAKOKITISWIPPAKGTGTDVAGADLYD 63
 Db 32 NGTLMQYFEWYAPSDNNHNRJLTDAENLAKOKITISWIPPAKGTGTDVAGADLYD 91
 QY 64 LGFENQKGTVRTKYGKKAQKSAIDALHKKNIDYGVVNMHKGADYETVTAVERDPA 123
 Db 92 LGFENQKGTVRTKYGKKAQKSAIDALHKKNIDYGVVNMHKGADYETVTAVERDPA 151
 QY 124 DNRNVIISGEHLIKAMTHFHPGRGSTYSDPKMWHYFDGTDWDESKLRIRYKFO--GKA 181
 Db 152 NRVNVEGSDYELISANTGFEPGRGDSYSFKKMKHHPDGTDMDEGRKLRIRYKFGIGKA 211
 QY 182 WMEVSNENGNNDYLMYADIDYDHPVAALIKRMGTWIANEQLDGFRLDAVKHIFKESFL 241
 Db 212 WMEVSNENGNNDYLMYADIDYDHPVAALIKRMGTWIANEQLDGFRLDAVKHIDHEYL 271
 QY 242 RDMVNHVREKTKEMFTVAEYWMNDLGALENTYLNKTENHSVFDVPLHYOFHAASQGGG 301
 Db 272 RDMVNHVREKTKEMFTVAEYWMNDLGALENTYLNKTENHSVFDVPLHYOFHAASQGGG 331
 QY 302 YDMRKLNGTVYSKHEPLKSVTFVDNHDTPGQSLESTVQWTKPLAYAFILTRREGYPOV 361
 Db 332 YDMRKLNGTVYSKHEPLKSVTFVDNHDTPGQSLESTVQWTKPLAYAFILTRREGYPOV 391
 QY 362 FYGDMYGTGDSQREIPALKKHIEPILKARKQYAGAHQDFDHDHIVGWTREGSSVAN 421
 Db 392 FYGDMYGTGDSQREIPALKKHIEPILKARKQYAGAHQDFDHDHIVGWTREGSSVAN 451
 QY 422 SGLAALITDGPQAKMYVGRONAGETWHDITGNRSEPVINSSENGEFTVNGSSVSIVY 481
 Db 452 SGLAALITDGPQAKMYVGRONAGETWHDITGNRSEPVINSSENGEFTVNGSSVSIVY 511
 QY 482 QR 483
 Db 512 QR 513

RESULT 5
 ID 082839 PRELIMINARY; PRT; 516 AA.
 AC 082839;
 DT 01-NOV-1998 (TREMBlrel. 08, Created)
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Amylase.
 OS Bacillus sp.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 CX NCBI_TaxID=1409;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=KSM-1378;
 RC MEDLINE=98342096; PubMed=9675143;
 RA Igarashi K., Hatada Y., Ikawa K., Arai H., Ozawa T., Kobayashi T.,
 RA Ozaki K., Ito S.;
 RT "Improved thermostability of a Bacillus alpha-amylose by deletion of
 RT an arginine-glycine residue is caused by enhanced calcium binding.";
 RL Biochem Biophys Res Commun. 248:372-377(1998).
 DR HSSP; P06278; IV05.
 DR EMBL; AB087653; BA32431.1; -
 DR GO; GO:0004556; F:alpha-amylose activity; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro; IPR006047; Alpha_amy1_cat.
 DR InterPro; IPR006589; Alp_amy1_cat_sub.
 DR Pfam; PF00128; alpha-amy1_cat_sub.
 DR PRINTS; PR00110; ALPHAAMYLASE.
 DR SMART; SM00642; Amy; 1.
 SQ SEQUENCE 516 AA; 58841 MW; D90A8C90ECC182F8 CRC64;

Query Match 71.6%; Score 1909; DB 2; Length 516;
 Best Local Similarity 69.1%; Pred. No. 8e-132;

Matches 335; Conservative 68; Mismatches 72; Indels 10; Gaps 4;

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QY 4 NGTLMQYFEWYMPNDGQWRRLONDASAYLAEHGITAWMIPPAKGTSGADVGAYDLYD 63
QY 37 NGTLMQYFEWYMPNDGQWRRLONDASAYLAEHGITAWMIPPAKGTSGADVGAYDLYD 96
QY 64 LGEPHOGKGTATKTKGTGELQSAIKSLHSRDINVGQVVIINHGADATPDYTAAYVDA 123
QY 97 LGEPHOGKGTATKTKGTGELQSAIKSLHSRDINVGQVVIINHGADATPDYTAAYVDA 156
QY 124 DRRNVIAGEHLIKMTHTFHFPGRGSTYSDPKMWHYFPGTDMDESRKL-NRIYKPO--GK 180
QY 157 NRNCEIAGEHTIEMTKEFDFGKGNTHSNFKMRHYHEDGTDMQSQLOKIKYKFGTCK 216
QY 181 AMDWEVSNENGNVYLYMADIDYDHPDYAAEIKRWGTWYANELQDGFRLDAVKIKFSF 240
QY 217 AMDWEVSNENGNVYLYMADIDYDHPDYAAEIKRWGTWYANELQDGFRLDAVKIKFSF 276
QY 241 LRDVNVHREKTKGEMFTVAEYQNDIGALENYLNTKTPNHSVDFVPLHYQFHAASSTQ 300
QY 277 TRDMLTHVRNTTGPMPAVAEFWQNDLAIENTYLNKTSNHSVDFVPLHYQFHAASSTQ 336
QY 301 GYDMRKLINGTVSKHPLKSVTFVNDHDTOPQSGLESTVQWTKPLAFAFILTREGCY 360
QY 337 YEDMKNILNGSVQKHPHATFVNDHDTOPQSGLESTVQWTKPLAFAFILTREGCY 396
QY 361 VFYGDWYMG--TKGDSOREIPALKKIEPIILKARKQYVGAOHDFHDDHVGWTRREGDS 418
QY 397 VFYGDWYMG--TKGDSOREIPALKKIEPIILKARKQYVGAOHDFHDDHVGWTRREGDS 451
QY 419 VANSGLAALITDGPCKAKMYVGRONAGETWHDITGNRSEPVVINSGEWGFHYNGSVS 478
QY 452 HPNSGLATIMSDGPGKMYVGRONAGETWHDITGNRSEPVVINSGEWGFHYNGSVS 511
QY 479 IYVOR 483
QY 512 VWVPR 516

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RESULT 6

031193 PRELIMINARY; PRT; 549 AA.

ID 031193

AC 031193 (PRELIMINARY; PRT; 549 AA.)

DT 01-JAN-1998 (TREMBlrel. 05, Created)

DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)

DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)

DE Alpha amylase.

GN AMT

OS Bacillus stearothermophilus.

OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.

NCBI_TaxID=1422;

NCBI_TaxID=1422;

RA da Silva A.C.R., Fernandes E., Pueyo M.T.;

RA Submitted (NOV-1997) to the EMBL/Genbank/DBJ databases.

DR EMBL; AF032864; AAB6961.1; -

DR PIR; A54541; A5451.

DR HSSP; P06278; IVUS.

DR GO; GO:0004556; F:alpha-amylase activity; IEA.

DR GO; GO:0005975; P:carbohydrate metabolism; IEA.

DR InterPro; IPR006047; Alpha_cat.

DR InterPro; IPR006047; Alpha_cat.

DR InterPro; IPR006046; Glyco_hydro_13.

DR Pfam; PF00128; alpha-amylase; 1.

DR PRINTS; PR00110; ALPHAMYLASE.

DR SMART; SM00642; Amy; 1.

DR SMART; SM00642; Amy; 1.

SEQUENCE 549 AA; 62651 MW; 2CA689EDACC4D262 CRC64;

Query Match 67.1%; Score 1789.5; DB 2; Length 549;
 Best Local Similarity 64.9%; Pred. No. 5.2e-123;
 Matches 315; Conservative 67; Mismatches 96; Indels 5; Gaps 2;

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QY 1 ANGLTMOYFEWYMPNDGQWRRLONDASAYLAEHGITAWMIPPAKGTSGADVGAYD 60
QY 36 APENGMQYFEWYMPNDGQWRRLONDASAYLAEHGITAWMIPPAKGTSGADVGAYD 95
QY 61 LYLDEPHOGKGTATKTKGTGELQSAIKSLHSRDINVGQVVIINHGADATPDYTAAYV 120
QY 96 LYLDEPHOGKGTATKTKGTGELQSAIKSLHSRDINVGQVVIINHGADATPDYTAAYV 155
QY 121 DPADNRVISEHILKMTHTFHFPGRGSTYSDPKMWHYFPGTDMDESRKL-NRIYKPO-- 178
QY 156 NPSDNCIEISTYIOLQMTKEFDFGKGNTHSNFKMRHYHEDGTDMQSQLOKIKYKFG 215
QY 179 GKAMDWEVSNENGNVYLYMADIDYDHPDYAAEIKRWGTWYANELQDGFRLDAVKIKFS 238
QY 216 GKAMDWEVSNENGNVYLYMADIDYDHPDYAAEIKRWGTWYANELQDGFRLDAVKIKFS 275
QY 239 SFLRNVHREKTKGEMFTVAEYQNDIGALENYLNTKTPNHSVDFVPLHYQFHAASSTQ 298
QY 276 SFLRNVHREKTKGEMFTVAEYQNDIGALENYLNTKTPNHSVDFVPLHYQFHAASSTQ 335
QY 299 GGGYDMRKLINGTVSKHPLKSVTFVNDHDTOPQSGLESTVQWTKPLAFAFILTREGCY 358
QY 336 GGGYDMRKLINGTVSKHPLKSVTFVNDHDTOPQSGLESTVQWTKPLAFAFILTREGCY 395
QY 359 POFVFGDMYGTGKDSOREIPALKKIEPIILKARKQYVGAOHDFHDDHVGWTRREGDS 418
QY 396 POFVFGDMYGTGKDSOREIPALKKIEPIILKARKQYVGAOHDFHDDHVGWTRREGDS 452
QY 419 VANSGLAALITDGPCKAKMYVGRONAGETWHDITGNRSEPVVINSGEWGFHYNGSVS 478
QY 453 KPGSGLAALITDGPCKAKMYVGRONAGETWHDITGNRSEPVVINSGEWGFHYNGSVS 512
QY 479 IYVOR 483
QY 513 VWVPR 517

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RESULT 7

P71034 PRELIMINARY; PRT; 521 AA.

ID P71034

AC P71034 (PRELIMINARY; PRT; 521 AA.)

DT 01-FEB-1997 (TREMBlrel. 02, Created)

DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)

DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)

DE Alpha-amylase precursor.

OS Bacillus sp. MK 716.

OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

NCBI_TaxID=54116;

NCBI_TaxID=54116;

RA Sridhar G.S., Chakrabarti T.;

RA Submitted (OCT-1996) to the EMBL/Genbank/DBJ databases.

DR EMBL; U75445; AAB18785.1; -

DR HSSP; P06278; IVUS.

DR GO; GO:0004556; F:alpha-amylase activity; IEA.

DR GO; GO:0005975; P:carbohydrate metabolism; IEA.

DR InterPro; IPR006047; Alpha_cat.

DR InterPro; IPR006047; Alpha_cat.

DR InterPro; IPR006046; Glyco_hydro_13.

DR Pfam; PF00128; alpha-amylase; 1.

DR PRINTS; PR00110; ALPHAMYLASE.

DR SMART; SM00642; Amy; 1.

DR SMART; SM00642; Amy; 1.

SEQUENCE 521 AA; 59311 MW; 5612A88596D922E1 CRC64;

Query Match 66.9%; Score 1784.5; DB 2; Length 521;
 Best Local Similarity 64.7%; Pred. No. 1.1e-122;
 Matches 314; Conservative 67; Mismatches 99; Indels 5; Gaps 2;

```

QY 1 ANLNGTLMQYFEMWYMPNDGQHMRLONDSAYLAEGHTAVWIPRAYKGTSGADVGAYD 60
D 36 APFNGTMOYFEMWYLPDDGTLMTKRVANENNLSSLGITRLMPLPAKYKTSRESDVGAYD 95
QY 61 LYLDSGEHOKGVYRTKGTGKGELOSALKSLSHRDINVYGDVYINHGADATEDVTAEV 120
D 96 LYLDSGEHOKGVYRTKGTGKGELOSALKSLSHRDINVYGDVYINHGADATEDVTAEV 155
QY 121 DPADRNRVISEGHLIKAMTHFHPGSGTYSDFKMWYHFDGTDWDESKLRIRYKFO-- 178
D 156 NPSDRNGEISGTQIQAMTKFDFPGKNTYSSFKRWYHFDGVDWDESKLRIRYKFGI 215
QY 179 GKAMDVEVSNENGYDYLMTADIDYDHPVAALIKRWGTWYANELQDGFRLDAYKHIF 238
D 216 GKAMDVEVDENENGYDYLMTADIDYDHPVAALIKRWGTWYANELQDGFRLDAYKHIF 275
QY 239 SFLRDWVNHREKTKGEMFTVAEYQNDLGALENYLNKTNFNHSVFDVPLHYQFHAASQ 298
D 276 SFFPDMLSYRSQTKGKPLFTVGEYMSYDINKLHNYITKNGTMSLFDALHNKFTYAKS 335
QY 299 GGGYDKRLKNGTVSKHPLKSVTFVNDHDTOPGQSLSTVQTWKPLAYAFILTRBSGY 358
D 336 GGAEDKRLMTNTLMTKDQPLTAVTFVNDHDTOPGQSLSTVQTWKPLAYAFILTRBSGY 395
QY 359 POVFYGDYGTGDSOREIPALKHKEPIFKARQYAGAHQDYPHNDIYGMTRESGS 418
D 396 PCVFYGDYGTGDSOREIPALKHKEPIFKARQYAGAHQDYPHNDIYGMTRESGS 452
QY 419 VANSGLAALITDGPAGAKMYVGRONAGETWHDITGNRSEPVYINSEGEFHYNGSGVS 478
D 453 KPSGGLAALITDGPAGAKMYVGRONAGETWHDITGNRSEPVYINSEGEFHYNGSGVS 512
QY 479 IYVOR 483
D 513 VWVPR 517

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RESULT 8

Q9KMY6 PRELIMINARY; PRT; 549 AA.

AC 09KMY6; (TREMblrel. 15, Created)

DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)

DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)

DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)

DB Alpha-amylase (EC 3.2.1.1).

OS Bacillus stearothermophilus.

OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.

OX NCBI_TaxID=1422;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=US100;

RA Bejar S.

RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL; Y11557; CAB93511.1; .

DR PIR; A54541; A54541.

DR HSSP; P06278; IVS.

DR GO; GO:0004556; F:alpha-amylase activity; IEA.

DR GO; GO:0016798; F:hydrolyase activity; acting on glycosyl bonds; IEA.

DR GO; GO:0005975; P:carbohydrate metabolism; IEA.

DR InterPro; IPR006047; Alpha_amyl_cat.

DR InterPro; IPR006589; Alp_amyl_cat_sub.

DR InterPro; IPR006046; Glyco_hydro_13.

DR Pfam; PF00128; alpha-amylase; 1.

DR PRINTS; PR00110; ALPHAMYLASE.

DR SMART; SM00642; Amyy; 1.

KW Glycosidase; Hydrolase.

SQ SEQUENCE 549 AA; 62582 MW; 8DA3B6DFF9120BCE CRC64;

Query Match 66.3%; Score 1784.5; DB 2; Length 549;
 Best Local Similarity 64.7%; Pred. No. 1.2e-122;
 Matches 314; Conservative 67; Mismatches 99; Indels 5; Gaps 2;

```

QY 1 ANLNGTLMQYFEMWYMPNDGQHMRLONDSAYLAEGHTAVWIPRAYKGTSGADVGAYD 60
D 36 APFNGTMOYFEMWYLPDDGTLMTKRVANENNLSSLGITRLMPLPAKYKTSRESDVGAYD 95
QY 61 LYLDSGEHOKGVYRTKGTGKGELOSALKSLSHRDINVYGDVYINHGADATEDVTAEV 120
D 96 LYLDSGEHOKGVYRTKGTGKGELOSALKSLSHRDINVYGDVYINHGADATEDVTAEV 155
QY 121 DPADRNRVISEGHLIKAMTHFHPGSGTYSDFKMWYHFDGTDWDESKLRIRYKFO-- 178
D 156 NPSDRNGEISGTQIQAMTKFDFPGKNTYSSFKRWYHFDGVDWDESKLRIRYKFGI 215
QY 179 GKAMDVEVSNENGYDYLMTADIDYDHPVAALIKRWGTWYANELQDGFRLDAYKHIF 238
D 216 GKAMDVEVDENENGYDYLMTADIDYDHPVAALIKRWGTWYANELQDGFRLDAYKHIF 275
QY 239 SFLRDWVNHREKTKGEMFTVAEYQNDLGALENYLNKTNFNHSVFDVPLHYQFHAASQ 298
D 276 SFFPDMLSYRSQTKGKPLFTVGEYMSYDINKLHNYITKNGTMSLFDALHNKFTYAKS 335
QY 299 GGGYDKRLKNGTVSKHPLKSVTFVNDHDTOPGQSLSTVQTWKPLAYAFILTRBSGY 358
D 336 GGAEDKRLMTNTLMTKDQPLTAVTFVNDHDTOPGQSLSTVQTWKPLAYAFILTRBSGY 395
QY 359 POVFYGDYGTGDSOREIPALKHKEPIFKARQYAGAHQDYPHNDIYGMTRESGS 418
D 396 PCVFYGDYGTGDSOREIPALKHKEPIFKARQYAGAHQDYPHNDIYGMTRESGS 452
QY 419 VANSGLAALITDGPAGAKMYVGRONAGETWHDITGNRSEPVYINSEGEFHYNGSGVS 478
D 453 KPSGGLAALITDGPAGAKMYVGRONAGETWHDITGNRSEPVYINSEGEFHYNGSGVS 512
QY 479 IYVOR 483
D 513 VWVPR 517

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RESULT 9

Q59222 PRELIMINARY; PRT; 613 AA.

AC 059222; (TREMblrel. 01, Created)

DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)

DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)

DT 01-JUN-2003 (TREMblrel. 24, Last annotation update)

DE Alpha-amylase (EC 3.2.1.1).

GN AMY.

OS Bacillus sp. TS-23.

OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

OX NCBI_TaxID=38441;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=TS-23;

RA Lin L.-J., Chu W.S., Hsu W.H.

RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.

DR EMBL; U22045; AAA63900.1; .

DR HSSP; P06278; IVS.

DR GO; GO:0004556; F:alpha-amylase activity; IEA.

DR GO; GO:0016798; F:hydrolyase activity; acting on glycosyl bonds; IEA.

DR GO; GO:0008777; F:putative nucleosidase activity; IEA.

DR GO; GO:0005975; P:carbohydrate metabolism; IEA.

DR InterPro; IPR006047; Alpha_amyl_cat.

DR InterPro; IPR006589; Alp_amyl_cat_sub.

DR InterPro; IPR002044; CBD_4.

DR InterPro; IPR006046; Glyco_hydro_13.

DR Pfam; PF00128; alpha-amylase; 1.

DR Pfam; PF00686; CBM_20; 1.

DR PRINTS; PR00110; ALPHAMYLASE.

DR PRODOM; PD001368; CBD_4; 1.

DR SMART; SM00642; Amyy; 1.

KW Glycosidase; Hydrolase.

SQ SEQUENCE 613 AA; 69537 MW; 14684A30FC2695E8 CRC64;

Query Match 65.8%; Score 1755.5; DB 2; Length 613;

Best Local Similarity 64.18; Pred. No. 1,9e-120;
Matches 311; Conservative 68; Mismatches 101; Indels 5; Gaps 2;

QY 1 ANLNGTMOYFEWYVNDGQHWRLONDSAYLAHGHTAVWIPPAKGTSGQADVGAYD 60
D 33 APINEMTMOYFEWYVNDGQHWRLONDSAYLAHGHTAVWIPPAKGTSGQADVGAYD 92
QY 61 LYDGEFHQKGTVRTKYGKGLQSAIKSLHSRDINVGDVVINKKGADATEDVTAVEY 120
D 93 LYDGEFHQKGTVRTKYGKGLQSAIKSLHSRDINVGDVVINKKGADATEDVTAVEY 152
QY 121 DPABNRVISEGHELIKMTFHFPGRGSTYSPFKMHYHPDGTWDSRKLNIYKQ-- 178
D 153 DPSNRNGTSGTYQIQMTKFDYFGRKNTYSPFKMHYHPDGTWDSRKLNIYKQ-- 212
QY 179 GKAMDVEVSNNGVDYLVADIDYDHPVAELIKRWGTWYANELQDGFELDAVKIKF 238
D 213 GKAMDVEVSNNGVDYLVADIDYDHPVAELIKRWGTWYANELQDGFELDAVKIKF 272
QY 239 SELDMVNVHVEKTEKEMFTVAEYVNDGLALENYLNTKTNHNSVFPVPLHYOFHAATQ 298
D 273 SFFPDMLYYVNRQKSKNIPAVGEFNSYVKNLHYITKNGSNLFPADPLNNFYTKSKS 332
QY 333 SGYFDMRYLNNITLMKQPSLAVTLVDNHTQPGQSLSWEPWFKFLAVAFILTRQEGY 392
D 359 PQVFQDMYGTGKSQREIIPALKEIPILKARKQYAGAOHDFDHDIVGWTREGDS 418
QY 393 PCVFQGDYGI--PKYNIPLKSKIDPLIARDDYAGTGRDIDHDIVGWTREGIDT 449
D 419 VANSGLALITDGPQAKMYVGRONAGETWHDITGNSEPEVINSSEGGEFHVNGSVS 478
QY 450 KPNISGLALITDGPQAKMYVGRONAGETWHDITGNSEPEVINSSEGGEFHVNGSVS 509
QY 479 TYVQR 483
D 510 IWVAK 514

RESULT 10
ID 093148 PRELIMINARY; PRT; 501 AA.
AC 093148;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Amylase.
GN AMYK38.
OS Bacillus sp. KSM-K38.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OC NCBI_TaxID=129736;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KSM-K38;
RA Hayashi Y.;
RT Submission of a new Bacillus alpha-amylase."
RT Submitted (NOV-2000) to the EMBL/GenBank/DBD databases.
DR EMBL: A8051102; BAB71820.1; --
DR GO: GO:0004556; F:alpha-amylase activity; IEA.
DR GO: GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro: IPR006047; Alpha_amy1_cat.
DR Pfam: PF00128; alpha-amylase; 1.
SQ SEQUENCE 501 AA; 57485 MW; 1240F46739A5CC11 CRC64;

Query Match 64.6%; Score 1723.5; DB 2; Length 501;
Best Local Similarity 62.8%; Pred. No. 3.2e-118;
Matches 302; Conservative 72; Mismatches 104; Indels 3; Gaps 1;

QY 3 LNLGTLMOYFEWYVNDGQHWRLONDSAYLAHGHTAVWIPPAKGTSGQADVGAYD 62
D 24 LNLGTLMOYFEWYVNDGQHWRLONDSAYLAHGHTAVWIPPAKGTSGQADVGAYD 83

QY 63 DLGEFHQKGTVRTKYGKGLQSAIKSLHSRDINVGDVVINKKGADATEDVTAVEVP 122
D 84 DLGEFHQKGTVRTKYGKGLQSAIKSLHSRDINVGDVVINKKGADATEDVTAVEVP 143
QY 123 ADNRVISEGHELIKMTFHFPGRGSTYSPFKMHYHPDGTWDSRKLNIYKQOKAW 182
D 144 TNRMODIGATLIDMTGFDPGSGNNAYSPDKMHYHPDGTWDSRKLNIYKQOKAW 203
QY 183 DWEVSENGNDYLVADIDYDHPVAELIKRWGTWYANELQDGFELDAVKIKF 242
D 204 DWEVSENGNDYLVADIDYDHPVAELIKRWGTWYANELQDGFELDAVKIKF 263
QY 243 DWEVSENGNDYLVADIDYDHPVAELIKRWGTWYANELQDGFELDAVKIKF 302
D 264 DWEVSENGNDYLVADIDYDHPVAELIKRWGTWYANELQDGFELDAVKIKF 323
QY 303 DWEVSENGNDYLVADIDYDHPVAELIKRWGTWYANELQDGFELDAVKIKF 362
D 324 DWEVSENGNDYLVADIDYDHPVAELIKRWGTWYANELQDGFELDAVKIKF 383
QY 363 YGDMYGTGKSQREIIPALKEIPILKARKQYAGAOHDFDHDIVGWTREGDSVANS 422
D 384 YGDMYGTGKSQREIIPALKEIPILKARKQYAGAOHDFDHDIVGWTREGDSVANS 440
QY 423 GLAALITDGPQAKMYVGRONAGETWHDITGNSEPEVINSSEGGEFHVNGSVSYQ 482
D 441 GLAALITDGPQAKMYVGRONAGETWHDITGNSEPEVINSSEGGEFHVNGSVSYQ 500
QY 483 R 483
D 501 Q 501

RESULT 11
ID 087HG6 PRELIMINARY; PRT; 507 AA.
AC 087HG6;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Alpha-amylase.
GN VPA0999.
OS Vibrio parahaemolyticus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OC NCBI_TaxID=670;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RIMD 2210633 / Serotype O3:K6;
RX MEDLINE=22508454; PubMed=12620739;
RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
RA Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
RA Yasunaga T., Honda T., Shingawa H., Hattori W., Tida T.,
RT "genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
RT distinct from that of V. cholerae.";
RT Lancet 361:743-749(2003).
DR EMBL: AP005087; BAC62342.1; --
DR GO: GO:0004556; F:alpha-amylase activity; IEA.
DR GO: GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro: IPR006047; Alpha_amy1_cat.
DR Pfam: PF00128; alpha-amylase; 1.
KW Complete proteome.
SQ SEQUENCE 507 AA; 58428 MW; 91B549E2BE0700BD CRC64;

Query Match 56.4%; Score 1502.5; DB 16; Length 507;
Best Local Similarity 55.8%; Pred. No. 5.6e-102;
Matches 271; Conservative 81; Mismatches 125; Indels 9; Gaps 7;

QY 1 ANLNGTMOYFEWYVNDGQHWRLONDSAYLAHGHTAVWIPPAKGTSGQADVGAYD 59
D 23 ANLNGTMOYFEWYVNDGQHWRLONDSAYLAHGHTAVWIPPAKGTSGQADVGAYD 82
QY 60 DVLGEFHQKGTVRTKYGKGLQSAIKSLHSRDINVGDVVINKKGADATEDVTAVE 119

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Db      83 DMYDGEFQKGSVTKYGTAKAYISALIAAHNNNNIQTIGDVVFHNRGADGSKSVWDTKR 142
Qy      120 VDPADNRKRTISEHLIKAMTHFHPGRGSTYSDFKMHWYHFGDTWDSRKLNRITYKQ-- 177
Db      143 VMDNRN-TEIGDKMTLEAVVEFNPGRRNDKYSNFHMTWTHFDGWDMDGKEKALFKKRG 201
Qy      178 QGKAMDVEVSNENGYDYLMTADIDYDHPVAEIKRWGTWYANELQDGFRLDAVKAIX 237
Db      202 EGRAMDVEVSEKGNVDYLMYADLDMDHFEVQELKMGWEYINNTGVDGFMADVKIKX 261
Qy      238 FEFRLDWNVHREKTKEMFTVAEYQNDLGALNNTKTNHSEFVPLHYQFHAAS 297
Db      262 YYLDEMIDHLRWKTKGKELFTVGEYVWYVNOJHNFITITSGSMSLFAPLHMNFYNSK 321
Qy      298 OGGGYDMRKLNGTVVSKPLKSVFVDNHDTPQGSLSTVQTFWFKPLAYAFILTRREG 357
Db      322 SGNATMRQIMNGTLMKCNPKVAVTLVENHDTQDLALSTYDWMFKPLAYAFILTRREG 381
Qy      358 YQVYFGDMYGTG-GDSREIPALK-HKLEPILKARKQYAGAQHDYDHDHIVGWTREG 415
Db      382 YSVFVADYGAQYSKGYNNMAKPYIEELVTLRKEYAYGKQNSYLDHMDVIGWTRRG 441
Qy      416 DSSVANSGLAALITDPPGAKMYVGRQNAGETWHDITGNRESEPVINSEGEFHVNG 475
Db      442 DAEHPNS-KAVINSDGPGGTGMWYTGKPSST-RYVDKLGIRTEVWTDANMAEPVNG 498
Qy      476 SVSIYV 481
Db      499 SVSVWV 504

RESULT 12
Q089YPI PRELIMINARY; PRT; 481 AA.
AC Q089YPI;
DT 01-JUN-2003 (TREMblrel. 24, Created)
DT 01-JUN-2003 (TREMblrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
DE Alpha-amylase precursor.
GN B74690.
OS Bacteroides thetaiotaomicron.
OC Bacterioidetes; Bacteroidales; Bacteroidaceae; Bacteroides.
OC NCBI_TaxID=818;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VPI-5482 / ATCC 29148;
RX MEDLINE=22550858; PubMed=12663928;
RA Xu J., Bjureell M.K., Hamrod J., Deng S., Carmichael L.K.,
  Chiang H.C., Hooper L.V., Gordon J.I.;
RT "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.";
RU Science 299:12074-2076(2003).
DR EMBL; A6016946; A6079795.1; -.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_ami1_cat.
DR InterPro; IPR006589; Alp_ami1_cat_sub.
DR Pfam; PF00128; alpha-amylase; 1.
DR SMART; SM00642; Amy; 1.
KW Complete proteome.
SQ SEQUENCE 481 AA; 55343 MW; 86BF237011F5EB1A CRC64;

Query Match 50.1%; Score 1336; DB 16; Length 481;
Best Local Similarity 49.6%; Pred. No. 8.9e-90;
Matches 239; Conservative 84; Mismatches 153; Indels 6; Gaps 2;

Qy      4 NGTLMQFEWYMPNDGQWRRLQDSAYLAHGITAVWIPPAKSGSQADVGAYDLYD 63
Db      3 NGWMOQFEWHLNDGDLKQIKEDALHLDIDGTVAWIPPAKADQEQDEGATAYDLYD 62
Qy      64 LGFHKQKTVRTKYGTGKELSAIKSLHSRDINYGVDVILNHKGADATEDVTAVEVPA 123

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Db      63 LGFEDQKRTIRTKYGTRELBKXALDELAKHYIAVYLDVYLNHKAAGDTEFKMVEVEVDEK 122
Qy      124 DNRVISEHLLIKAMTHFHPGRGSTYSDFKMHWYHFGDTWDSRKLNRITYKQ--GKA 181
Db      123 ERTKALGEPELIGMTGYSTHGKDKGSDPKMHWYHFGSTGDDAQKRGVQIQGEKGA 182
Qy      182 WDEVSNENGYDYLMTADIDYDHPVAEIKRWGTWYANELQDGFRLDAVKAIXFSL 241
Db      183 WSEGVSESNENGYDFLLCNLDIDLHPVSEINRWGKVSNEINLQMRDLAIKHKMDQPV 242
Qy      242 RDWNVHREKTKEMFTVAEYQNDLGALNNTKTNHSEFVPLHYQFHAAS 301
Db      243 AQFLDAVSRERNGDFTAVGVEYMGDLBALDAYLEAVGHKNPLFDVLIHNMQAQSEGD 302
Qy      302 YDMRKLNGTVVSKPLKSVTFVDNHDTPQGSLSTVQTFWFKPLAYAFILTRREGSPV 361
Db      303 YDLRDLKDTLVEHHPOLAVTIVDNHDTPQSSLESNVEDWFKPLAYGILLMKEGYPL 362
Qy      362 FYGDMYGTGDSQREIPALKHKELEPILKARKQYAGAQHDYDHDHIVGWTREGDSSVAN 421
Db      363 FYGDMYGTGDSQREIPALKHKELEPILKARKQYAGAQHDYDHDHIVGWTREGDSSVAN 418
Qy      422 SGLAALITDPPGAKMYVGRQNAGETWHDITGNRESEPVINSEGEFHVNGSVSIYV 481
Db      419 SGLVFLMSNDAGSKINSLEKTKGVEYHETISISEITLDEGNGEFSVESRLAVWV 478
Qy      482 QR 483
Db      479 KK 480

RESULT 13
Q03657 PRELIMINARY; PRT; 483 AA.
AC Q03657;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMblrel. 24, Last annotation update)
DE Amylase.
GN AMYE.
OS Bacillus circulans.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OC NCBI_TaxID=1397;
RN [1]
RP SEQUENCE FROM N.A.
RA Marcel T.;
RL Nucleic Acids Res. 0:0-0(0).
DR EMBL; X60779; CAA43194.1; -.
DR PIR; S15713; S15713.
DR HSSP; P06278; IVUS.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_ami1_cat.
DR InterPro; IPR006589; Alp_ami1_cat_sub.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAMYLASE.
DR SMART; SM00642; Amy; 1.
SQ SEQUENCE 493 AA; 56537 MW; FECD2F805BB4694 CRC64;

Query Match 47.3%; Score 1262; DB 2; Length 493;
Best Local Similarity 47.6%; Pred. No. 2.5e-84;
Matches 230; Conservative 75; Mismatches 166; Indels 12; Gaps 3;

Qy      4 NGTLMQFEWYMPNDGQWRRLQDSAYLAHGITAVWIPPAKSGSQADVGAYDLYD 63
Db      4 NHTWMOQFEWHLNADGDHMKRLAEMAPELKAKGIDITWVPPVTKAVSAEDTGYGVYDLYD 63
Qy      64 LGFHKQKTVRTKYGTGKELSAIKSLHSRDINYGVDVILNHKGADATEDVTAVEVPA 123
Db      64 LGFEDQKTVRTKYGTGKELSAIKSLHSRDINYGVDVILNHKGADATEDVTAVEVPA 123
Qy      124 DRNVISEHLLIKAMTHFHPGRGSTYSDFKMHWYHFGDTWDSRKLNRITYKQ--KA 181

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Db      124 DRTKISPEFLEGTKTTFPRGQGYSSFKNSHFGTDPDAREBRTGFRLAGENK 183
Qy      182 WMEVSNENGVNDYLMVADIDYHPDVAEIKRWGTAYANELQDGFRLDAVKIKSFL 241
Db      184 WMEVNDDEFGVNDYLMFANIDYNHDPVREMI DMGKMLDITLQCGGFRLDAIKHINEFI 243
Qy      242 RDWVNHVEKTKGKEMFTVAEYVNDIGALEVNLKTNHNSVFPVPLHYOPHAASTOGG 301
Db      244 KEFAEMTRKQGDYIVGEFNNSLDCREFLDIVDQIDLFVYSLHKHEBSLGRD 303
Qy      302 YDMRLKLTGVVSKPLKSVTFVNDHDTQPGQSLESTVQTFKPLAYAFILITRESGYPQV 361
Db      304 PLSKIPDITLVQTPHTAVTFVDNHDSPHEALSMIGDFKPSAYALTLLRRDGYFVV 363
Qy      362 FPGDVMYGTGK----DSQREIPALKKIEPILKARQYAYGAOHDFDHDIVGWTREDS 417
Db      364 FPGDYYGIGGPPVDGKEI-----LDLISARCNKAYGEDEYFDHANTIGWTRGVE 417
Qy      418 SVANGSLAALITDGPAGKMYVGRONAGETWHDITGNRSEPVVINSGEWGEFHVNGSV 477
Db      418 EIEGGCAVIVISNGDGEKMFIEGRAGEVWVDTLTKSCDQITIEEDGMATFHVCGGV 477
Qy      478 STY 480
Db      478 SVM 480

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RESULT 14

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ID      08YU21      PRELIMINARY;      PRT;      492 AA.
AC      08YU21;

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DT      01-MAR-2002 (TREMBLrel. 20, Created)
DT      01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DE      01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE      Alpha-amylase.
GN      ALR2190.
OS      Anabaena sp. (strain PCC 7120).
OC      Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
NCBI_TaxID=103690;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=2159285; PubMed=11759840;
RA      Kaneke T., Nakamura Y., Molk C.P., Kuritz T., Sasamoto S.,
RA      Mateneko A., Iriuchihara M., Ishikawa A., Kawashima K., Kimura T.,
RA      Kishida Y., Kohara M., Matsumoto M., Matsumoto A., Muraki A.,
RA      Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
RA      Yasuda M., Tabata S.;
RT      "Complete genomic sequence of the filamentous nitrogen-fixing
RT      cyanobacterium Anabaena sp. strain PCC 7120.";
RL      DNA Res. 8:205-213 (2001).
DR      EMBL: AP003588; BAB73889.1; -
DR      PIR: AH2079; AH2079.
DR      GO: GO:0004556; F:alpha-amylase activity; IEA.
DR      GO: GO:0005975; P:carbohydrate metabolism; IEA.
DR      InterPro: IPR006047; Alpha_amy1_cat.
DR      InterPro: IPR006046; Glyco_hydro_13.
DR      Pfam: PF00128; alpha-amylase; 1.
DR      PRINTS: PR00110; ALPHAAMYLASE.
DR      Complete proteome.
KM      SEQUENCE 492 AA; 57063 MW; 11B5D6CE2F1828 CRC64;

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Query Match      46.7%; Score 1244; DB 16; Length 492;
Best Local Similarity 47.5%; Pred. No. 5, 2e-83;
Matches 234; Conservative 84; Mismatches 161; Indels 14; Gaps 6;

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Qy      1 ANLNGLMGYFEMVYNDGQHWRLONDSAYLAEGHITVWIPPAVKG-TSQADYGVAY 59
Db      2 AQMGNGMAYFHYIINDGNLNGKVASAPALADAGFTLWMLPPAYKAGSFDYGVY 61
Qy      60 DLYDLGEFHQKGVTRTKYGTGKLGSAISLSHRDINVGDVVINKSGADTEPVTAVE 119
Db      62 DLYDLGEFHQKGVTRTKYGTGKLGSAISLSHRDINVGDVVINKSGADTEPVTAVE 121

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Qy      120 VDPADNRNVI SGEHLIKAMTHPEPRGSTYSDFKHHYFDGTDWDESRKLR--IYKF 177
Db      122 FPDQDRLNKGGLQIKITTYHNFPRGOKYSNFMHMHDDAVDYNEVNSGDSSTVLL 181
Qy      178 OGKAMDVEVSNENGVNDYLMVADIDYHPDVAEIKRWGTAYANELQDGFRLDAVKIKSFL 237
Db      182 EGNRFDYVALKEKNFAYLMGCDLDFONBWVGEVTVYKGCCLPTTKYDGFRLDAIKIS 241
Qy      238 FSLRNVNHVEKTKGKEMFTVAEYVNDIGALEVNLKTNHNSVFPVPLHYOPHAAST 297
Db      242 TWFFPEWIDALRRHAKGLFMYGVTYNDINTLLVYAVKMSVDFVPLHYNHQSK 301
Qy      298 OGQYDMRLKLTGVVSKPLKSVTFVNDHDTQPGQSLESTVQTFKPLAYAFILITRESG 357
Db      302 SGGNYDMRLITDGTWVQRPHTAVTFVENHDSPQLALESVYEPWFKPLAYAILLRQEG 361
Qy      358 YPQVFGDMYGTGK----GDSQRE--IPALKKIEPILKARQYAYGAOHDFDHDIV 409
Db      362 YPQVHADYVGAIEYEDWKGDNRYNIFMFSHMLIDKLVAKKYAYVQPYVLDHNTI 421
Qy      410 GWTREDSVSVANGSLAALITDGPAGKMYVGRONAGETWHDITGNRSEPVVINSGEWGE 469
Db      422 GWTRELDAD-HPGMAVIMSDSGEIKMVEVGKPT--KFIDLTBIKEAVYTNEWGE 478
Qy      470 FHVNGSVSTIYQ 482
Db      479 FRCLGGSVSWVQ 491

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RESULT 15

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ID      097049      PRELIMINARY;      PRT;      484 AA.
AC      097049;

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DT      01-OCT-2001 (TREMBLrel. 18, Created)
DT      01-OCT-2001 (TREMBLrel. 18, Last sequence update)
DE      01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE      Alpha-amylase.
GN      SPI382.
OS      Streptococcus pneumoniae.
OC      Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC      Streptococcus.
NCBI_TaxID=1313;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      STRAIN=ATCC BAA-334 / TIGR4;
RA      Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,
RA      Peterson S., Heidelberg J., Deboy R.T., Haft D.H., Dodson R.J.,
RA      Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,
RA      Umayam L.A., White O., Salzberg S.L., Lewis M.R., Raudenb D.,
RA      Holtzapfel E., Khouli H., Wolf A.M., Uetebach T.R., Hansen C.L.,
RA      McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey E.K.,
RA      Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,
RA      Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;
RT      "Complete genome sequence of a virulent isolate of Streptococcus
RT      pneumoniae";
RL      Science 293:498-506 (2001).
DR      EMBL: AE007435; AAK75480.1; -
DR      PIR: G95160; G95160.
DR      TIGR: SPI382; -
DR      GO: GO:0004556; F:alpha-amylase activity; IEA.
DR      GO: GO:0005975; P:carbohydrate metabolism; IEA.
DR      InterPro: IPR006047; Alpha_amy1_cat.
DR      InterPro: IPR006048; Alp_amy1_cat_sub.
DR      InterPro: IPR006046; Glyco_hydro_13.
DR      Pfam: PF00128; alpha-amylase; 1.
DR      PRINTS: PR00110; ALPHAAMYLASE.
DR      SMART: SM00642; Amy; 1.
DR      Complete proteome.
KM      SEQUENCE 484 AA; 55918 MW; 4E90A450A90EFB8C CRC64;

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Query Match      46.2%; Score 1233; DB 16; Length 484;

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Best Local Similarity 48.6%; Pred. No. 3.3e-82; Matches 234; Conservative 72; Mismatches 167; Indels 8; Gaps 4;

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QY 4 NCTLMQYFEMWPNNDQOHRRRLONDSAYLAEHGITAWMIPRAYKGTSGQADVGAYDYD 63
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 3 NCTLMQYFEMWLPHDQHWTRLAENAPHLALGISHWMPFPAFKATNEQDVGYYDLFD 62
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 64 LGFHHQKGTVRTYKYGKGLQSAIKSLHSRDINVGDVYINHGADATEDVTAVENDBA 123
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 63 LGFHHQKGTVRTYKYGKEDYLOALQALKAQGIQPMADVVLNKAADHREAFQVLEVDV 122
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 124 DRNRVSGEHLIKAWTHFHPGSGSTYSDFKWMTYHFDGTWDESRKLNRIYKFG--KA 181
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 123 DRVHVGEPFTINGWTSFTFDGRQDPTYNGFHWHFTGTDYDAKRSKSGIYLIGDNKG 182
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 182 WDME--VSNENGYDYLTADIDYDHPDVAALIKWGTYANELQDGFRLDAVKIKFS 239
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 183 WANEELVDNENGYDYLTADIDYDHPDVAALIKWGTYANELQDGFRLDAVKIKFS 242
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 240 FLBDWNVHREKTKGKEMFTVAEYQNDLGALENVLKNKTNFNSVFPDPLHYQFHAAS 299
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 243 FMRNFTRDMEKKGDPFYVGFEPNPDKEANIDYLEKTEHFDVYVRLHQNLFEASQAG 302
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 300 GGYDMKRLNGTVVSKHPLKSVTFVDNHDTPQGSLESTVQTFEKLAYAFILTRSGYP 359
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 303 ANYDLRGIFTDLSIVELKPDKAVTFVDNHDTPQGSLESTVQTFEKLAYAFILTRSGYP 362
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 360 QVYSGMYGKTKGSDSOREIPALKHIEPIIKARQVAYGAQHDFDHDIVGWTREGDS 419
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 363 CVFYGDYIGSQYAOE--DFKEILDRLAIRKDLAYGEONDFDHANCIGWVRSAGEN- 419
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 420 ANSGLAALITDGGAKRMVYGRQNAGETMHDITGNRSEPVYINSGGEFHVNGGSVSI 479
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 420 -QSPYAVLISNDQENSKSMFVGQEMTNGTFVDILGNHQGVITIDEGYGFVVSARSVSV 478
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 480 Y 480
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 479 W 479
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

Search completed: May 3, 2004, 20:53:12
Job time : 38.3365 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 3, 2004, 20:36:03 ; Search time 11.1361 Seconds
(without alignments)
2403.363 Million cell updates/sec

Title: US-10-644-187-6

Perfect score: 2847

Sequence: 1 AAFNGTGMQGFYFWYLPDDG.....TTREPTGSEFVRWTEPRIVAW 514

Scoring table: BLASTSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2780	97.6	549	1 AMY_BACST	P06279 bacillus st
2	1874.5	65.8	518	1 AMYB_BACST7	P15571 bacillus sp
3	1797.5	63.1	512	1 AMY_BACLI	P06278 bacillus li
4	1773.5	62.3	514	1 AMY_BACAM	P00692 bacillus am
5	1110.5	35.0	494	1 AMY2_SALTU	P26612 salmoneilla
6	1074.5	37.7	495	1 AMY2_ECOLI	P26612 escherichia
7	313	11.0	713	1 CDGT_BACSP	P30921 bacillus sp
8	307	10.8	1196	1 AMYB_PABPO	P21543 paenibacill
9	302.5	10.6	440	1 AMY3_ORYSA	P27932 oryza sativ
10	302	10.6	713	1 CDGT_BACSS	P17692 bacillus sp
11	300	10.5	713	1 CDGU_BACCI	P43379 bacillus ci
12	286.5	10.1	712	1 CDGT_BACCS	P09121 bacillus sp
13	286	10.0	718	1 CDGT_BACLI	P14014 bacillus li
14	284.5	10.0	713	1 CDGT_BACSO	P05618 bacillus sp
15	283	9.9	421	1 AMY4_VIGMU	P17859 vigna mungo
16	282	9.9	718	1 CDGT_BACSS	P31747 bacillus sp
17	280	9.8	413	1 AMY3_WHEAT	P08117 triticum ae
18	278	9.8	718	1 CDGT_BACCI	P30920 bacillus ci
19	275.5	9.7	564	1 AMY4_SCHPO	O9789 schizosach
20	274.5	9.6	438	1 AMYB_ORYSA	P27937 oryza sativ
21	274.5	9.6	528	1 AMY_BACCI	P08137 bacillus ci
22	273	9.6	710	1 CDGT_THETU	P26827 thermomane
23	272.5	9.6	428	1 AMY1_ORYSA	P17654 oryza sativ
24	271.5	9.5	437	1 AMY3_ORYSA	P27939 oryza sativ
25	268.5	9.4	438	1 AMY1_HORVU	P00693 hordeum vul
26	268	9.4	711	1 CDGT_BACST	P13197 bacillus st
27	266.5	9.4	429	1 AMYB_HORVU	P04750 hordeum vul
28	266	9.3	435	1 AMYB_ORYSA	P27935 oryza sativ
29	262.5	9.2	427	1 AMY2_HORVU	P04063 hordeum vul
30	262	9.2	703	1 CDGT_BACCS2	P31146 bacillus sp
31	258.5	9.1	368	1 AMY3_HORVU	P04747 hordeum vul
32	257.5	9.0	437	1 AMY3_ORYSA	P27934 oryza sativ
33	253.5	8.9	494	1 AMY1_SACFI	P21567 saccharomyc

34	249	8.7	443	1 AMY2_ORYSA	P27935 oryza sativ
35	248	8.7	498	1 AMYB_ASAPW	Q02905 aspergillus
36	248	8.7	499	1 AMYB_ASAPW	Q02906 aspergillus
37	247	8.7	499	1 AMYB_ASAPW	P10529 aspergillus
38	245	8.6	499	1 AMYB_ASAPW	P10529 aspergillus
39	244	8.6	519	1 AMYB_ASAPW	O05884 streptomyc
40	242	8.5	445	1 AMY2_ORYSA	P27941 oryza sativ
41	238.5	8.4	498	1 AMY3_DICHT	P14899 dictyoglomu
42	236	8.3	581	1 AMY1_SCHPO	Q09840 schizosach
43	230.5	8.1	713	1 CDGT_PABPO	P31835 paenibacill
44	224.5	7.9	704	1 CDGT_BACCH	P27036 bacillus ch
45	224	7.9	624	1 AMY1_LIPKO	Q01117 lipomyces k

ALIGNMENTS

RESULT 1
ID AMY_BACST STANDARD, PRT, 549 AA.
AC P06279; Q45519;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-FEB-1996 (Rel. 33, last sequence update)
DT 15-MAR-2004 (Rel. 43, last annotation update)
DE Alpha-amylase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
DE glucanohydrolase).
GN AMYS.
OS Bacillus stearothermophilus.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.
OX NCBI_Taxid=1422;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 35-39.
RX MEDLINE=85234394; PubMed=3924897;
RA Nakajima K., Imanaka T., Aiba S.;
RT "Nucleotide sequence of the Bacillus stearothermophilus alpha-amylase
RT gene.";
RL J. Bacteriol. 163:401-406 (1985).
RN [2]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=DV5/PHI300.
RX MEDLINE=86008166; PubMed=3876333;
RA Ihara H., Sasaki T., Tsuboi A., Yamagata H., Tsukagoshi N., Ueda S.;
RT "Complete nucleotide sequence of a thermophilic alpha-amylase gene:
RT homology between prokaryotic and eukaryotic alpha-amylases at the
RT active sites.";
RL J. Biochem. 98:95-103 (1985).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=NZ-3;
RX MEDLINE=86195857; PubMed=3099417;
RA Gray G.L., Mainzer S.E., Rey M.W., Lamsa M.H., Kindle K.L.,
CA Carmona C., Reuquard C.;
RT "Structural genes encoding the thermophilic alpha-amylases of
RT Bacillus stearothermophilus and Bacillus licheniformis.";
RL J. Bacteriol. 166:635-643 (1986).
RN [4]
RP SEQUENCE FROM N.A.
RA Suominen I., Karp M., Lautamo J., Knowles J., Mantseelae P.;
RT "Recombinant alpha amylase of Bacillus stearothermophilus: cloning,
RT expression, and secretion by Escherichia coli.";
RL (in) Chaloupka J., Krumphanz V. (eds.);
RL Extracellular enzymes of microorganisms, pp.129-137, Plenum Press,
RL New York (1987).
RN [5]
RP SEQUENCE OF 1-122 FROM N.A., AND SEQUENCE OF 35-48.
RC STRAIN=DV-5;
RX MEDLINE=86059211; PubMed=2999073;
RA Tsukagoshi N., Iritani S., Sasaki T., Takemura T., Ihara H.,
ID Iida Y., Yamagata H., Ueda S.;
RT "Efficient synthesis and secretion of a thermophilic alpha-amylase by
RT protein-producing Bacillus brevis 47 carrying the Bacillus
RT stearothermophilus amylase gene.";
RL J. Bacteriol. 164:1182-1187 (1985).
RL

RN [6]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
 RX MEDLINE=21125602; PubMed=11226887;
 RA Stud D., Fujimoto Z., Takase K., Matsumura M., Mizuno H.;
 RT "Crystal structure of Bacillus stearotherophilus alpha-amylase:
 RL J. Biochem. 129:461-468(2001).
 CC possible factors determining the thermostability.";
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
 CC linkages in oligosaccharides and polysaccharides.
 CC -1- COFACTOR: Binds 3 calcium ions and 1 sodium ion per subunit.
 CC -1- SUBUNIT: Monomer.
 CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC EMBL; M11450; AAA22235.2; -;
 DR EMBL; X02769; CAA26547.1; -;
 DR EMBL; M57457; AAA22227.1; -;
 DR EMBL; M13255; AAA22241.1; -;
 DR PIR; A24436; A24436.
 DR PIR; A91999; ALBSF.
 DR PDB; 1HVX; 05-AUG-03.
 DR InterPro; IPR006589; Alp amyl cat sub.
 DR InterPro; IPR006047; Alp amyl cat.
 DR InterPro; IPR006046; Glyco_hydro_13.
 DR Pfam; PF00128; alpha-amylase_1.
 DR PRNRS; PR00110; ALPHAMYLASE.
 DR SMART; SM00642; Amy; 1.
 KW Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
 KW Signal; 3D-structure.
 FT CHAIN 1 34
 FT SIGNAL 1 34
 FT ACT_SITE 35 549 ALPHA-AMYLASE.
 FT ACT_SITE 272 272
 FT ACT_SITE 365 365
 FT METAL 139 139
 FT METAL 196 196
 FT METAL 218 218
 FT METAL 220 220
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 FT METAL 464 464
 FT CONFLICT 13 13
 FT CONFLICT 19 19
 FT CONFLICT 23 23
 FT CONFLICT 31 31
 FT CONFLICT 107 107
 FT CONFLICT 167 167
 FT CONFLICT 179 179
 FT CONFLICT 251 251
 FT CONFLICT 260 260
 FT CONFLICT 284 284
 FT CONFLICT 312 312
 FT CONFLICT 338 338
 FT CONFLICT 342 342
 FT CONFLICT 346 346
 FT CONFLICT 376 376
 FT CONFLICT 526 527
 FT CONFLICT 527 527
 FT CONFLICT 535 535
 D -> V (IN REF. 3).
 L -> W (IN REF. 3).
 L -> S (IN REF. 2 AND 3).
 P -> H (IN REF. 2 AND 5).
 A -> T (IN REF. 2 AND 3).
 T -> I (IN REF. 4).
 P -> N (IN REF. 2).
 S -> N (IN REF. 2, 3 AND 4).
 TNI -> RTL (IN REF. 4).
 D -> Y (IN REF. 2, 3 AND 4).
 M -> T (IN REF. 2 AND 3).
 T -> A (IN REF. 2 AND 3).
 R -> S (IN REF. 3).
 V -> N (IN REF. 3).
 V -> C (IN REF. 2 AND 3).
 WS -> RD (IN REF. 2).
 D -> G (IN REF. 2 AND 3).

SQ SEQUENCE 549 AA; 62670 MW; 3A2DD93A955E79D3 CRC64;
 Query March 97.6%; Score 2780; DB 1; Length 549;
 Beet Local Similarity 98.1%; Pred. No. 3.2e-190;
 Matches 504; Conservative 2; Mismatches 8; Indels 0; Gaps 0;
 QY 1 AAPNGTMOQFEYVLPDDGLTKVANEANNSSLSGLTLMPLPAVKGRSDVGVY 60
 DB 35 AAPNGTMOQFEYVLPDDGLTKVANEANNSSLSGLTLMPLPAVKGRSDVGVY 94
 QY 61 DLYLGEFNQKGTARTKGTAKQYLQAIQAHAAGQVADVDFDHGAGDGEWDVAVE 120
 DB 95 DLYLGEFNQKGTARTKGTAKQYLQAIQAHAAGQVADVDFDHGAGDGEWDVAVE 154
 QY 121 VNPSDRNGEISGTQIQAMTKFDFPGKNTYSSFKRWYHFDGVWDSEKLSRIYFRG 180
 DB 155 VNPSDRNGEISGTQIQAMTKFDFPGKNTYSSFKRWYHFDGVWDSEKLSRIYFRG 214
 QY 181 IGRKMDWEVDTEFNQVYIMADLDMHPYVTELKMGKMYVNTNIDGFRIDAVGHK 240
 DB 215 IGRKMDWEVDTEFNQVYIMADLDMHPYVTELKMGKMYVNTNIDGFRIDAVGHK 274
 QY 241 FSEFPDMLSYVRSQGRPLFTVGEWYSDINKLNNYITKTGWTSLDAPLANKFYTASK 300
 DB 275 FSEFPDMLSDVRSQGRPLFTVGEWYSDINKLNNYITKTGWTSLDAPLANKFYTASK 334
 QY 301 SGGAFAVATLNTLTKDQPLATFVDNHDTEFGQALQSWDPWFEPFLAVAFILTRQEG 360
 DB 335 SGGFEDMTLNTLTKDQPLATFVDNHDTEFGQALQSWDPWFEPFLAVAFILTRQEG 394
 QY 361 YPCVFYGVYGIPOYNIPSLKSKIDPLLIARDVATQHDYDHSIDILGTEGGEIEKP 420
 DB 395 YPCVFYGVYGIPOYNIPSLKSKIDPLLIARDVATQHDYDHSIDILGTEGGEIEKP 454
 QY 421 GSGLAALITDGPQSGKMYTVGKHAKVFDYLTNRSDYTTINSNGEGRKVGSGISVW 480
 DB 455 GSGLAALITDGPQSGKMYTVGKHAKVFDYLTNRSDYTTINSNGEGRKVGSGISVW 514
 QY 481 VPRKTVSTIARPIITRPMTGEFVRMTPEPRLVAN 514
 DB 515 VPRKTVSTIARPIITRPMTGEFVRMTPEPRLVAN 548
 RESULT 2
 ID AMT6_BACS7 STANDARD; PRT; 518 AA.
 AC P19571;
 DT 01-FEB-1991 (rel. 17, Created)
 DT 01-FEB-1991 (rel. 17, Last sequence update)
 DT 10-OCT-2003 (rel. 42, Last annotation update)
 DE Glucan 1,4-alpha-maltohexosidase precursor (EC 3.2.1.98) (66-amylase)
 DE (Maltotetraose-producing amylase) (Exo-maltohexoamylase).
 OS Bacillus sp. (strain 707).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 NCBI_TaxID=1416;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 34-36.
 RX MEDLINE=88162814; PubMed=3258152;
 RA Tsukamoto A., Kimura K., Ishii Y., Takano T., Yamane K.;
 RT "Nucleotide sequence of the maltotetraose-producing amylase gene from
 RT an alkalophilic Bacillus sp. #707 and structural similarity to
 RT liquefying type alpha-amylases.";
 RL Biochem. Biophys. Res. Commun. 151:25-31(1988).
 CC -1- CATALYTIC ACTIVITY: Hydrolysis of 1,4-alpha-D-glucosidic linkages
 CC in amylicaceous polysaccharides so as to remove successive
 CC maltotetraose residues from the non-reducing chain ends.
 CC -1- COFACTOR: Binds 2 calcium ions and 1 sodium ion per subunit (By
 CC similarity).
 CC -1- PATHWAY: Starch degradation.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
 CC
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 CC or send an email to license@ebi.ac.uk).

CC EMBL; M18862; AAA22231.1; -
 DR PIR; A27705; A27705.
 DR HSP; P06278; 1VCS.
 DR InterPro; IPR006589; Alp_amy1_cat_sub.
 DR InterPro; IPR006047; Alp_amy1_cat.
 DR InterPro; IPR006046; Glyco_hydro_13.
 DR Pfam; PF00128; alpha-amy1ase; 1.
 DR PRINTS; PR00110; ALPHAMYLASE.
 DR SMART; SM00642; Amy; 1.
 KM Hydrolase; Glycosidase; Carbohydrate metabolism; signal.
 FT SIGNAL 1 33
 FT CHAIN 1 33
 FT ACT_SITE 269 269 GLUCAN 1,4-ALPHA-MALTOHEXAOSIDASE.
 FT ACT_SITE 273 273 BY SIMILARITY.
 FT ACT_SITE 366 366 BY SIMILARITY.
 FT METAL 139 139 CALCIUM 1 (BY SIMILARITY).
 FT METAL 196 196 CALCIUM 2 AND SODIUM (BY SIMILARITY).
 FT METAL 219 219 CALCIUM 2 (VIA CARBONYL OXYGEN) (BY
 FT METAL 219 219 SIMILARITY).
 FT METAL 221 221 CALCIUM 2 AND SODIUM (BY SIMILARITY).
 FT METAL 232 232 CALCIUM 1 AND SODIUM (BY SIMILARITY).
 FT METAL 238 238 CALCIUM 1 AND SODIUM (BY SIMILARITY).
 FT METAL 240 240 CALCIUM 2 (BY SIMILARITY).
 FT METAL 242 242 CALCIUM 2 (BY SIMILARITY).
 FT METAL 273 273 CALCIUM 1 (VIA CARBONYL OXYGEN) (BY
 FT METAL 273 273 SIMILARITY).
 SQ SEQUENCE 518 AA; 59009 MM; 3A961E21612682C4 CR664;

Query Match 65.8%; Score 1874.5; DB 1; Length 518;
 Best Local Similarity 67.2%; Pred. No. 6.6e-126;
 Matches 321; Conservative 76; Mismatches 80; Indels 1; Gaps 1;

QY 5 NCTMMQPEWYLPDGTMTKXANENNNSSGTTALMPPRYKGTSSRDVGYVYDLYD 64
 DB 39 NGTMMQPEWYLPDGTMTKXANENNNSSGTTALMPPRYKGTSSRDVGYVYDLYD 98
 QY 65 LGFENQKGTVRTYGTGAQYLOIAQAHAAGQVADVYFDHKGAGDGTWDAVEVNP 124
 DB 99 LGFENQKGTVRTYGTGAQYLOIAQAHAAGQVADVYFDHKGAGDGTWDAVEVNP 158
 QY 125 DRNGEISGTIOAQWTKPPRGNGYTSFKRWYHFDVVDDESRKL-SRTYKRGYIGK 183
 DB 159 NRGQEVYGTETLEAWRFPFGNGHSSFKRWYHFDVVDDESRKL-SRTYKRGYIGK 218
 QY 184 AMDMEVDTEGNVYDYLMDHDEVEVTEKMGKWTNTNIDGRLDAVKIKESF 243
 DB 219 AMDMEVDTEGNVYDYLMDHDEVEVTEKMGKWTNTNIDGRLDAVKIKESF 278
 QY 244 FPMWLSYVSQGTSLPTVGEYSYDINKLHYITTDGTMLEPDAFLNRYTSKSG 303
 DB 279 TRDMINHSATGKKNFAVAEFKNDLGAIENTLOQTNHNSHVPDPLVNLNYSKSG 338
 QY 304 AFPMRTIMNTLMKDOPTLAVTFVDNHTDEPQALQSWDPFVKPLAVAFILTRQGYPC 363
 DB 339 NYMNRIMFNCTVYQRRPASHAVTFVDNHDQSPREALSPFEMFKPLAVALTITREGYVS 398
 QY 364 VFGVDYVIGPQVNTIBSKKIDPLILARDYAVGTHVDLHSDIIGMREGTEKPSG 423
 DB 399 VFGVDYVIGPQVNTIBSKKIDPLILARDYAVGTHVDLHSDIIGMREGTEKPSG 458
 QY 424 LAALLITDPPGSGSWMYVGKOHAKVFPYDLGNRSDVTINSQDMGKFXNKGSGSVYV 481
 DB 459 LAALLITDPPGSGSWMYVGKOHAKVFPYDLGNRSDVTINSQDMGKFXNKGSGSVYV 516

RESULT 3

AMY BACLI STANDARD; PRT; 512 AA.
 ID AMY BACLI
 AC P06278; Q84171;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Alpha-amy1ase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
 DE glucanohydrolase) (BLA).
 GN AMYS OR AMYL.
 OS Bacillus licheniformis.
 CX Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 NCBI Taxid=1402;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 27811.
 RX MEDLINE=86111694; PubMed=2418011;
 RA Yuki T., Nomura T., Tezuka H., Teuboi A., Yamagata H.,
 RA Tsukagoshi N., Ueda S.;
 RT "Complete nucleotide sequence of a gene coding for heat- and
 RT pH-stable alpha-amy1ase of Bacillus licheniformis: comparison of the
 RT amino acid sequences of three bacterial liquefying alpha-amy1ases
 RT deduced from the DNA sequences."
 RL J. Biochem. 98:1147-1156(1985).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86195857; PubMed=3009417;
 RA Gray G.L., Mainzer S.E., Rey M.W., Lamsa M.H., Kindle K.L.,
 RA Carmona C., Requadt C.;
 RT "Structural genes encoding the thermophilic alpha-amy1ases of
 RT Bacillus stearotherophilus and Bacillus licheniformis."
 RL J. Bacteriol. 166:635-643(1986).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Shaboshvili M., Zisel A.A., Ghaemi N., Pourbaeei A.A.;
 RT "An unusual DNA sequence encoded a hyperthermostable alpha-amy1ase.";
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 1-104 FROM N.A.
 RX MEDLINE=8418455; PubMed=6609154;
 RA Stephens M.A., Ortlepp S.A., Ollington J.F., McConnell D.J.;
 RT "Nucleotide sequence of the 5' region of the Bacillus licheniformis
 RT alpha-amy1ase gene: comparison with the B. amy1oliquefaciens gene";
 RL J. Bacteriol. 158:369-372(1984).
 RN [5]
 RP SEQUENCE OF 1-29 FROM N.A.
 RX MEDLINE=89213924; PubMed=2540150;
 RA Lacle B.M., Chambliss G.H., McConnell D.J.;
 RT "Bacillus licheniformis alpha-amy1ase gene, amy1, is subject to
 RT promoter-independent catabolite repression in Bacillus subtilis";
 RL J. Bacteriol. 171:2435-2442(1989).
 RN [6]
 RP SEQUENCE OF 30-47.
 RX MEDLINE=82098050; PubMed=6172418;
 RA Kuhn H., Fietzek P.P., Lampen J.O.;
 RT "N-terminal amino acid sequence of Bacillus licheniformis
 RT alpha-amy1ase: comparison with Bacillus amy1oliquefaciens and
 RT Bacillus subtilis enzymes.";
 RL J. Bacteriol. 149:372-373(1982).
 RN [7]
 RP MAPPING OF SUBSTRATE-BINDING SITE.
 RX MEDLINE=21992788; PubMed=11997021;
 RA Kandra L., Gyeant G., Remenyik J., Hovanaszi G., Liptak A.;
 RT "Action pattern and substrate mapping of Bacillus licheniformis
 RT alpha-amy1ase (BLA) with modified maltotriosecarbohydrate substrates.";
 RL PEBB Lett. 518:79-82(2002).
 RN [8]
 RP MUTAGENESIS OF HIS-64; HIS-162; HIS-276; HIS-322; HIS-435 AND HIS-479.
 RC STRAIN=ATCC 6598;
 RX MEDLINE=90368748; PubMed=2394736;
 RA Declerck N., Joyet P., Galliard C., Masson J.M.;
 RT "Use of amber suppressors to investigate the thermostability of
 RT Bacillus licheniformis alpha-amy1ase. Amino acid replacements at 6
 RT histidine residues reveal a critical position at His-123.";

QY 185 MDWEVDTEGNGYDYLMTADLMDHPEVYTELKNWGYVNTTNDGFRIDAVKIKRSEF 244
 DB 213 MDWEVSSSENGYDYLMTADVDYDHPDVAETKKGIVYAMELSDGFRIDAAKIKRSEF 272
 QY 245 PDMLSVYRSGTQKGLFTVGEYWSYDINKLHNITKTDGMSLFPDAPLHNKFTYASKSGA 304
 DB 273 RDWQARQATGKGMFTVAEYWNQNNAGLENYLNTKTSFNSGVDFPDPHFLQAASSGGG 332
 QY 305 FDMRTMTNTLMKQOPTLATFVNDHTEPQALQSWNDPWFKLALAFILTRQEGPCV 364
 DB 333 YDMRLDGTGVVSRHPEKAVTFVENHDTQPGQSLSTVQTFKPLAVALITRESGPV 392
 QY 365 FYGDYVGI-----PQYNIPSLKSKIDPLLIARDYAYGTHDHSDIIGWTEGTEKP 420
 DB 393 FYGDYVGIKTSKPK-EIPLSDKNIEPIKAKREYAYGQHDIIDHPVIGTRGDSAA 451
 QY 421 GSGLAALITDGPQSKMYVQKQAKVFDLTGNSRTYTINDGGEFKNGGSVW 480
 DB 452 KSGLAALITDGPQSKMYVQKQAKVFDLTGNSRTYTINDGGEFKNGGSVW 511
 QY 481 VPR 483
 DB 512 VQK 514
 RESULT 5
 AMY2_SALTY STANDARD; PRT; 494 AA.
 ID AMY2_SALTY STANDARD; PRT; 494 AA.
 AC P26613;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Cytoplasmic alpha-amylase (EC 3.2.1.1) (1/4-alpha-D-glucan
 DE glucanhydrolase).
 GN AMYA OR STM1963.
 OS Salmoneella typhimurium.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Salmoneella.
 OX NCBI_TaxID=602;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SUM1103;
 RX MEDLINE=93015717; PubMed=1400215;
 RA Raha M., Kawagishi I., Mueller V., Kihara M., Macnab R.M.;
 RT "Escherichia coli produces a cytoplasmic alpha-amylase, AmyA";
 RL J. Bacteriol. 174:6644-6652(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LT2 / SGSC1412 / ATCC 700720;
 RX MEDLINE=21534948; PubMed=11677609;
 RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
 RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
 RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
 RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
 RA Waterston R., Wilson R.K.;
 RT "Complete genome sequence of Salmoneella enterica serovar Typhimurium
 RT LT2";
 RL Nature 413:852-856(2001).
 RN [3]
 RP SEQUENCE OF 1-6 FROM N.A.
 RC STRAIN=SUM1103;
 RX MEDLINE=92407478; PubMed=1527488;
 RA Kawagishi I., Mueller V., Williams A.W., Irikura V.M., Macnab R.M.;
 RT "Subdivision of flagellar region III of the Escherichia coli and
 RT Salmoneella typhimurium chromosomes and identification of two
 RT additional flagellar genes";
 RL J. Gen. Microbiol. 138:1051-1065(1992).
 RN [4]
 RP SEQUENCE OF 476-494 FROM N.A.
 RX MEDLINE=93181452; PubMed=8371104;
 RA Raha M., Kihara M., Kawagishi I., Macnab R.M.;
 RT "Organization of the Escherichia coli and Salmoneella typhimurium
 RT chromosomes between flagellar regions Itra and Iiib, including a

RT large non-coding region."
 RL J. Gen. Microbiol. 139:1401-1407(1993).
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
 CC linkages in oligosaccharides and polysaccharides.
 CC -1- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
 CC -1- SUBUNIT: Monomer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: Belongs to family 13 of glycoyl hydrolases.
 CC
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 CC
 CC EMBL, L01643; AAA27110.1; -
 DR EMBL, AE008787; AAL20875.1; -
 DR EMBL, M85241; AAA27079.1; -
 DR EMBL, L13280; AAA71970.1; -
 DR PIR, B45238; 345738.
 DR HSSP, P06278; 1VUS.
 DR StyGene, SG10011; AMYA.
 DR InterPro, IPR006869; Alp_amyl_cat_sub.
 DR InterPro, IPR006047; Alpha_amyl_cat.
 DR Pfam, PF00128; alpha-amylase; 1.
 DR SMART, SMO0642; Amy; 1.
 KW Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
 KM Complete proteome.
 FT ACT_SITE 235..235 BY SIMILARITY.
 FT ACT_SITE 265..265 BY SIMILARITY.
 FT ACT_SITE 332..332 BY SIMILARITY.
 FT METAL 104..104 CALCIUM (BY SIMILARITY).
 FT METAL 239..239 CALCIUM (VIA CARBOXYL OXYGEN) (BY
 FT SIMILARITY).
 FT
 FT CONFLICT 462..462 L -> S (IN REF. 1).
 SQ SEQUENCE 494 AA; 56522 MW; 5C1E862FEDD5C47C CRC64;
 Query Match 39.0%; Score 1110.5; DB 1; Length 494;
 Best Local Similarity 44.0%; Pred. No. 1.2e-71;
 Matches 216; Conservative 82; Mismatches 176; Indels 17; Gaps 5;
 QY 5 NGNMVQFEWYPPDDGTLTKVANEANNISGITALMTPAYKTSRS-DVGYGVYDLY 63
 DB 3 NPTLQYFHWYPPDGSKLSELAEPADGINDIGIMWVLPKCKASGSGYGVGYTYDLY 62
 QY 64 DLGEFNQKGTVRKYGTAKQYLOAIQAAGMAYADVPDHRGADGTEWDAVEYNP 123
 DB 63 DLGEFNQKGTITKYGDKRQLTALDKNNIAVLDDVVVHKKGADKEKIRVQRYNQ 122
 QY 124 SPRNGEISTYQIOMTKDFEGRGNTYSSFKRWYHFDGVWDGSRKLSRYKRG--I 181
 DB 123 DDTQIDENITIECKRTTPRARGYSNFIWDYHCSGIDHINPBDGIFKIVNDYT 182
 QY 182 GRAMWEVDTEGNGYDYLMTADLMDHPEVYTELKNWGYVNTTNDGFRIDAVKIKF 241
 DB 183 GGMNDQVDENGENEDYLMGENIDPRNHAVTEIKYMARWMEQTHCGFRIDAVKHPA 242
 QY 242 SFPEDLSTYRSGTQKGLFTVGEYWSYDINKLHNITKTDGMSLFPDAPLHNKFTASKS 301
 DB 243 WFKEMIEHVOAVAPPLFVAEYVSHVEDKQYIYDQDGTMLFDAPLQMKFEASRQ 302
 QY 302 GGAFDRTMTNTLMKQOPTLATFVNDHTEPQALQSWNDPWFKLALAFILTRQEGY 361
 DB 303 GAEYDWRHIFGTGLVADPFAVTLVANHDTQPLALEAPVPEPKPLAYALILRENGV 362
 QY 362 PCFYGYDYGIPI-----QYNIPSLKSKIDPLLIARDYAYGTHDHSDIIG 410
 DB 363 PSVFYFDLYGASVEYSGENETCRVDMPT-NQLRLLIARORFAHGQTLFDPNCA 421
 QY 411 WTEGTEKPSGIALITDGPQSKMYVQKQAKVFDLTGNSRTYTINDGGEFKNGGSVW 470

DB 422 FSRSGTEENP--GCVVVLSNGDDGKTLILLGDNVANKTWBPLGNBDEYVVTNDGEATF 475
 QY 471 KMGGSVSVMV 481
 DB 480 FCNAGSVSMV 490

RESULT 6
 AMY2_ECOLI STANDARD; PRT; 495 AA.
 ID AMY2_ECOLI
 AC P26612; P78072;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Cytoplasmic alpha-amylase (EC 3.2.1.1) (1,4-alpha-D-glucan
 glucanohydrolase).
 GN AmyA OR B1927.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_Taxid=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Jall;
 RC MEDLINE=93015717; PubMed=1400215;
 RA Raha M., Kawagishi I., Mueller V., Kihara M., Macnab R.M.;
 RT "Escherichia coli produces a cytoplasmic alpha-amylase, AmyA.";
 RL J. Bacteriol. 174:6644-6652(1992).
 RP [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12 / MG1655;
 RC MEDLINE=97426517; PubMed=9278503;
 RA Blatner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12.";
 RL Science 277:1453-1474(1997).
 RN [3]
 RN SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RC MEDLINE=97251358; PubMed=9097040;
 RA Itoh T., Alba H., Baba T., Fujita K., Hayashi K., Inada T.,
 RA Isono K., Kasai H., Kimura S., Kikukawa M., Kikugawa M.,
 RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
 RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T.,
 RA Saito N., Sampaio G., Seki Y., Sivasubramanian S., Tagami H.,
 RA Takeda J., Takemoto K., Wada C., Yamamoto Y., Horikuchi T.;
 RT "A 460-kb DNA sequence of the Escherichia coli K-12 genome
 corresponding to the 40.1-50.0 min region on the linkage map.";
 RL DNA Res. 3:379-392(1996).
 RN [4]
 RN SEQUENCE OF 1-5 FROM N.A.
 RC STRAIN=Jall;
 RC MEDLINE=92407478; PubMed=1527488;
 RA Kawagishi I., Mueller V., Williams A.W., Irikura V.M., Macnab R.M.;
 RT "Subdivision of flagellar region III of the Escherichia coli and
 RT additional flagellar genes.";
 RL J. Gen. Microbiol. 138:1051-1065(1992).
 RN [5]
 RN SEQUENCE OF 475-495 FROM N.A.
 RC STRAIN=Jall;
 RC MEDLINE=93381452; PubMed=8371104;
 RA Raha M., Kihara M., Kawagishi I., Macnab R.M.;
 RT "Organization of the Escherichia coli and Salmonella typhimurium
 RT chromosomes between flagellar regions IIIa and IIb, including a
 RT large non-coding region.";
 RL J. Gen. Microbiol. 139:1401-1407(1993).
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
 CC linkages in oligosaccharides and polysaccharides.
 CC -2- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
 CC -1- SUBUNIT: Monomer (By similarity).

CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
 CC -----
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DR EMBL; L01642; AAA23810.1; -;
 DR EMBL; AE000285; AAC74994.1; -;
 DR EMBL; D90833; BA15755.1; -;
 DR EMBL; M85240; -; NOT ANNOTATED_CDS.
 DR EMBL; L13279; AAA82575.1; -;
 DR PIR; D64956; A45738.
 DR HSP; P06278; 1YUS.
 DR EcoGene; Egl1387; amyA.
 DR InterPro; IPR006589; Alp_amy1_cat_sub.
 DR InterPro; IPR006047; Alpha_amy1_cat.
 DR Pfam; PF00128; alpha-amylase; 1.
 DR SMART; SMC0642; Amyy; 1.
 KW Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
 KM Complete proteome.
 FT ACT_SITE 235
 FT ACT_SITE 235
 FT ACT_SITE 265
 FT ACT_SITE 332
 FT METAL 104
 FT METAL 239

FT CONFLICT 19
 FT CONFLICT 109
 FT CONFLICT 149
 FT CONFLICT 234
 SQ SEQUENCE 495 AA; 56639 MW; 26AFF6797DDA54d6 CRC64;

Query Match 37.7%; Score 1074.5; DB 1; Length 495;
 Best Local Similarity 42.9%; Pred. No. 4,3e-69;
 Matches 210; Conservative 83; Mismatches 182; Indels 15; Gaps 4;

QY 5 NGTMOGYEYVLPDDGLTMTKTVANEANNTSSLGITLMLPAPYKTSRS-DVGYGYDLY 63
 DB 3 NPTLQCFHMYEYEGGLMPELBRADGFNDIDINWVWLPAYKAGSGYSGVSDYDLF 62
 QY 64 DLGSENGKGVTRTKYTGKAYLOAIOAHNAAGQYVADYVFDHKGAGDGTWDAVEVNP 123
 DB 63 DLGSEFDKGSIPKYGKQALNIDLKNDIAVLVDVYVNHKMGADKEAARQRYNA 122
 QY 124 SDRQNEISGYLOCAWTKFPDPFGNGNTYSSPKRWYHFDGVDMDESKTSRIYKFRG-I 181
 DB 123 DRRQIDBEIEEGCGWTRYPFAPRAGQYSQFIDPFKFSIGDIHENDEDEGIFKIVNDYT 182
 QY 182 GKAMDWEVDNENGVYDILAMADLDMDHREYVTELKMGSKYVNTTINDGRLDVAKHIXF 241
 DB 183 GEGANDVDDELGNFDLMBENIDFRNHAATBEIKIARWVMEQTCODGRDLDAVXIPA 242
 QY 242 SFPDMLSYVRSQYKGLFTVGEWYSYDINKLNNYIKTKDTGMSLFDAPLANKFYTASKS 301
 DB 243 WFKYEWIEHVQEVAPKFLFVAYEWSHEVDKLTQYIDQVGGKMTLFPAPLQMKFHEASRM 302
 QY 302 GGADFMRTLMTNLMKQOPLTAVFVNNDHTEPQALQSVWDMPEKRLAFAFLITREGY 361
 DB 303 GRDYDMQIFGTGLVENDPFAVTLVANHDTQPOLAEVBEPEKFLAYALILIRENGV 362
 QY 362 PCVFYGYGYPQYNIPS-----LKSXIDPLLIARDVAYVGTQHDYLDHSDIIGW 411
 DB 363 PSVFPDLYGAHYDVGDDQGYPIDWPITIEQDELILARQFAHGVQTLFFDHPNCIAF 422
 QY 412 TREGELEPSSGLAALLITDGGGSKMYVKGQAHGKFFYLLTNGRSDTYVINSGWGEFK 471
 DB 423 SRSQTEDEP--GCVVVLSNGDDGKTHLGENYANKTWBPLGNRQREVVTDENGEATFF 480

QY 472 VNGSVSVWV 481
 DB 481 CNGSVSVWV 490
 RESULT 7
 CDGT_BACSP STANDARD; PRT; 713 AA.
 ID CDGT_BACSP PRT; 713 AA.
 AC P30921.
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Cyclomaltodextrin glucanotransferase precursor (EC 2.4.1.19)
 GN (Cyclodextrin-glucosyltransferase) (Gltase).
 OS Bacillus sp. (strain 17-1).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 CX NCBI_TaxId=1409;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 28-44.
 RA MEDLINE=90257592; PubMed=2534600; Kudo T, Horikoshi K;
 RA Kaneo T., Song K.B., Hamamoto T., Kudo T, Horikoshi K;
 RT "Construction of a chimeric series of Bacillus cyclomaltodextrin
 RT glucanotransferases and analysis of the thermal stabilities and pH
 RT optima of the enzymes."
 RL J. Gen. Microbiol. 135:1447-1457(1989).
 CC -1- CATALYTIC ACTIVITY: Degrades starch to cyclodextrins by formation
 CC of a 1,4-alpha-D-glucosidic bond.
 CC -1- COFACTOR: Binds 2 calcium ions per subunit (By similarity).
 CC -1- SUBUNIT: Monomer.
 CC -1- MISCELLANEOUS: COTASE MAY CONSIST OF TWO PROTEIN DOMAINS: THE ONE
 CC IN THE AMINO-TERMINAL SIDE CLEAVES THE ALPHA-1,4-GLUCOSIDIC BOND
 CC IN STARCH, AND THE OTHER IN THE C-TERMINAL SIDE CATALYZES OTHER
 CC ACTIVITIES, INCLUDING THE RECONSTITUTION OF AN
 CC ALPHA-1,4-GLUCOSIDIC LINKAGE FOR CYCLIZING THE
 CC MALTOOLIGOSACCHARIDE PRODUCED.
 CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
 CC
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 CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
 CC or send an email to license@sib-sib.ch).
 CC
 CC EMBL: M28053; AAA2310.1; .
 CC HSSP: P43379; 1CDG.
 DR InterPro: IPR006589; A1D_amy1_cat_sub.
 DR InterPro: IPR006048; Alpha_amy1_C.
 DR InterPro: IPR006047; Alpha_amy1_cat.
 DR InterPro: IPR002044; CBD_4.
 DR InterPro: IPR006046; Glyco_hydro_13.
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR002909; IPT_TIG.
 DR Pfam: PF00128; alpha-amy1ase; 1.
 DR Pfam: PF02806; alpha-amy1ase_C; 1.
 DR Pfam: PF06886; CBM_20; 1.
 DR Pfam: PF01833; TIG; 1.
 DR PRINTS; PR00110; ALPHAMYLASE.
 DR PRODOM; PD001568; CBD_4; 1.
 DR SMART; SM00642; Amyy; 1.
 DR SMART; SM00632; Amyy_C; 1.
 KM Transferase; Glycosyltransferase; Calcium-binding; Signal.
 FT SIGNAL; 1
 FT CHAIN; 28
 FT DOMAIN; 28
 FT DOMAIN; 166
 FT DOMAIN; 229
 FT DOMAIN; 230
 FT DOMAIN; 433
 FT DOMAIN; 434
 FT DOMAIN; 522
 FT DOMAIN; 523
 FT DOMAIN; 610
 FT ACT_SITE; 256
 BY SIMILARITY.

FT ACT_SITE 284 284 BY SIMILARITY.
 FT ACT_SITE 355 355 BY SIMILARITY.
 FT METAL 54 54 CALCIUM 2 (BY SIMILARITY).
 FT METAL 56 56 CALCIUM 2 (VIA CARBONYL OXYGEN) (BY
 FT METAL 59 59 SIMILARITY).
 FT METAL 60 60 CALCIUM 2 (BY SIMILARITY).
 FT METAL 60 60 CALCIUM 2 (BY SIMILARITY).
 FT METAL 78 78 CALCIUM 2 (VIA CARBONYL OXYGEN) (BY
 FT METAL 80 80 SIMILARITY).
 FT METAL 166 166 CALCIUM 1 (BY SIMILARITY).
 FT METAL 217 217 CALCIUM 1 (VIA CARBONYL OXYGEN) (BY
 FT METAL 226 226 SIMILARITY).
 FT METAL 260 260 CALCIUM 1 (BY SIMILARITY).
 FT METAL 260 260 CALCIUM 1 (VIA CARBONYL OXYGEN) (BY
 FT METAL 260 260 SIMILARITY).
 SQ DISULFID 70 77 BY SIMILARITY.
 FT SEQUENCE 713 AA; 77389 MW; D13AEF6C507FE45E CRC64;
 Query Match 11.0%; Score 313; DB 1; Length 713;
 Best local Similarity 24.7%; Pred. No. 8.6e-15;
 Matches 135; Conservative 82; Mismatches 188; Indels 142; Gaps 29;
 QY 19 DQTL-----WTKYANRNN--LSSGTLALMLPP---AYKTSRSDVGVGVLD 62
 DB 67 DDTCTNRLRYCGSDWGGIINKINDYLTGMEVTAIWSQPVNTYSVINYSGVNNYHG 126
 QY 63 YDGEFNQKGVTRTKYQYQYLOAIAAQAQVADVVDHKGGA--DGEWDAVE 120
 DB 127 YNADPK---INPAGTIDADQNLIAPAAKNIKIVITIDFAPNHTSPASLDQSPFAENGK 183
 QY 121 VNPSDRNQSISGTYOIAATKDFPGRGNITSSFKRKYRHDGVWDSRKLRIYKRG 180
 DB 184 LYNGRDE--GGY-----INDTNLF--HNGGDFG----- 211
 QY 181 IGMAMWEVDTEGNYDYLM--YADLMDHEVETELKMGKXYVTNTIDGFRDLAVGI 239
 DB 212 -----TTENGIKYKYLADLNHNSTVDYTLKAIKRWLD-LIDGIRMDAVGEM 261
 QY 240 KFSFEDWLSYVRSQTKPLFTVGEYSYDINKL--HNYITDGTMSLFPAPLHKKYT 297
 DB 262 PFGWQKSPMATVNNY--KVFTEGE--WELGVNEVAENKFAVNSGMSLLDPRFAQXK 318
 QY 298 ASK--SGCAFMDKTLMTNL-----MKDPTLAVFVNDHDE--PGALGSWDPWFK 347
 DB 319 VFQNDTNNYGLSMLEGSATDYAQMEDQ---VFIDHDERFHNSNANRKLQ--- 371
 QY 348 PLAYAFILTRQEGYPCVFYGDYGIPOY-----NIFS-----LKSRIPL 387
 DB 372 --ALAFILTR--SRGVPAI-----YGTQVYSGNDPDRARIPSFSTTAYGVSKLA 424
 QY 388 LIRRDYAYGTQDYDHDHDIIGMTREGE-----KPGSLALITDGPQSGKW 437
 DB 425 KSNPAIYVGTQDERNDVLYERKFFNNYAVIANRNVTSASITGLVSLPAGS-- 482
 QY 438 MYVKGHAKGVFYDLGN--RSDPTVINSNGME--FKVNGSVSVW--VERKTVSTIAR 492
 DB 483 -----YDVLGGLNGNLIVSGGSASIFTLAAGTAWQYTTAAPTIGHV 531
 QY 493 -PITTRP 498
 DB 532 GPMWAKP 538
 RESULT 8
 AMYB_PABPO STANDARD; PRT; 1196 AA.
 ID AMYB_PABPO
 AC P21543;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Beta/alpha-amy1ase precursor [Includes: Beta-amy1ase (EC 3.2.1.2);
 DE Alpha-amy1ase (EC 3.2.1.1)].

OS Paenibacillus polymyxa (Bacillus polymyxa).
 OC Bacteria; Firmicutes; Bacillales; Paenibacillaceae; Paenibacillus.
 NCBI_TaxID=1406;
 RN [1]
 RP SEQUENCE OF 1-936 FROM N.A., AND PARTIAL SEQUENCE.
 RC STRAIN=72;
 RX MEDLINE=87165765; PubMed=2435707;
 RA Kawazu T., Nakamshi Y., Uozumi N., Sasaki T., Yamagata H.,
 RT Tsukagoshi N., Uda S.;
 RT "Cloning and nucleotide sequence of the gene coding for enzymatically
 active fragments of the Bacillus polymyxa beta-amylose.";
 RL J. Bacteriol. 169:1564-1570(1987).
 RN [2]
 RP SEQUENCE OF 689-1196 FROM N.A., AND PARTIAL SEQUENCE.
 RC STRAIN=72;
 RX MEDLINE=89123046; PubMed=2464578;
 RA Uozumi N., Sakurai K., Sasaki T., Takekawa S., Yamagata H.,
 RT Tsukagoshi N., Uda S.;
 RT "A single gene directs synthesis of a precursor protein with beta-
 and alpha-amylose activities in Bacillus polymyxa.";
 RL J. Bacteriol. 171:375-382(1989).
 RN [3]
 RP SEQUENCE OF 1-776 FROM N.A.
 RC STRAIN=ATCC 8523;
 RX MEDLINE=87231094; PubMed=2438660;
 RA Rhodes C., Strasser J., Friedberg F.;
 RT "Sequence of an active fragment of B. polymyxa beta amylose.";
 RL Nucleic Acids Res. 15:3934-3934(1987).
 RN [4]
 RP DISULFIDE BOND, AND MUTAGENESIS OF CYSTEINE RESIDUES.
 RX MEDLINE=91215008; PubMed=1827035;
 RA Uozumi N., Matsuda T., Tsukagoshi N., Uda S.;
 RT "Structural and functional roles of cysteine residues of Bacillus
 polymyxa beta-amylose.";
 RL Biochemistry 30:4594-4599(1991).
 CC -1- FUNCTION: THE PRECURSOR PROTEIN IS PROTEOLYTICALLY CLEAVED TO
 PRODUCE MULTIFORM BETA-AMYLASES AND A 48 KDa ALPHA-AMYLASE AFTER
 SECRETION.
 CC -1- CATALYTIC ACTIVITY: Hydrolysis of 1,4-alpha-glucosidic linkages in
 polysaccharides so as to remove successive maltose units from the
 non-reducing ends of the chains.
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
 linkages in oligosaccharides and polysaccharides.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: In the N-terminal section; belongs to family 14 of
 glycosyl hydrolases.
 CC -1- SIMILARITY: In the C-terminal section; belongs to family 13 of
 glycosyl hydrolases.
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 or send an email to license@isb-sib.ch).
 CC EMBL, M15817; AAA65446.1; -
 DR EMBL, Y00150; AAG68344.1; -
 DR PIR, A29130; A29130.
 DR HSSP, P36924; 1892.
 DR InterPro, IPR006589; A1p_aml_cat_sub.
 DR InterPro, IPR006048; Alpha_aml1_C.
 DR InterPro, IPR006047; Alpha_aml1_cat.
 DR InterPro, IPR005085; CBM_25.
 DR InterPro, IPR006046; Glyco_hydro_13.
 DR InterPro, IPR001554; Glyco_hydro_14.
 DR Pfam, PF00128; alpha-amylose_1.
 DR Pfam, PF02806; alpha-amylose_C_1.
 DR Pfam, PF03423; CBM_25_2.
 DR Pfam, PF01373; Glyco_hydro_14_1.
 DR PRINTS, PR00110; ALPHAMYLASE.
 DR PRINTS, PR00750; BETAMYLASE.

DR SMART, SM00642; Amy, 1.
 DR SMART, SM00632; Amy_C, 1.
 DR PROSITE, PS00506; BETA_AMYLASE_1; 1.
 DR PROSITE, PS00679; BETA_AMYLASE_2; 1.
 DR Multifunctional enzyme: Hydrolase; Glycosidase; Signal;
 KM Polysaccharide degradation; Repeat.
 KM SIGNAL 1 35
 FT CHAIN 36 1196
 FT DOMAIN 36 454
 FT REPEAT 455 558
 FT REPEAT 565 668
 FT DOMAIN 669 1196
 FT DISULFID 118 126
 FT ACT_SITE 198 198
 FT ACT_SITE 394 394
 FT MUTAGEN 118 118
 FT MUTAGEN 126 126
 FT MUTAGEN 358 358
 FT CONFLICT 1 1
 FT CONFLICT 67 67
 FT CONFLICT 100 100
 FT CONFLICT 154 154
 FT CONFLICT 177 177
 FT CONFLICT 227 228
 FT CONFLICT 330 330
 FT CONFLICT 425 425
 FT CONFLICT 493 493
 FT CONFLICT 532 532
 FT CONFLICT 559 559
 FT CONFLICT 665 665
 FT CONFLICT 681 681
 FT CONFLICT 686 686
 FT CONFLICT 725 728
 FT CONFLICT 736 736
 FT CONFLICT 741 741
 FT CONFLICT 758 758
 SQ SEQUENCE 1196 AA; 130893 MW; A41E6B70F257064 CRC64;
 Query Match 10.84; Score 307; DB 1; Length 1196;
 Best Local Similarity 23.04; Pred. No. 4,3e-14;
 Matches 123; Conservative 68; Mismatches 186; Indels 158; Gaps 27;
 QY 4 FNGTMQYFHWLPDDGTLMTKYANBANNSIGITATMLPFAKYGTSR-SDYGVGVYVL 62
 DB 770 FNSNNSDQRKMH-----GDPFGIINKLDYKNGKGFATWTFPMQKSEAYVGHHTYDF 825
 QY 63 YDLGEFQKGTATKTKGTAKVLOATQAAHAAQMOYVADVPFKGSGADGTEVAVENV 122
 DB 826 Y-----AVDGHLSIMDKLQELVKAKDKRIAVVDVNVNHTG----- 862
 QY 123 PSDRNOISGTYYQIQTWTFDF-PGRGNTYSSF-KRWYHFDG---VWDSRKLSRIY 176
 DB 863 -----DFOGNGFAFAPDKADMYHNDITDGDYNSNNQ----- 897
 QY 177 KFRSIGAMWEVDTEGNVDYLMVADLDMDHBEVTELEKNWKKYVNTNIDGFLDAY 236
 DB 898 -----WKI--ENG--DVAGLDLNLNENPATNELKMWIKMLNETGIDGLRDIV 943
 QY 237 KHIFSEFPMLSVRSQTKPLFTVGEVYWSYDINKLHNYITKDTGMSLFAPLHNKFY 296
 DB 944 KHVPKGLKDF-----DQANFTNGEIPHGPAVAGDTRVLDAL--DFPM--XY 991
 QY 297 TAAK-SGGAFDKRL-----MTNLMKDQPLATVPVNDHT-----EPQALQSWV 342
 DB 992 TIKDVFPHDSMRKIKRYSDDRYRDAQNGV-FIDNHVKRFLNDASGKPAANTDKW- 1049
 QY 343 DPFKPLAVAFILTRCGEPCVFGYGVYGIPOYNISLSKIDPLLIARRDYVYGTQHDY 402
 DB 1050 -POLK-AALGFTLL-SNGIPIIITVGTGEGYSGDDPA-----NRENKMFNANHDL 1096
 QY 403 LDHSDITIGWRGEGTEPFGSGLAALITDGPSSKMTVQGHAKGYFYDL--IGNSDTV 460
 DB 1097 YQYIAKLNIVYNN-----HPALONGSQRKRV-----DSFYSFQRKNGDEAI 1140

QY 461 TINSDEW-----GEF-----KUNGSVSVMV-PRKTYST 489
 Db 1141 VFINSMNSQRTITGNFDNLNSGRLTNLSQNSDSVOJNNGSIITVLAPEVAKFT 1195

RESULT 9
 AM3A_ORYSA STANDARD; PRT; 440 AA.

AC P27932;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Alpha-amylase isozyme 3A precursor (EC 3.2.1.1) (1,4-alpha-D-glucan glucanohydrolase).
 GN AMY1.2 OR AMY3A.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Euphorbiaceae; Oryzaeae; Oryza.
 OC NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N. A.
 RC STRAIN=cv. Japonica M202; TISSUE=Etioolated leaf;
 RA MEDLINE=9132892; PubMed=1714318;
 RA Sutilif T.D., Huang N., Lites J.C., Rodriguez R.L.;
 RT "Characterization of an alpha-amylase multigene cluster in rice";
 RL Plant Mol. Biol. 16:579-591(1991).
 CC -1- FUNCTION: Important for breakdown of endosperm starch during germination.
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic linkages in oligosaccharides and polysaccharides.
 CC -1- COFACTOR: Binds 3 calcium ions per subunit (By similarity).
 CC -1- SUBUNIT: Monomer.
 CC -1- TISSUE SPECIFICITY: Most abundant in embryo-derived callus tissue.
 CC -1- DEVELOPMENTAL STAGE: Expressed at a high level during germination in the aleurone cells under the control of the plant hormone gibberellic acid and in the developing grains at a low level.
 CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
 CC -----
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 CC -----
 CC EMBL: X56336; CAA39776.1; -
 CC DR PIR: S14958; S14958.
 CC DR HSSP: P04063; IAVA.
 CC DR Gramene: P27932; -
 CC DR InterPro: IPR006589; Alp_amy1_cat_sub.
 CC DR InterPro: IPR006547; Alpha_amy1_cat.
 CC DR InterPro: IPR006046; Glyco_hydro_13.
 CC DR Pfam: PF00128; alpha-amylase; 1.
 CC DR PRINTS: PR00110; ALPHAAMYLASE.
 CC DR SMART: SMO0642; Aamy; 1.
 CC DR Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
 CC KW Signal; Multigene family.
 CC FT SIGNAL 1 26
 CC FT CHAIN 27 440 POTENTIAL.
 CC FT ACT_SITE 207 440 ALPHA-AMYLASE ISOZYME 3A.
 CC FT ACT_SITE 315 440 BY SIMILARITY.
 CC FT METAL 119 119 BY SIMILARITY.
 CC FT METAL 145 145 CALCULUM 1 (BY SIMILARITY).
 CC FT METAL 155 155 CALCULUM 2 (BY SIMILARITY).
 CC FT METAL 166 166 CALCULUM 3 (BY SIMILARITY).
 CC FT METAL 169 169 CALCULUM 3 (VIA CARBONYL OXYGEN) (BY SIMILARITY).
 CC FT METAL 170 170 CALCULUM 1 (BY SIMILARITY).
 CC FT METAL 171 171 CALCULUM 1 (VIA CARBONYL OXYGEN) (BY SIMILARITY).

FT METAL 174 174 CALCULUM 3 (VIA CARBONYL OXYGEN) (BY
 FT METAL 176 176 SIMILARITY).
 FT METAL 440 440 CALCULUM 1 AND 3 (BY SIMILARITY).
 SQ SEQUENCE 440 AA; 48872 MW; 5E9B78C29AA91C2B CRC64;

Query Match 10.6%; Score 302.5; DB 1; Length 440;
 Best Local Similarity 28.4%; Pred. No. 2.6e-14;
 Matches 117; Conservative 47; Mismatches 147; Gaps 21;

QY 8 MMQYFEW-YLPDDGLTWKTVANEANLNSIGITALMLPARYKTSRSDVGYVDYDLG 66
 Db 31 LFQGFNMDSWKQGGWNTMLDQVGDIAAGVTHVLPPTH--SVFQGYMPGRLYDLN 88
 QY 67 EFNOKGVRTYKTKAYOLAIQAAAGQVADVDPDKGADGTEWDAVENS DR 126
 Db 89 -----ASKRYGKAEIKSLIAFAHAKIKCVADIVNHRCADP----- 125
 QY 127 NOEISGVYQIQAMTKFDPGRGNTYSSFKRMWHFDPDVEDNDESKLSRIYFR-GIGKAW 185
 Db 126 -KQGRGVYCI-----FKGGGR-----GLDMQPSMICDDPDQYSDGTGHR- 165
 QY 166 DEWVDTEGNYDYLMYADLDMDPEVTELEKMGKATVNTNIDGFLDAVKHKIESFPF 245
 Db 166 -----DT-----GADFAAPDIDHNLPLVQRELSDWLRMRDVGFGWRLDPAKYSAAVA- 217
 QY 246 DMLSVRSQTKPLFTVGEYW---SYD-----INKLHNYTKTDGTWLSFDAP 290
 Db 218 -RTIV--QNAPEFVAIEKNSLSYDGDGKPAANOQGRVLYNWKQVGPATADFT 273
 QY 291 LHNKFTYASKGAGAFDKMTLMTNTLMKD-----OPTLVTFVNDHTPEQALQSW 341
 Db 274 TKGILQSAVQ--GELMRKD-----KDGKAPGMIGWPEKAVFVFNHDT--GSTORMW 323
 QY 342 VDPWFKP-LAAVFLTRQEGYPCVFGYDYGIPQYNIPLSKIDPLLIAR 392
 Db 324 PEPSSKVLIGAVYILT-HPGVCFIYQGVF---DNR---LKEINLMAATRK 368

RESULT 10
 CDGT_BACS8 STANDARD; PRT; 713 AA.

AC P17652;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Cyclomatodextrin glucanotransferase precursor (EC 2.4.1.19)
 DE (Cyclodextrin-glycosyltransferase) (CGTase) (Raw-starch-digesting amylase)
 OS Bacillus sp. (strain B1019)
 OC Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus.
 OC NCBI_TaxID=1417;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 28-47.
 RX MEDLINE=90147765; PubMed=1689153;
 RA Itokor P., Tsukagoshi N., Ueda S.;
 RT "Nucleotide sequence of the raw-starch-digesting amylase gene from Bacillus sp. B1018 and its strong homology to the cyclodextrin RT glucanotransferase genes";
 RT Biochem. Biophys. Res. Commun. 166:630-636(1990).
 CC -1- FUNCTION: This endo-type adsorbable amylase is capable to digest raw starch.
 CC -1- CATALYTIC ACTIVITY: Degrades starch to cyclodextrins by formation of a 1,4-alpha-D-glucosidic bond.
 CC -1- COFACTOR: Binds 2 calcium ions per subunit (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
 CC -----
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CC or send an email to licensee@sb.eib.ch).
CC -----
DR EMBL/ M33302; AAA2239.1;
DR EMBL/ D90112; BAA1440.1;
DR PIR/ S09196; S09196.
DR HSSP/ P43379; 1CDG.
DR InterPro; IPR006589; Alp_amy1_cat_sub.
DR InterPro; IPR006048; Alpha_amy1_C.
DR InterPro; IPR006047; Alpha_amy1_cat.
DR InterPro; IPR002044; CBD_4.
DR InterPro; IPR006046; Glyco_hydro_13.
DR InterPro; IPR007110; Ig_1like.
DR InterPro; IPR002909; IPr_TiG.
DR Pfam; PF00128; alpha-amy1ase; 1.
DR Pfam; PF02806; alpha-amy1ase_C; 1.
DR Pfam; PF00886; CBM_20; 1.
DR Pfam; PF01833; TiG; 1.
DR PRINTS; PR00110; ALPHAMYLASE.
DR ProDom; PD001568; CBD_4; 1.
DR SMART; SM00643; Amy; 1.
DR SMART; SM00633; Amy; C; 1.
DR Transferrase; Glycosyltransferase; Calcium-binding; signal.
FT SIGNAL 1 27
FT CHAIN 1 27
FT ACT SITE 28 713
FT ACT SITE 256 713
FT ACT SITE 284 284
FT ACT SITE 355 355
FT METAL 54 54
FT METAL 56 56
FT METAL 59 59
FT METAL 60 60
FT METAL 80 80
FT METAL 166 166
FT METAL 217 217
FT METAL 226 226
FT METAL 260 260
FT METAL 260 260
SQ SEQUENCE 713 AA; 77420 MW; 85FB616DA687888 CRC64;

Query Match 10.6%; Score 302; DB 1; Length 713;
Best Local Similarity 24.7%; Pred. No. 5.2e-14;
Matches 136; Conservative 80; Mismatches 205; Indels 130; Gaps 29;

2 APENGTMOYFEWYLPDGLTWKVNAN--LSSLGITATMLP---AYKGTGRSDV 55
64 AADGCTN-LRLYCGSD--WGIINKINDGYLTGMGTALWISQVENIYSIIYSGV 119
56 GYGVYDLYLGEFNQGYRTKGTGAOYLQAIQAHAAGQVYADVFDHSGADGTEM 115
120 NNTAYGYWADKCK--TNPAVGTADFQNTLAAHAANKIKITIDFANHSRPSASSDP 176
116 VDAVEVPSDRNOEISGYQIQMTKFPDPGRNTYSFKRWYHFDGVMDSEKRLSRI 175
177 SFENGRALVD-NETLIGY-----TNDTQNLF---HHNGGTFDS----- 211
176 YKRGIGKAMDVEVDENGVYDIATADLDMHPEVYTE--LKNCKKVVYNTINIDGFL 233
212 -----TTENGIGYKNL--VDLNLNNSTSDVYLDAIKKMLD-LGIDGIM 255
234 DAVKHKESFPFPMLSVRSQTKPLFTVGEVMSYDINKL--HNYITKTIDGWSLFDAPL 291
256 DAYKHPFGQKSPMAVNNY--KPVYTFGE-WFLGNEVGRPNHFKFANESGSLDFRF 312
292 HNKFYTA--SKSGAEDMRTLMNTL-----MDQPLATFPVDNHTREGQLQSWDP 344
313 AOKRQVFRDNTNMGKAMLRGSADVAQVDDQ---VTFDNDHMERFHSANRRK 368
345 WPKDLAFAFLTROBGVPCVFYGYGYGIPY-----NIPSLKS-----KI 384
369 LEQALATTLILAR---VPAT-----YVGTEDYMSGTDPDNRALIPSTSTTAYVYIQL 421

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QY 385 DPLLRRADYAYGTOHDYLDHSDIIGMTREGT-----EKPSPGAALITDPG 433
DB 422 APLAKSNPAIAYGSGQERWINNDVILYERKFSNVAVAVNRNLAPAS-LSGLVTSLPQ 480
QY 434 GSKRMVYGKQHAQKQFYDITGN--RSDVYITNSDQ-WSEPKNGSVSW-VPRKTYST 489
DB 481 GS-----YNDVGLGGLNGNLTVVSGGAASFTLAAGTAVWQYTAATATPT 527
QY 490 IAR--PIITRP 498
DB 528 IGHVGPMAKP 538

RESULT 11
CDGU_BACCI STANDARD; PRT; 713 AA.
AC P43378;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cyclodextrin-glucanotransferase precursor (EC 2.4.1.19)
DE (Cyclodextrin-glycosyltransferase) (CGTase).
OS Bacillus circulans.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1397;
[1]
SEQUENCE FROM N.A., SEQUENCE OF 28-37, AND X-RAY CRYSTALLOGRAPHY (2.0
ANGSTROMS).
RP STRAIN=251;
RC MEDLINE=94149761; PubMed=8107143;
RX Lawson C.L., van Montfort R., Strokopylov B., Rozedoom H.J.,
RA Kalk K.H., de Vries G.E., Penninga D., Dijkhuizen L.,
RT "Nucleotide sequence and X-ray structure of cyclodextrin
dependent crystal form."
RL J. Mol. Biol. 236:590-600(1994).
[2]
X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
RP STRAIN=251;
RC MEDLINE=96094317; PubMed=7493956;
RX Knegetel R.M.A., Strokopylov B., Penninga D., Faber O.G.,
RA Rozedoom H.J., Kalk K.H., Dijkhuizen L., Dijkstra B.W.,
RT "Crystallographic studies of the interaction of cyclodextrin
glycosyltransferase from Bacillus circulans strain 251 with natural
substrates and products."
RL J. Biol. Chem. 270:29256-29264(1995).
[3]
X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RP MEDLINE=97115811; PubMed=8955113;
RX Penninga D., van der Veen B.A., Knegetel R.M.A., van Hijum S.A.F.T.,
RA Rozedoom H.J., Kalk K.H., Dijkstra B.W., Dijkhuizen L.,
RT "The raw starch binding domain of cyclodextrin glycosyltransferase
from Bacillus circulans strain 251."
RL J. Biol. Chem. 271:32777-32784(1996).
[4]
X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF COMPLEX WITH INHIBITOR.
RP STRAIN=251;
RC MEDLINE=96264806; PubMed=8672460;
RX Strokopylov B., Knegetel R.M.A., Penninga D., Rozedoom H.J., Kalk K.H.,
RA Dijkhuizen L., Dijkstra B.W.,
RT "Structure of cyclodextrin glycosyltransferase complexed with a
maltonase inhibitor at 2.6-A resolution. Implications for product
specificity."
RL Biochemistry 35:4241-4249(1996).
CC -1- CATALYTIC ACTIVITY: Degrades starch to cyclodextrins by formation
of a 1,4-alpha-D-glucosidic bond.
CC -1- CORFACTOR: Binds 2 calcium ions per subunit.
CC -1- SUBUNIT: Monomer.
CC -1- DOMAIN: May consist of two protein domains: the one in the amino-
terminal side cleaves the alpha-1,4-glucosidic bond in starch, and
the other in the C-terminal side catalyzes other activities,
including the reconstruction of an alpha-1,4-glucosidic linkage
for cyclizing the maltooligosaccharide produced.

```

CC -! SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X78145; CAA55023.1; -
CC PIR: A58800; A58800
DR PDB: 1CDG; 08-MAR-95.
DR PDB: 1CGV; 27-FEB-95.
DR PDB: 1CGM; 27-FEB-95.
DR PDB: 1CGX; 07-FEB-95.
DR PDB: 1CGY; 07-FEB-95.
DR PDB: 1CXE; 15-DEC-95.
DR PDB: 1CXF; 15-DEC-95.
DR PDB: 1CXH; 15-DEC-95.
DR PDB: 1CXI; 15-DEC-95.
DR PDB: 1CXK; 07-FEB-00.
DR PDB: 1CXL; 03-SEP-99.
DR PDB: 1D3C; 22-DEC-99.
DR PDB: 1DTU; 06-MAR-00.
DR PDB: 1E05; 22-NOV-00.
DR PDB: 1E07; 22-NOV-00.
DR PDB: 1KCK; 16-JAN-02.
DR PDB: 1KCL; 16-JAN-02.
DR PDB: 1TCM; 21-APR-97.
DR PDB: 2CXG; 14-OCT-98.
DR PDB: 2DIJ; 13-JAN-99.
DR InterPro: IPR006589; Alp_amy1_cat_sub.
DR InterPro: IPR006048; Alpha_amy1_C.
DR InterPro: IPR006047; Alpha_amy1_cat.
DR InterPro: IPR002044; CBD_4.
DR InterPro: IPR006046; Glyco_hydro_13.
DR InterPro: IPR007110; Ig-1ike.
DR InterPro: IPR002909; IPT_TIG.
DR Pfam: PF00128; alpha-amy1ase_1.
DR Pfam: PF02806; alpha-amy1ase_C_1.
DR Pfam: PF00686; CBK_20_1.
DR Pfam: PF01833; TIG_1.
DR PRINTS: PR00110; ALPHAMYLAASE.
DR ProDom: PD001568; CBD_4; 1.
DR SMART: SM00642; Amy; 1.
DR SMART: SM00632; Amy; C; 1.
KM transferase; Glycosyltransferase; Calcium-binding; signal;
3d-structure.
FT SIGNAL. 1 27
FT CHAIN 28 713
FT DOMAIN 28 165
FT DOMAIN 166 229
FT DOMAIN 230 433
FT DOMAIN 434 522
FT DOMAIN 523 609
FT DOMAIN 610 713
FT DISULFID 70 77
FT ACT_SITE 256 256
FT ACT_SITE 284 284
FT ACT_SITE 355 355
FT METAL 54 54
FT METAL 55 55
FT METAL 56 56
FT METAL 59 59
FT METAL 60 60
FT METAL 80 80
FT METAL 166 166
FT METAL 217 217
FT METAL 226 226
FT METAL 260 260
FT TURN 30 31
FT TURN 33 34
FT TURN 36 37
CYCLOMALTODEXTRIN GLUCANOTRANSFERASE.
A1.
B.
A2.
C.
D.
E.
NUCLEOPHILE.
PROTON DONOR.
SUBSTRATE BINDING.
CALCIUM 1 (VIA CARBONYL OXYGEN).
CALCIUM 1.
CALCIUM 1.
CALCIUM 1.
CALCIUM 2 (VIA CARBONYL OXYGEN).
CALCIUM 2.
CALCIUM 2 (VIA CARBONYL OXYGEN).
CALCIUM 2 (VIA CARBONYL OXYGEN).

FT TURN 40 41
FT STRAND 44 46
FT HELIX 49 52
FT HELIX 57 59
FT HELIX 63 65
FT STRAND 66 66
FT TURN 68 69
FT TURN 73 74
FT STRAND 76 76
FT HELIX 81 89
FT TURN 90 91
FT HELIX 92 96
FT TURN 97 97
FT STRAND 100 103
FT STRAND 107 109
FT STRAND 114 116
FT TURN 117 118
FT STRAND 119 121
FT TURN 124 125
FT STRAND 129 135
FT STRAND 137 139
FT TURN 142 154
FT HELIX 155 158
FT TURN 158 163
FT TURN 165 166
FT STRAND 167 170
FT TURN 173 174
FT TURN 175 177
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FT TURN 187 188
FT STRAND 189 192
FT TURN 195 196
FT STRAND 202 202
FT STRAND 207 207
FT HELIX 213 218
FT STRAND 220 220
FT TURN 222 223
FT STRAND 224 227
FT TURN 229 230
FT HELIX 232 248
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FT HELIX 294 302
FT STRAND 306 308
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FT TURN 321 321
FT HELIX 327 340
FT TURN 342 343
FT HELIX 344 346
FT STRAND 348 349
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FT TURN 362 363
FT HELIX 366 378
FT STRAND 382 386
FT TURN 387 388
FT HELIX 389 391
FT TURN 392 392
FT TURN 398 399
FT HELIX 400 402
FT HELIX 413 421
FT TURN 422 423
FT HELIX 424 427
FT HELIX 429 433

Query Match 10.5%; Score 300; DB 1; Length 713;
Best Local Similarity 24.8%; Pred. No. 7.2e-14;
Matches 138; Conservative 77; Mismatches 200; Indels 142; Gaps 30;

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QY 2 AAFNGTMMQYFEMWLPDDGLMTKVAEANN--LSIGITALMLP-----AYKGTSRSDV 55
DB 64 AAFDQTCN-LRLVCGGD---WQGIINKINDGYLTGMGVATMIISQPEVNIYSIINSGV 119
QY 56 GYGVYDLYDLGEFNRQKTVRTKGYKQVLAIQAAHAAGQVADYVFDHKGADGTEW 115
DB 120 NNTAHGWWARDFFK---TNPAYGTIADPQMLIAAHAKNIKVIIDPAHNTSPASSDQ 176
QY 116 VDAVEVNSDRNOEISGTYOICAMTKFDPGRGNVYSSFFKRWYHFDGVDESRKLSRI 175
DB 177 SPAENGRLYD-NGTLGGY-----TNDIQNF-----HNGGTDS----- 211
QY 176 YKFRGIGKAMWEVDTEGNNDYLM-VADLMDHEVYTELKNNGKVTNTINDGRFLD 234
DB 212 -----TTENGIVKNLYDLADLNHNSTGVYIKDLIKWMLD-LGIDGIRMD 256
QY 235 AVKHIFSFPPDMLSVRSQTKPLFTVGEWYSYDINKL--HNYITKIDGTMSPDAPLH 292
DB 257 AVKHIFPFQKQSFMAAVNNY--KPVFTTGE-WFLGVNVSPEKHFANESGMSLIDRFA 313
QY 293 NKFYTA--SKSGAAPDMETLMTNTL-----MKDPTLAIVFDNHDEPQGA-----L 338
DB 314 QKVRQVFDNDMDNMGKAMLEGSADYAOVDDQ---VTFIDNHMERFHASNANRKL 369
QY 339 QSWVDPWPKPLAYAFILTRQEGYPCVFYGDYGIPOY-----NIPSLKS----- 382
DB 370 E-----ALATLT-SRGVPAL-----YGTGQVNSGGTDPNRARIPTFSTTAY 415
QY 393 ----KIDPLLIARDYAGTCHDYLHSDIIGWTRREGT-----EKPSGGLAL 427
DB 416 QVIGTLAPLRKCNPAIAYGSTDERINNDVLIYERKFSNVAVVAVNNLNAFAPS-ISGL 474
QY 438 ITDGGSGKMYVYGQKAGKVFYDLTGN--RSDTITISDG-WGEFKYNGSSVW-VPR 483
DB 475 VTSHPGS-----TNDVGLGGLNGNTLSVSGGAASFTLAAGGTAWQYTA 521
QY 484 KTVVSTIAR--PITTRP 498
DB 522 ATATPTLGHVPMMAKP 538

RESULT 12
CDGT_BACS3 STANDARD; PRT; 712 AA.
ID AC 209121;
AC 01-MAR-1989 (Rel. 10, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cyclomalto-dextrin glucanotransferase precursor (EC 2.4.1.19)
DE (Cyclodextrin-glycosyltransferase) (CGTase).
GN CGT.
OS Bacillus sp. (strain 38-2).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
ON NCBI_TaxId=1412;
RX MEDLINE=89036108; PubMed=2972812;
RA Kaneko T., Hamamoto T., Horikoshi K.;
RT "Molecular cloning and nucleotide sequence of the cyclomalto-dextrin
RT glucanotransferase gene from the alkalophilic Bacillus sp. strain no.
RT 38-2."
RL J. Gen. Microbiol. 134:97-105 (1988).
RN 121
RP SEQUENCE OF 1-586 FROM N.A.
RA Hamamoto T., Kaneko T., Horikoshi K.;
RT "Nucleotide sequence of the cyclomalto-dextrin glucanotransferase
RT (CGTase) gene from alkalophilic Bacillus sp. strain No. 38-2."
RT Agric. Biol. Chem. 51:2019-2022 (1987).
CC -1- CATALYTIC ACTIVITY: Degrades starch to cyclodextrins by formation
CC of a 1,4-alpha-D-glucosidic bond.
CC -1- COFACTOR: Binds 2 calcium ions per subunit (By similarity).
CC -1- SUBUNIT: Monomer.

```

```

CC -1- MISCELLANEOUS: CGTASE MAY CONSIST OF TWO PROTEIN DOMAINS: THE ONE
CC IN THE AMINO-TERMINAL SIDE CLEAVES THE ALPHA-1,4-GLUCOSIDIC BOND
CC IN STARCH, AND THE OTHER IN THE C-TERMINAL SIDE CATALYZES OTHER
CC ACTIVITIES, INCLUDING THE RECONSTITUTION OF AN
CC ALPHA-1,4-GLUCOSIDIC LINKAGE FOR CYCLIZING THE
CC MALTOOLIGOSACCHARIDE PRODUCED.
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M19880; AAA22309.1; -.
DR EMBL; D00129; BAA00077.1; -.
DR HSSP; P05618; IPAM.
DR InterPro; IPR006589; Alp_amy1_cat_sub.
DR InterPro; IPR006048; Alpha_amy1_C.
DR InterPro; IPR006047; Alpha_amy1_cat.
DR InterPro; IPR002044; CBD_4.
DR InterPro; IPR006046; Glyco_hydro_13.
DR InterPro; IPR007110; Ig_1like.
DR InterPro; IPR002909; IPT_TIG.
DR Pfam; PF00128; alpha-amy1ase; 1.
DR Pfam; PF02896; alpha-amy1ase_C; 1.
DR Pfam; PF00686; CBM_20; 1.
DR Pfam; PF01833; TIG; 1.
DR PRINTS; PR00110; ALPHAMYLASE.
DR PRODOM; PD001568; CBD_4; 1.
DR SMART; SM00642; Aamy; 1.
DR SMART; SM00632; Aamy_C; 1.
KM Transferase; Glycosyltransferase; Calcium-binding; signal.
FT SIGNAL 1 27
FT CHAIN 28 712
FT DOMAIN 28 165 CYCLOMALTODEXTRIN GLUCANOTRANSFERASE.
FT DOMAIN 166 229 A1.
FT DOMAIN 230 433 B.
FT DOMAIN 434 522 A2.
FT DOMAIN 523 608 C.
FT DOMAIN 609 712 D.
FT ACT_SITE 256 256 B.
FT ACT_SITE 284 284 BY SIMILARITY.
FT ACT_SITE 355 355 BY SIMILARITY.
FT ACT_SITE 54 54 BY SIMILARITY.
FT METAL 56 56 CALCIUM 2 (BY SIMILARITY).
FT METAL 59 59 CALCIUM 2 (BY SIMILARITY).
FT METAL 60 60 CALCIUM 2 (BY SIMILARITY).
FT METAL 78 78 CALCIUM 2 (VIA CARBONYL OXYGEN) (BY
FT METAL 80 80 CALCIUM 2 (BY SIMILARITY).
FT METAL 166 166 CALCIUM 1 (BY SIMILARITY).
FT METAL 217 217 CALCIUM 1 (VIA CARBONYL OXYGEN) (BY
FT METAL 226 226 CALCIUM 1 (BY SIMILARITY).
FT METAL 260 260 CALCIUM 1 (VIA CARBONYL OXYGEN) (BY
FT METAL 277 277 CALCIUM 1 (BY SIMILARITY).
FT DISULFID 70 77 BY SIMILARITY.
FT CONFLICT 582 586 VPGGI -> SMRLI (IN REF. 2).
SQ SEQUENCE 712 AA; *78249 MW; 4FAA8F0BE818F9 CRG64;

Query Match 10.1%; Score 286.5; DB 1; Length 712;
Best Local Similarity 24.5%; Pred. No. 6, 5e-13;
Matches 127; Conservative 75; Mismatches 190; Indels 127; Gaps 27;

QY 23 WTKVAEANN--LSIGITALMLP-----AYKGTSRSDVGYGVYDLYDGEFNRQKTVRT 76
DB 81 WQGIINKINDGYLTGMGVATMIISQPEVNIYSIINSGVHNTAHGWWARDFFK---TNP 137
QY 77 KYGTAKQVLAQIAHAAGQVADYVFDHKGADGTEWVDAVEVNSDRNOEISGTYOI 136

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Db 138 AYGMNDFPKNLDIAHANNIKVILIDFAHNHTSPASDDPSFAENGRLYD--NGNLLGCV-- 194
Oy 137 QAMTKFDPFGNGNTYSSFKRWYHFDGDYDWDSEKLSRIYKFGIGAMDEVDTEGNY 196
Db 195 -----TNDTONLF-----HHYGTDFG-----TIENGIV 218
Oy 197 DYLM-YADLMDHEVVTTELKMGKMYNTNIDGFRDAVKHIFSPFDMLSYVSQT 255
Db 219 KNLVDLADLNENNSSVDYLLDAIKMWLD-LGVGIVADAKHMFQMSFMSNTINNY- 276
Oy 256 GKPLFTVEEYWSYDINKL---HNITKTDTMSLFDAPLNKRYTA--SKSGAFAFMRT 309
Db 277 -KPVNFGE-WFLGNEISPEYHOFANESG--MSLDFPFQAKARQVFRDNTDMYGLKA 332
Oy 310 LMTNT-----LMKDPPLATVTFVDHCHTEPGCALQSWVDPWFKPLAAYAFILTRQEGYPCV 364
Db 333 MLEGEVYVAQVNDQ---VTFIDNHMERHTNSG--DRKRLQALAFILIT-SRGVPAI 385
Oy 365 FYGDYIGIPQY-----NIPSLKS-----KIDPLIARRDYVGTQHDYLD 404
Db 386 ---YGGSEQYWSGGNDPDNRARIPFSITTTAVQVLOKAPLKRKSPALAYGSTOERMI 441
Oy 405 HSDITGWMREGGT-----EKPSGLAALITDPGSKXMMVYQKQAGKVFYDLT 453
Db 442 NNDVLIYERKFGNNVAVAINRMNTTPAS-ITGLVTSIPQGS-----YNDVL 487
Oy 454 GN--RSDVTITNSDG-WGEFVNGGSVSWVPRKTVST 489
Db 488 GGLINGNTLITVAGAGASNFILAPGRTAVW--QYTTDAT 524

RESULT 13
CDGT_BACLI STANDARD; PRT; 718 AA.
ID CDGT_BACLI
AC P14014;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cyclomaltoedextrin glucanotransferase precursor (EC 2.4.1.19)
GN (Cyclodextrin-glycosyltransferase) (CGTase).
OS CGTA.
OS Bacillus licheniformis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1402;
RN [1]

SEQUENCE FROM N.A.
MEDLINE=90174931; PubMed=2137908;
RA Hill D.B., Alape R., Rozzell J.D.;
RT "Nucleotide sequence of a cyclodextrin glucosyltransferase gene,
RT cgtA, from Bacillus licheniformis.";
RL Nucleic Acids Res. 18:199-199(1990).
CC -1- CATALYTIC ACTIVITY: Degrades starch to cyclodextrins by formation
CC of a 1,4-alpha-D-glucosidic bond.
CC -1- CORPACTOR: Binds 2 calcium ions per subunit (By similarity).
CC -1- SUBUNIT: Monomer.
CC -1- MISCELLANEOUS: CGTase may consist of two protein domains: THE ONE
CC IN THE AMINO-TERMINAL SIDE CLEAVES THE ALPHA-1,4-GLUCOSIDIC BOND
CC ACTIVITIES, INCLUDING THE RECONSTITUTION OF AN
CC ALPHA-1,4-GLUCOSIDIC LINKAGE FOR CYCLIZING THE
CC MALTOOLIGOSACCHARIDE PRODUCED.
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X15752; CAA3763.1; -

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DR PIR; S15920; ALBSX.
DR HSSP; P30920; ICGF.
DR InterPro; IPR006589; Alp_amy1_cat_sub.
DR InterPro; IPR006048; Alpha_amy1_C.
DR InterPro; IPR006047; Alpha_amy1_cat.
DR InterPro; IPR002044; CBD_4.
DR InterPro; IPR006046; Glyco_hydro_13.
DR InterPro; IPR007110; 19-1ike.
DR InterPro; IPR002909; 1PT_TIG.
DR Pfam; PR02806; alpha-amy1ase; 1.
DR Pfam; PR00686; CW_20; 1.
DR Pfam; PR01833; TIG_1.
DR PRINTS; PRO0110; ALPHAMYLASE.
DR ProDom; PD001568; CBD_4; 1.
DR SMART; SM00642; Amy; 1.
DR SMART; SM00632; Amy_C; 1.
KM Transferase; Glycosyltransferase; Calcium-binding; Signal.
FT SIGNL 1 34
FT CHAIN 35 718
FT DOMAIN 35 172
FT DOMAIN 173 236
FT DOMAIN 237 440
FT DOMAIN 441 528
FT DOMAIN 529 614
FT DOMAIN 615 718
FT ACT_SITE 258 258
FT ACT_SITE 291 291
FT ACT_SITE 362 362
FT METAL 61 61
FT METAL 63 63
FT METAL 65 66
FT METAL 67 67
FT METAL 85 85
FT METAL 87 87
FT METAL 173 173
FT METAL 224 224
FT METAL 223 223
FT METAL 267 267
FT DISULFID 77 84
SQ SEQUENCE 718 AA; 78002 MW; B3DE14A81D5DC4E CRC64;

Query Match 10.0%; Score 266; DB 1; Length 718;
Best Local Similarity 23.1%; Pred. No. 7,2e-13;
Matches 136; Conservative 78; Mismatches 196; Indels 166; Gaps 30;

Oy 2 APPNGTMOYFEMWYFDGTLTKVANEAN--LSSLGITALMPPA-----YKG 49
Db 71 AAFDGTCSN-LKLYCGSD--WGLVKNKINDYFSDLGVTALMISQPVENIPATINYGCV 126
Oy 50 TSSRDVGYGVYDYLDEGFNGKGVTRKGTGAOYLQAIQAHAAGMAYADVFEDHKGK 109
Db 127 TNAHYGVYARDPKKNPY-----FGMTDQNLVTTAAAGIKIILDFAHNHSP 177
Oy 110 ADGTWDAVEVNPDRNCEISGTQIQAWYKFDPPGKNTYSSFRKMYHFDGDYDWDSE 169
Db 178 AMETDTSFANGKLYDNGMLVGG-----YTNDTNGY-----FHHNGSDFS-- 218
Oy 170 RKLSRIYKRGIGKAMDWEVDTEGNGYDYL-YADLMDHPEVVTTELKMGKMYNTNVI 228
Db 219 -----TIENGIVKULYDLADLNENNSTIDYFKDALILMD-MGV 257
Oy 229 DGRFLDAVKHIFSPFDMLSYVSQTGPLFTVEEYWSYDINKLHNITKTGDT----- 283
Db 258 DGIKRVDAVKAMPQGMKNMMSIYAH--KPVFTFGEMF-----LGSAPDADNDIDFANE 309
Oy 284 --MSL-----FDALHNKFTYASGSGAPKRLMNTL-----MKDQPLATVFDVNDHT 332
Db 310 SGMSLIDFRNLSAVRNVFRDNTSNKYALD--SMLTATADYVQVNDQ---VTFIDNHDM 363

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QY 333 EPGQALQSWDPWFKFLAVAFILITROGYCVFYGDYGIPOY-----NIPSLX 381
DB 364 D--RFTSAVNNRRLDQALFILT-SRGVPAL---YGTBQILTNGDPNDRGKMPHS 416
QY 382 -----SKIDPELLIARDVAYG-TQHDYLD----- 404
DB 417 KSTTAFNVISKLAPLRKSNPAIAYGSTQGWNNNDYIERKKGKGVAVAVNRMLTPT 476
QY 405 -----HSDIIGWTRGCGTEKRGSSGLAALITDGPQSK-MWTVGKQ-----H 444
DB 477 STNNLTSLPSGTYTDLGVLNGNNITSSGNISFTLAAGTAVAWQYTASETTPTIGH 536
QY 445 AGKRFYDLTGNRSDTYTINSDGWGEFR-----VNGGSVVM--VERKTTVSTIA 491
DB 537 VGPVM-----GKPGNVVTLIDGRGFGSAKGTVFYFTTAVTSATSWMEDTQIKVTIPVA 590

RESULT 14
CDGT_BACSO STANDARD; PRT; 713 AA.
AC P05618;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cyclomalodextrin glucanotransferase precursor (EC 2.4.1.19)
GN Cyclodextrin-glucosyltransferase (Cgtase).
OC Bacillus sp. (strain 1011).
OX Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
RT NCBI_TaxID=1410;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87308036; PubMed=2957361;
RA Kiuma K., Kataoka S., Ishii Y., Takano T., Yamane K.;
RT "Nucleotide sequence of the beta-cyclodextrin glucanotransferase gene
of alkalophilic Bacillus sp. strain 1011 and similarity of its amino
acid sequence to those of alpha-amylases.";
RT J Bacteriol. 169:4399-4402(1987).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
RA Harata K., Haga K., Nakamura A., Aoyagi M., Yamane K.;
RT "X-ray structure of cyclodextrin glucanotransferase from alkalophilic
Bacillus Sp. 1011. Comparison of two independent molecules at 1.8-A
resolution.";
RT Acta Crystallogr. D 52:1136-1145(1996).
CC -1- CATALYTIC ACTIVITY: Degrades starch to cyclodextrins by formation
of a 1,4-alpha-D-glucosidic bond.
CC -1- COFACTOR: Binds 2 calcium ions per subunit.
CC -1- SUBUNIT: Monomer.
CC -1- MISCELLANEOUS: CGTASE MAY CONSIST OF TWO PROTEIN DOMAINS: THE ONE
IN THE AMINO-TERMINAL SIDE CLEAVES THE ALPHA-1,4-GLUCOSIDIC BOND
ACTIVITIES, INCLUDING THE RECONSTITUTION OF AN
ALPHA-1,4-GLUCOSIDIC LINKAGE FOR CYCLIZING THE
MULTIOLIGOSACCHARIDE PRODUCED.
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
CC -----
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or send an email to license@isb-sib.ch).
CC -----
EMBL: M17366; AAA23308.1; -
DR PIR; A26678; ALBSC3;
DR PDB; 1D7F; 17-MAR-00.
DR PDB; 1DED; 07-APR-00.
DR PDB; 1I75; 11-APR-01.
DR PDB; 1PAM; 11-JAN-97.
DR InterPro; IPR006589; Alp_amyl_cat_sub.

DR InterPro; IPR006048; Alpha_amyl_C.
DR InterPro; IPR006047; Alpha_amyl_cat.
DR InterPro; IPR002044; CBD_4
DR InterPro; IPR006046; Glyco_hydro_13.
DR InterPro; IPR007110; 19-like.
DR InterPro; IPR02909; IPT_TIG.
DR Pfam; PF00128; alpha-amylase_1.
DR Pfam; PF02806; alpha-amylase_1.
DR Pfam; PF00685; CBM 20; 1.
DR Pfam; PF01833; TIG_1.
DR PRINTS; PR00110; ALPHAMYLASE.
DR ProDom; PD001568; CBD_4; 1.
DR SMART; SM00642; Amyy; 1.
DR SMART; SM00632; Amyy_C; 1.
KM Transferase; Glycosyltransferase; Calcium-binding; signal;
KM 3D-structure.
FT SIGNAL 1 27
FT CHAIN 28 713
FT DOMAIN 166 165
FT DOMAIN 166 229
FT DOMAIN 230 433
FT DOMAIN 434 522
FT DOMAIN 523 609
FT DOMAIN 610 713
FT ACT_SITE 256 256
FT ACT_SITE 284 284
FT ACT_SITE 354 355
FT ACT_SITE 54 54
FT METAL 54 54
FT METAL 56 56
FT METAL 59 59
FT METAL 60 60
FT METAL 80 80
FT METAL 166 166
FT METAL 217 217
FT METAL 226 226
FT METAL 260 260
FT DISULFID 70 77
FT TURN 30 31
FT TURN 33 34
FT TURN 40 41
FT TURN 44 44
FT STRAND 44 46
FT HELIX 49 51
FT TURN 52 52
FT HELIX 57 57
FT HELIX 63 63
FT STRAND 66 66
FT TURN 68 69
FT TURN 73 74
FT STRAND 76 76
FT HELIX 81 89
FT TURN 90 93
FT HELIX 94 96
FT TURN 97 97
FT STRAND 100 103
FT STRAND 107 109
FT STRAND 114 116
FT TURN 117 118
FT STRAND 119 121
FT STRAND 124 125
FT STRAND 129 135
FT TURN 137 139
FT HELIX 142 154
FT TURN 155 156
FT STRAND 158 163
FT TURN 165 166
FT STRAND 167 170
FT TURN 176 177
FT TURN 179 182
FT STRAND 184 186
FT TURN 187 188
FT STRAND 189 192
FT TURN 195 196
FT TURN 198 199

CYCLOMALDODEXTRIN GLUCANOTRANSFERASE.
A1.
B.
A2.
C.
D.
E.
CALCIUM 1.
CALCIUM 1 (VIA CARBONYL OXYGEN).
CALCIUM 1.
CALCIUM 1.
CALCIUM 2.
CALCIUM 2 (VIA CARBONYL OXYGEN).
CALCIUM 2.
CALCIUM 2 (VIA CARBONYL OXYGEN).
CALCIUM 2.

Query	Match	Score	DB 1	Length	713
Best Local Similarity	23.4%	Pred. No. 9.1e-13			
Matches 135	Conservative	70	Mismatches 192	Indels 181	Gaps 28
QY	23 WTKVANEANN--LSLSGITLALMLP----	AYKGTSSDSDVGYVDDLYDGEFNQKGTVRT	76		
QY	81 WOGIINKINDYLTGGMGTIAITWISQ	PENITYSVINSGVNTAIVHGMARDFKK--TNP	137		
QY	77 KGTGAOYLQAIQAAHAAQMQYADV	YVDHKGAGDGTGWDVAVVPSRDNQISGTQYI	136		
QY	138 AAGTQWODRKLLIDTAHANNTKVI	ITDPAHNTSPASSDDPEFAENGRLLYD-NGTLGGY--	194		
QY	137 QAWKTFDPPGKQNTYSSFKMKRYTF	DFDGVDDDESKRLRIYKFGIKGAKMDWEVDENSGNY	196		
QY	195 -----TNDTQNLNF-----	HHYGGTDS-----TIENGXY	218		
QY	197 DYLM-YADIDMDHPEVVTTELKMG	KWYVNTNIDGFLDAVKHIIKESFPEDWL	255		
QY	219 KKLVDLADLNENNSVDYLLDALIK	MLLD-LGVGCIKVDVAVKHMPGCMQKSP	276		
QY	256 GKPLFTVGSYMSYDINKL----	HNITKTGDTSLFPAHLNKFYTKSKGCAF-----	305		
QY	277 -KPVFFTFGS-WFLGNEISPEYH	OFANESG--MLLD-----FRFQKARQVFRDNTDN	326		
QY	306 --DMRTLMNT-----LMKDQ	PTLAVTVVDNHDHPDQALQSWDPEFKFLAYAFILTRQ	358		
QY	327 MGLKMKLGESEVDVAQVNDQ----	VTFIDHMDHERFHTSNG--DRKRLQALAFILTL-S	379		
QY	359 EGYPCVYFYDYGITQY-----	NITSLKS-----KIDPLLIARDVAYGT	398		
QY	380 RGVPAL-----YYGSBQYMSG	NDPDRRLPFSFTTTTAYOVIOQLKALPKRS	435		
QY	399 QHD-----	YLDHSIIIGTREGGT	417		
QY	436 THERMTINDVITIERKFGNNNA	VVAIINNMTPASITGLVTSLEBRASYN	495		
QY	418 EKPQGLAAL-ITDGPQSK-WMT-----	VGRKHAKGYFDLTGNRSPTVYINS	464		
QY	496 LTVAGAGAAANFTLAPGGTA	VWQYTTDATPIIGNVGWMA-----KPGVLTITDG	546		
QY	465 DGWGEFK-----VNGGS	VWVPRKTYSTIARP	493		
QY	547 RGFSGSGKTVYFCTATVAGAD	IVAMEDQIQVKIPAVP	584		
DB	RESULT 15				
DB	AMYA_VIGMU	STANDARD;	PRT;	421	AA.
DB	AC	PI7859;			
DB	DT	01-AUG-1990 (Rel. 15, Last	sequence update)		
DB	DT	01-AUG-1990 (Rel. 15, Last	sequence update)		
DB	DT	10-OCT-2003 (Rel. 42, Last	annotation update)		
DB	DE	Alpha-amylase precursor (EC	3.2.1.1) (1,4-alpha-D-glucan		
DB	DE	glucanohydrolase).			
DB	GN	AMY1.1.			
DB	OS	Vigna mungo (Rice bean) (Black	gram).		
DB	OS	Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
DB	OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;			
DB	OC	eurosid1; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Vigna.			
DB	OK	NCBI_TaxId=3915;			
DB	RN	SEQUENCE FROM N.A.			
DB	RP	TISSUE=Cotyledon;			
DB	RX	MEDLINE=90333425; PubMed=2377468;			
DB	RA	Yamauchi D., Miranekawa T.;			
DB	RT	"Nucleotide sequence of cDNA for alpha-amylase from cotyledons of			
DB	RL	germinating Vigna mungo seeds ";			
DB	RL	Nucleic Acids Res. 18:4250-4250(1990).			
DB	RN	SEQUENCE FROM N.A.			
DB	RP	MEDLINE=94120017; PubMed=8290640;			

RA Takeuchi H., Yamauchi D., Wada S., Minamikawa T.;
RT "Nucleotide sequence of the alpha-amylase gene from *Vigna mungo*,";
RL Plant Physiol. 103:1459-1459(1993).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -1- COFACTOR: Binds 3 calcium ions per subunit (By similarity).
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
CC
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CC
CC
CC EMBL; X53049; CAA37217.1; -;
CC EMBL; X73301; CAA51734.1; -;
CC PIR; S10514; S10514.
CC HSSP; P04063; IAVA.
CC InterPro: IPR006589; Alp_amy1_cat sub.
CC InterPro: IPR006047; Alpha_amy1_cat.
CC InterPro: IPR006046; Glyco_hydro_13.
CC Pfam; PF00128; alpha-amylase; 1.
CC PRINTS; PR00110; ALPHAAMYLASE.
CC SMART; SMO0642; Amy; 1.
CC Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
CC Signal.
CC
CC FT SIGNAL 1 23 PROBABLE.
CC FT CHAIN 24 421 ALPHA-AMYLASE.
CC FT ACT SITE 201 201 BY SIMILARITY.
CC FT ACT SITE 309 309 BY SIMILARITY.
CC FT METAL 113 113 CALCIUM 1 (BY SIMILARITY).
CC FT METAL 130 130 CALCIUM 2 (BY SIMILARITY).
CC FT METAL 133 133 CALCIUM 2 (BY SIMILARITY).
CC FT METAL 135 135 CALCIUM 2 (BY SIMILARITY).
CC FT METAL 139 139 CALCIUM 2 (BY SIMILARITY).
CC FT METAL 149 149 CALCIUM 3 (BY SIMILARITY).
CC FT METAL 160 160 CALCIUM 3 (BY SIMILARITY).
CC FT METAL 168 168 CALCIUM 3 (VIA CARBONYL OXYGEN) (BY
CC SIMILARITY).
CC
CC FT METAL 170 170 CALCIUM 1 AND 3 (BY SIMILARITY).
CC
CC SQ SEQUENCE 421 AA; 46888 MW; 15CA0DAB3DB4656 CRC64;
Query Match 9.9%; Score 283; DB 1; Length 421;
Best Local Similarity 26.3%; Pred. No. 6,1e-13;
Matches 103; Conservative 48; Mismatches 142; Indels 98; Gaps 17;
QY 8 MMQYFEMYLDDDTLTWTKVANEANNLSGITLWLPAPYKGTSRSDVGAVYDYLGE 67
DB 26 LFGFTWESKSKGKGNLSKSLPDLANGITHWLP--PSQSVSPGTLFGRLLYLD- 82
QY 68 FNQKGVTRKYGTGAQYLAIQAAAGQYVAVVFDKGG--ADGTEWDAVEVNPSD 125
DB 83 -----ASKYGSKNELKSLIAFHEKGIKCLADIVINHTAERKDRGIYCFEGGTPD 135
QY 126 RNQEIGSTVOIQMTKFPDPRGNTYSSPKRWYHFDGVDWDSRKLRIYKFRGIGKAM 185
DB 136 SRQDMGSPFICRDTAYS--DGTGNDS-----GEGY 165
QY 186 DWEVDTEENGNYDYLMYADLMDH--PEVYTELKNWGWYVNTNIDGFRLLDAVKIKESF 243
DB 166 D-----AAPDIDLNPQVORELSEWNNMLKTEIGFGMRFDYK---GY 206
QY 244 FPDMLSVRSQSGKPLFTYGEVW---SY-----DINK--LHNVTKTGDMSLFD 288
DB 207 APS-ISKIYVQTKPFAVGEKWDISLYGGDGKPNYNQSHRGALVNWVESAGAITAFD 265
QY 289 -----APLNKFTYASKSGGAFDMRTLMTNTLLKDOPTLAVTFVDNHDTEPGQALQS 340
DB 266 FTTKGIQAAVQGEIWRLLDPNG-----KPPGMIQVKNPENAIVTFIDNHDT--GSTQRL 316

QY 341 WVDPEFKPLAYAFILTRQSGYPCVFYGDY 370
DB 317 WPFSDKVMQGYAYILT-HPGTPSIFYDHF 346

Search completed: May 3, 2004, 20:51:15
Job time : 12.1361 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 3, 2004, 20:34:58 ; Search time 49.0521 Seconds
(without alignments)
2782.151 Million cell updates/sec

Title: US-10-644-187-2
Perfect score: 2666
Sequence: 1 ANLNGTLMQYEFWYVNDGQ.....SEGNGEPHNGSVSYVQR 483

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_28Jan04:*
1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001s:*
5: Geneseq2002s:*
6: Geneseq2003as:*
7: Geneseq2003bs:*
8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2666	100.0	483	2	AA72447 Bacillus
2	2666	100.0	483	2	AA72447 Bacillus
3	2666	100.0	483	2	AA72447 Bacillus
4	2666	100.0	483	2	AA72447 Bacillus
5	2666	100.0	483	2	AA72447 Bacillus
6	2666	100.0	483	2	AA72447 Bacillus
7	2666	100.0	483	2	AA72447 Bacillus
8	2666	100.0	483	2	AA72447 Bacillus
9	2666	100.0	483	2	AA72447 Bacillus
10	2666	100.0	483	2	AA72447 Bacillus
11	2666	100.0	483	2	AA72447 Bacillus
12	2666	100.0	483	2	AA72447 Bacillus
13	2666	100.0	483	2	AA72447 Bacillus
14	2666	100.0	483	2	AA72447 Bacillus
15	2666	100.0	483	2	AA72447 Bacillus
16	2666	100.0	483	2	AA72447 Bacillus
17	2666	100.0	483	2	AA72447 Bacillus
18	2666	100.0	483	2	AA72447 Bacillus
19	2666	100.0	483	2	AA72447 Bacillus
20	2666	100.0	483	2	AA72447 Bacillus
21	2666	100.0	483	2	AA72447 Bacillus
22	2666	100.0	483	2	AA72447 Bacillus
23	2666	100.0	483	2	AA72447 Bacillus
24	2666	100.0	483	2	AA72447 Bacillus
25	2666	100.0	483	2	AA72447 Bacillus

26	2663	99.9	512	1	AA70753	AA70753 phea arof
27	2663	99.9	512	2	AA73509	AA73509 Alpha-amy
28	2663	99.9	512	2	AA700769	AA700769 B. lichen
29	2663	99.9	512	4	AA707097	AA707097 Bacillus
30	2663	99.9	512	4	AA65875	AA65875 B. lichen
31	2663	99.9	512	4	AA65877	AA65877 B. lichen
32	2661	99.8	483	5	AA72165	AA72165 Bacillus
33	2661	99.8	483	5	AA72161	AA72161 Bacillus
34	2660	99.8	483	2	AA58000	AA58000 M197L alp
35	2660	99.8	483	2	AA58002	AA58002 M304L alp
36	2660	99.8	483	2	AA58735	AA58735 M15L alp
37	2660	99.8	483	2	AA57992	AA57992 M15L alp
38	2660	99.8	483	2	AA80192	AA80192 Bacillus
39	2660	99.8	483	5	AA72162	AA72162 Bacillus
40	2660	99.8	483	5	AA72163	AA72163 Bacillus
41	2660	99.8	487	2	AA80215	AA80215 A4 form a
42	2660	99.8	487	2	AA80191	AA80191 A4 form a
43	2660	99.8	653	2	AA57437	AA57437 NAM1.0 fu
44	2659	99.7	483	2	AA70576	AA70576 Mutant a1
45	2659	99.7	483	2	AA58007	AA58007 M197L alp

ALIGNMENTS

RESULT 1	AA72447	standard; protein; 483 AA.
ID	AA72447	
XX	AA72447	
AC	AA72447	
XX	AA72447	
DT	25-MAR-2003	(revised)
DT	01-DEC-1995	(first entry)
XX		
DE	Bacillus licheniformis alpha amylase (mature protein).	
XX		
KM	Alpha amylase; variant; enzyme; detergent; additive; dishwashing;	
KM	washing; Bacillus licheniformis; Bacillus amyloliquefaciens;	
KM	Bacillus stearothermophilus; dyeing; bleaching; scouring; textile;	
XX	thermostable.	
OS	Bacillus licheniformis.	
XX		
PN	WO9510603-A1.	
XX		
PD	20-APR-1995.	
XX		
PF	05-OCT-1994; 94WO-DK000370.	
XX		
PR	08-OCT-1993; 93DK-00001133.	
PR	02-FEB-1994; 94DK-00000140.	
XX		
PA	(NOVO) NOVO-NORDISK AS.	
XX		
PI	Borchert TV, Bisgard-Frantzen H, Svendsen A, Thellersen M;	
PI	Van Der Zee P;	
XX		
DR	WPI: 1995-161790/21.	
DR	N-PSDB; AAC88066.	
XX		
PT	New Bacillus derived alpha-amylase variants - having amino acid	
PT	modifications to improve washing and/or dishwashing performance.	
XX		
PS	Claim 6; Page 72; 105pp; English.	
XX		
CC	Variant alpha amylase enzymes which have improved washing and/or as	
CC	detergent additives. The enzymes have one or more amino acid residues	
CC	added, deleted or substituted. The variants can also be used for textile	
CC	bleaching prior to scouring, bleaching and dyeing. The variants have	
CC	improved thermostability, acid/alkaline stability, low temperature	
CC	optimum; pH optimum; higher hydrolysis velocity and improved tolerance	
CC	to other composition constituents, e.g. oxidation agents. (Updated on 25-MAR	
CC	-2003 to correct pn field.) (Updated on 25-MAR-2003 to correct pi field.)	

XX Sequence 483 AA;
 SQ Query Match 100.0%; Score 2666; DB 2; Length 483;
 Best Local Similarity 100.0%; Pred. No. 1.7e-224;
 Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANLNGTLMQYFEMWMPNDGQHRRLQNDSDAYLAHGTATWIPPAKGTSGADVGYGAD 60
 DB 1 ANLNGTLMQYFEMWMPNDGQHRRLQNDSDAYLAHGTATWIPPAKGTSGADVGYGAD 60
 QY 61 LYDGEFHQKGTATKTKGTGKELQSAIKSLHSRDINYGVDVINHKGADATEDVTAVEV 120
 DB 61 LYDGEFHQKGTATKTKGTGKELQSAIKSLHSRDINYGVDVINHKGADATEDVTAVEV 120
 QY 121 DPADNRVISEGHELIKAWTHFHPGRGSTYSDFKMWHYHFDGTDWDSRKLNRITYKQSK 180
 DB 121 DPADNRVISEGHELIKAWTHFHPGRGSTYSDFKMWHYHFDGTDWDSRKLNRITYKQSK 180
 QY 181 AMDWEVSENGNNDYLMYADIDYDHPVAAEIKRWGTWYANELQDGFRLDAVGHKFSF 240
 DB 181 AMDWEVSENGNNDYLMYADIDYDHPVAAEIKRWGTWYANELQDGFRLDAVGHKFSF 240
 QY 241 LRDMVNHVREKTKGEMFTVAEYMONDICALENTLNKNHNSVFDVPLHQFHAASQGG 300
 DB 241 LRDMVNHVREKTKGEMFTVAEYMONDICALENTLNKNHNSVFDVPLHQFHAASQGG 300
 QY 301 GYDKRKLNGTVSGHPKSVTFVDNHDTPQGSLSTVQTWKPLAYAFILTRSGYPO 360
 DB 301 GYDKRKLNGTVSGHPKSVTFVDNHDTPQGSLSTVQTWKPLAYAFILTRSGYPO 360
 QY 361 VFYGMVGTGKDSQREIPALKHKEIPILKARKQYAYAGOHYFDHDIYGMTREGDSSVA 420
 DB 361 VFYGMVGTGKDSQREIPALKHKEIPILKARKQYAYAGOHYFDHDIYGMTREGDSSVA 420
 QY 421 NSGLAALITDGPQGAKEKMYVGRONAGETWHDITGNRSEPVVINSBGGEFHVNGGSVSIY 480
 DB 421 NSGLAALITDGPQGAKEKMYVGRONAGETWHDITGNRSEPVVINSBGGEFHVNGGSVSIY 480
 QY 481 VQR 483
 DB 481 VQR 483

RESULT 2
 AAR78267
 ID AAR78267 standard; protein; 483 AA.
 XX AAR78267;
 AC AAR78267;
 XX 17-JAN-1996 (first entry)
 DT 17-JAN-1996 (first entry)
 DE Bacillus licheniformis alpha amylase (mature protein).
 XX Alpha amylase; oxidation; desizing; bleaching; scouring; fabric; starch;
 KW thermostable; methionine; Bacillus licheniformis;
 KW Bacillus amyloliquefaciens; Bacillus stearothermophilus.
 XX Bacillus licheniformis.
 OS Bacillus licheniformis.
 XX W09521247-A1.
 PN W09521247-A1.
 XX 10-AUG-1995.
 PD 10-AUG-1995.
 XX 05-OCT-1994; 94MO-DK000371.
 PE 05-OCT-1994; 94MO-DK000371.
 XX 02-FEB-1994; 94DK-00000141.
 PR 02-FEB-1994; 94DK-00000141.
 XX (NOVO) NOVO-NORDISK AS.
 PA (NOVO) NOVO-NORDISK AS.
 XX Toft AH, Marcher D, Pedersen HH, Nilesen TE;
 PI Toft AH, Marcher D, Pedersen HH, Nilesen TE;
 XX WPI: 1995-283767/37.
 DR

DR N-PSDB; AAQ95031.
 XX Use of an oxidation stable alpha-amylase - for simultaneous desizing and
 PT bleaching or scouring of fabrics contg. starch or starch derivs.
 XX Claim 6; Page 22; 37pp; English.
 PS
 XX Oxidation stable alpha amylases can be used for the simultaneous desizing
 CC and bleaching or scouring of a fabric comprising starch or starch
 CC derivatives. They exhibit a better heat stability, especially in the
 CC presence of oxidizing agents. They are obtained from a parent alpha
 CC amylase by replacing one or more methionine residues with any amino acid
 CC different from Cys or Met, preferably Leu, Thr, Ala, Gly, Ser, Ile or
 CC Asp. The parent alpha amylase is derived from a Bacillus species. This is
 CC the wild type (unmodified) alpha amylase

XX Sequence 483 AA;
 SQ Query Match 100.0%; Score 2666; DB 2; Length 483;
 Best Local Similarity 100.0%; Pred. No. 1.7e-224;
 Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANLNGTLMQYFEMWMPNDGQHRRLQNDSDAYLAHGTATWIPPAKGTSGADVGYGAD 60
 DB 1 ANLNGTLMQYFEMWMPNDGQHRRLQNDSDAYLAHGTATWIPPAKGTSGADVGYGAD 60
 QY 61 LYDGEFHQKGTATKTKGTGKELQSAIKSLHSRDINYGVDVINHKGADATEDVTAVEV 120
 DB 61 LYDGEFHQKGTATKTKGTGKELQSAIKSLHSRDINYGVDVINHKGADATEDVTAVEV 120
 QY 121 DPADNRVISEGHELIKAWTHFHPGRGSTYSDFKMWHYHFDGTDWDSRKLNRITYKQSK 180
 DB 121 DPADNRVISEGHELIKAWTHFHPGRGSTYSDFKMWHYHFDGTDWDSRKLNRITYKQSK 180
 QY 181 AMDWEVSENGNNDYLMYADIDYDHPVAAEIKRWGTWYANELQDGFRLDAVGHKFSF 240
 DB 181 AMDWEVSENGNNDYLMYADIDYDHPVAAEIKRWGTWYANELQDGFRLDAVGHKFSF 240
 QY 241 LRDMVNHVREKTKGEMFTVAEYMONDICALENTLNKNHNSVFDVPLHQFHAASQGG 300
 DB 241 LRDMVNHVREKTKGEMFTVAEYMONDICALENTLNKNHNSVFDVPLHQFHAASQGG 300
 QY 301 GYDKRKLNGTVSGHPKSVTFVDNHDTPQGSLSTVQTWKPLAYAFILTRSGYPO 360
 DB 301 GYDKRKLNGTVSGHPKSVTFVDNHDTPQGSLSTVQTWKPLAYAFILTRSGYPO 360
 QY 361 VFYGMVGTGKDSQREIPALKHKEIPILKARKQYAYAGOHYFDHDIYGMTREGDSSVA 420
 DB 361 VFYGMVGTGKDSQREIPALKHKEIPILKARKQYAYAGOHYFDHDIYGMTREGDSSVA 420
 QY 421 NSGLAALITDGPQGAKEKMYVGRONAGETWHDITGNRSEPVVINSBGGEFHVNGGSVSIY 480
 DB 421 NSGLAALITDGPQGAKEKMYVGRONAGETWHDITGNRSEPVVINSBGGEFHVNGGSVSIY 480
 QY 481 VQR 483
 DB 481 VQR 483

RESULT 3
 AAM31404
 ID AAM31404 standard; protein; 483 AA.
 XX AAM31404;
 AC AAM31404;
 XX 17-OCT-2003 (revised)
 DT 17-OCT-2003 (revised)
 DE Bacillus licheniformis [Termamy] alpha-amylase.
 XX [Termamy]; alpha-amylase; enzyme engineering; protein engineering; starch;
 KW liquefaction; saccharification; sweetener; textile desizing;
 KW detergent additive.
 KM

XX Bacillus licheniformis, strain ATCC 27811.
 OS WO9741213-A1.
 XX 06-NOV-1997.
 XX 30-APR-1997; 97WO-DK000197.
 XX 30-APR-1996; 96DK-00000515.
 XX 28-JUN-1996; 96DK-00000712.
 XX 11-JUL-1996; 96DK-00000775.
 XX 08-NOV-1996; 96DK-00001263.
 XX (NOVO) NOVO-NORDISK AS.
 XX Svendsen A, Borchert TV, Bisgaard-Frantzen H;
 PI WPI; 1997-549718/50.
 DR WPI; 1997-549718/50.
 DR N-PSDB; AAV02471.
 XX Termamyl-like alpha-amylase variants with improved properties - e.g.
 PT increased stability at low pH and low calcium, useful as detergent
 PT additives and in industrial starch processing e.g. liquefaction.
 XX Claim 1; Page 82; 101pp; English.
 XX This protein comprises Termamyl alpha-amylase (see AAW31404) of Bacillus
 CC licheniformis ATCC 27811. The invention relates to novel variants
 CC (mutants) of Termamyl-like alpha-amylases that have alpha-amylase
 CC activity and exhibit an alteration in at least one property selected
 CC from: substrate specificity; binding or cleavage pattern; thermal
 CC stability; pH/activity or pH/stability profile; stability towards
 CC oxidation; Ca²⁺ dependency and specific activity. The variant has one or
 CC more mutations selected from: (a) the mutations A181E, D, Q, N, V; I201
 CC (bulkier amino acid) including I201W, F, L, Y203Q, Q9K, L, E; F11R, K, E;
 CC E120; D100N, L, V101H, R, K, D, E, F, V102A, T, I103H, K, N104R, K, D, I;
 CC H105R, K, D, E, W, F, I116R, K, D, E, F, Y, I121R, K, D, E, L230H, K, I;
 CC A232G, H, F, S, V; V233D, K234L, E, I236R, K, N, H, D, E, L241R, K, D, E,
 CC F, A260S; W263H; Q264R, D, K, E; N265K, R, D; A269R, K, D, E, L270R, K,
 CC H, D, E; J283H, D; F284H; D285N, L; V286R, K, H, D, E, Y290R, E, K;
 CC V312R, K, D, E; F323H; D325N; N326K, H, D, L; H327Q, N, E, D, F, Q220L, E
 CC ; G332D; Q333R, K, H, E, L; S334A, V, T, L, I, D; L335G, A, S, T, N, N,
 CC E336R, R337E, T337D, K, T338D, E, T338D, Q360K, R, E, D365N; G372D, R;
 CC (b) substitutions at positions H66, H91, H247, R305, K306, H382, K389,
 CC H405, H406, H450 or R483; (c) the mutations H140Y, H142Y, H145Y, H145D +
 CC H145R, H140K + H142D; or H142Y + H156Y; (d) deletion of 3 amino acids
 CC within the partial sequence from T369 to I377, including K370-D372 or
 CC D372-Q374; (e) replacement of T369-I377 by IPTHSV, IPTHGV or IPQYNI; (f)
 CC substitutions at positions R169 or R173, including R169I, L, F, T or
 CC R173I, L, F, T; (g) the mutations H156D, I201F, I212F, A209I, or T, or
 CC V208I; (h) substitutions at positions N172, A181, N188, N190, H205, D207,
 CC A209, A210, E211, Q264 or N265, including N172R, H, K, A181T, N188P;
 CC N190L, F, H205C; D207Y, A209L, T, V; A210S, E211Q, Q264A, E, L, K, S, T;
 CC N265A, S, T, Y; or (Q264S + N265Y); and (i) the mutations H156Y + A181T +
 CC A209V; H156Y + A181T + N190F + A209V + Q264S; A1* + N2* + L3V + M15T +
 CC R23K + S29A + A30E + Y31H + A33S + E34D + H35I + H156Y + A209V
 CC (where * indicates deletion of the amino acid residue); A1* + N2* + L3V +
 CC M15T + R23K + S29A + A30E + Y31H + A33S + E34D + H35I + H156Y + A181T +
 CC N90F + A205V; or A1* + N2* + L3V + M15T + R23K + S29A + A30E + Y31H +
 CC A33S + E34D + H35I + H156Y + A181T + N190F + A209V + Q264S. Also claimed
 CC are constructs comprising DNA (see AAV02471) encoding such a variant, and
 CC recombinant expression vectors and transformed cells containing the DNA.
 CC The alpha-amylase variant is useful as a detergent additive and can also
 CC be used in industrial starch processing e.g. liquefaction (claimed) or
 CC saccharification to produce sweeteners, and in textile desizing
 CC (claimed). (Updated on 17-OCT-2003 to standardise OS field)
 CC
 XX
 XX Sequence 483 AA;
 Query Match 100.0%; Score 2666; DB 2; Length 483;
 Best Local Similarity 100.0%; Pred. No. 1,7e-224;
 Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANLNGTLMOYFEWMPNDGQWRRLQNDSAVLAESHGTAWMIIPAYKGTSGADYGYAYD 60
 DB 1 ANLNGTLMOYFEWMPNDGQWRRLQNDSAVLAESHGTAWMIIPAYKGTSGADYGYAYD 60
 QY 61 LVDLGEFHQKGTVRTKYGKGLQSAIKLSHRDINVGDVVNHKGGADATDVAVEV 120
 DB 61 LVDLGEFHQKGTVRTKYGKGLQSAIKLSHRDINVGDVVNHKGGADATDVAVEV 120
 QY 121 DPADRRRVISGEHLIKAMTHFFPGRGSTYSDPKKWHFPGDTMDESRKINRIYKFGK 180
 DB 121 DPADRRRVISGEHLIKAMTHFFPGRGSTYSDPKKWHFPGDTMDESRKINRIYKFGK 180
 QY 181 AMDWEVSNENGVYDLMYADIDYDHPVAAEIKRNGTWANELQDGRDLDAVKHIFSF 240
 DB 181 AMDWEVSNENGVYDLMYADIDYDHPVAAEIKRNGTWANELQDGRDLDAVKHIFSF 240
 QY 241 LRDVNVHVEKTKGEMFTVAEYQNDLGLLENYLNKTNFNSVFPVPLHYOPHASTQGG 300
 DB 241 LRDVNVHVEKTKGEMFTVAEYQNDLGLLENYLNKTNFNSVFPVPLHYOPHASTQGG 300
 QY 301 GYMRKLINGTVSKAPLKSATFVFNHNDTPQGSLESTVQTWFKELAVAFILTRSGYPO 360
 DB 301 GYMRKLINGTVSKAPLKSATFVFNHNDTPQGSLESTVQTWFKELAVAFILTRSGYPO 360
 QY 361 VFYGDWYGTGDSQREIPALKKIEPILKARKQVAYGAQHDYFDHHDYVGTREDDSYA 420
 DB 361 VFYGDWYGTGDSQREIPALKKIEPILKARKQVAYGAQHDYFDHHDYVGTREDDSYA 420
 QY 421 NSGLAALINDGPGARWYVGRONAGETWHDITGNRSEPVVINSBGGEFHNQGSVSII 480
 DB 421 NSGLAALINDGPGARWYVGRONAGETWHDITGNRSEPVVINSBGGEFHNQGSVSII 480
 QY 481 VQR 483
 DB 481 VQR 483
 RESULT 4
 ID AAV15418 standard; protein; 483 AA.
 AC AAV15418;
 XX 22-JUL-1999 (first entry)
 DT 22-JUL-1999 (first entry)
 XX Bacillus licheniformis alpha-amylase protein.
 DE Bacillus licheniformis alpha-amylase protein.
 XX Termamyl-like; alpha-amylase; variant; washing; dishwashing; production;
 KW sweetener; ethanol; starch; textile desizing; starch liquefaction;
 KM saccharification process.
 XX Bacillus licheniformis.
 OS WO9923211-A1.
 XX 14-MAY-1999.
 XX 30-OCT-1998; 98WO-DK000471.
 XX 30-OCT-1997; 97DK-00001240.
 XX 14-JUL-1998; 98DK-00000936.
 XX (NOVO) NOVO-NORDISK AS.
 XX Borchert TV, Svendsen A, Andersen C, Nielsen BR, Nissen TV;
 PI Kjærulff S;
 XX WPI; 1999-326987/27.
 XX New Termamyl-like alpha-amylase variants.
 PT Claim 38; Page 82-84; 115pp; English.
 PS

XX The specification describes termamy1-like alpha-amylase variants that
 CC have altered amino acid sequences to improve properties. The variants are
 CC produced by creating one or more of the following mutations in amino acid
 CC sequence of the parent termamy1-like alpha-amylase: T141, K142, F143,
 CC D144, F145, G146, G147, R148, G149, Q174, R181, G182, D183, G184, K185,
 CC A186, W189, S193, N195, K108, G109, D166, W167, D168, Q169, S170,
 CC R171, Q172, F173, F267, W268, K269, N270, D271, L272, G273, A274, L275,
 CC K311, E346, K385, N456, N457, K458, P459, G460, T461, V462, T463. The
 CC variants can be used for washing and/or dishwashing. They can also be
 CC used in the production of sweeteners and ethanol from starch, and/or for
 CC textile desizing, and in starch liquefaction and/or saccharification
 CC processes. The present amylase can function as the parent sequence in the
 CC production of the variants of the invention

XX Sequence 483 AA:

Query Match 100.0%; Score 2666; DB 2; Length 483;
 Best Local Similarity 100.0%; Pred. No. 1.7e-224;
 Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANLNGTLMQFEYMYMNDGQHWRLQNDASVLAHSGITVWIPPAKGTSGQADVGYAYD 60
 DB 1 ANLNGTLMQFEYMYMNDGQHWRLQNDASVLAHSGITVWIPPAKGTSGQADVGYAYD 60
 QY 61 LYDLGEFHOKGTVRTKYGKGELOSALKSLSRDINVGDVVINKGADATEDVTAVEV 120
 DB 61 LYDLGEFHOKGTVRTKYGKGELOSALKSLSRDINVGDVVINKGADATEDVTAVEV 120
 QY 121 DPADRRNVISGEHLIKAMTHFHPGSGSTYSPDKMWHYFDGTDWDESKLNRIYKFGQK 180
 DB 121 DPADRRNVISGEHLIKAMTHFHPGSGSTYSPDKMWHYFDGTDWDESKLNRIYKFGQK 180
 QY 121 DPADRRNVISGEHLIKAMTHFHPGSGSTYSPDKMWHYFDGTDWDESKLNRIYKFGQK 180
 DB 181 AMDMEVSNENGVNDYLMYADIDYDHPDVAAEIKRGWTYANELQDGFRLDAVKIKESF 240
 QY 181 AMDMEVSNENGVNDYLMYADIDYDHPDVAAEIKRGWTYANELQDGFRLDAVKIKESF 240
 DB 181 AMDMEVSNENGVNDYLMYADIDYDHPDVAAEIKRGWTYANELQDGFRLDAVKIKESF 240
 QY 241 LRDVNVHVRKTKGEMFTVAEYVQNDLGALENYLNTKNHNSVFPVPLHYQFHAASGSG 300
 DB 241 LRDVNVHVRKTKGEMFTVAEYVQNDLGALENYLNTKNHNSVFPVPLHYQFHAASGSG 300
 QY 241 LRDVNVHVRKTKGEMFTVAEYVQNDLGALENYLNTKNHNSVFPVPLHYQFHAASGSG 300
 DB 241 LRDVNVHVRKTKGEMFTVAEYVQNDLGALENYLNTKNHNSVFPVPLHYQFHAASGSG 300
 QY 301 GYDMRKLTNGTVVSKHPLKSVTFVDNHDTPQGSLSTVQTFKPLAFAFILTRESGYPO 360
 DB 301 GYDMRKLTNGTVVSKHPLKSVTFVDNHDTPQGSLSTVQTFKPLAFAFILTRESGYPO 360
 QY 301 GYDMRKLTNGTVVSKHPLKSVTFVDNHDTPQGSLSTVQTFKPLAFAFILTRESGYPO 360
 DB 301 GYDMRKLTNGTVVSKHPLKSVTFVDNHDTPQGSLSTVQTFKPLAFAFILTRESGYPO 360
 QY 361 VFYGDWYGTGDSQREIPALKKIEBILKARKQYVGAQHDYFDHHDIVGWTREGDSVA 420
 DB 361 VFYGDWYGTGDSQREIPALKKIEBILKARKQYVGAQHDYFDHHDIVGWTREGDSVA 420
 QY 421 NSGLAALITDGPAGAKRMVYGRONAGETWHDITGNRSEPVVINSBGGEFHHVNGGSVSIY 480
 DB 421 NSGLAALITDGPAGAKRMVYGRONAGETWHDITGNRSEPVVINSBGGEFHHVNGGSVSIY 480
 QY 481 VQR 483
 DB 481 VQR 483

RESULT 5
 ID AAY29852 standard; protein; 483 AA.

XX AAY29852;

DT 18-NOV-1999 (first entry)

XX Bacillus licheniformis Termamy1-like alpha-amylase Val54.

XX Alpha-amylase; Termamy1-like alpha-amylase; glucose syrup; starch.

XX Bacillus licheniformis.

PN WO9946399-A1.

XX 16-SEP-1999.
 XX 08-MAR-1999; 99WO-DK000114.
 XX 09-MAR-1998; 98DK-00000321.
 XX (NOVO) NOVO-NORDISK AS.
 XX Norman BE, Hendriksen HV,
 XX WPI; 1999-551422/46.
 DR N-PSDB; AA221078.
 XX Preparation of a glucose syrup, using a Termamy1-like alpha-amylase.
 PT Claim 8; Page 26-28; 36pp; English.
 XX A method has been developed for the preparation of a glucose syrup using
 CC a Termamy1-like alpha-amylase containing a substitution at Val(54). The
 CC glucose syrup obtained by the process is useful as an ingredient in food
 CC products. The Termamy1-like alpha-amylase facilitates the preparation of
 CC glucose syrups suitable for the food industry, previously only possible
 CC using acid hydrolysis. The present sequence represents Bacillus
 CC licheniformis Termamy1-like alpha-amylase

XX Sequence 483 AA:

Query Match 100.0%; Score 2666; DB 2; Length 483;
 Best Local Similarity 100.0%; Pred. No. 1.7e-224;
 Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANLNGTLMQFEYMYMNDGQHWRLQNDASVLAHSGITVWIPPAKGTSGQADVGYAYD 60
 DB 1 ANLNGTLMQFEYMYMNDGQHWRLQNDASVLAHSGITVWIPPAKGTSGQADVGYAYD 60
 QY 61 LYDLGEFHOKGTVRTKYGKGELOSALKSLSRDINVGDVVINKGADATEDVTAVEV 120
 DB 61 LYDLGEFHOKGTVRTKYGKGELOSALKSLSRDINVGDVVINKGADATEDVTAVEV 120
 QY 121 DPADRRNVISGEHLIKAMTHFHPGSGSTYSPDKMWHYFDGTDWDESKLNRIYKFGQK 180
 DB 121 DPADRRNVISGEHLIKAMTHFHPGSGSTYSPDKMWHYFDGTDWDESKLNRIYKFGQK 180
 QY 121 DPADRRNVISGEHLIKAMTHFHPGSGSTYSPDKMWHYFDGTDWDESKLNRIYKFGQK 180
 DB 121 DPADRRNVISGEHLIKAMTHFHPGSGSTYSPDKMWHYFDGTDWDESKLNRIYKFGQK 180
 QY 181 AMDMEVSNENGVNDYLMYADIDYDHPDVAAEIKRGWTYANELQDGFRLDAVKIKESF 240
 DB 181 AMDMEVSNENGVNDYLMYADIDYDHPDVAAEIKRGWTYANELQDGFRLDAVKIKESF 240
 QY 181 AMDMEVSNENGVNDYLMYADIDYDHPDVAAEIKRGWTYANELQDGFRLDAVKIKESF 240
 DB 181 AMDMEVSNENGVNDYLMYADIDYDHPDVAAEIKRGWTYANELQDGFRLDAVKIKESF 240
 QY 241 LRDVNVHVRKTKGEMFTVAEYVQNDLGALENYLNTKNHNSVFPVPLHYQFHAASGSG 300
 DB 241 LRDVNVHVRKTKGEMFTVAEYVQNDLGALENYLNTKNHNSVFPVPLHYQFHAASGSG 300
 QY 241 LRDVNVHVRKTKGEMFTVAEYVQNDLGALENYLNTKNHNSVFPVPLHYQFHAASGSG 300
 DB 241 LRDVNVHVRKTKGEMFTVAEYVQNDLGALENYLNTKNHNSVFPVPLHYQFHAASGSG 300
 QY 301 GYDMRKLTNGTVVSKHPLKSVTFVDNHDTPQGSLSTVQTFKPLAFAFILTRESGYPO 360
 DB 301 GYDMRKLTNGTVVSKHPLKSVTFVDNHDTPQGSLSTVQTFKPLAFAFILTRESGYPO 360
 QY 301 GYDMRKLTNGTVVSKHPLKSVTFVDNHDTPQGSLSTVQTFKPLAFAFILTRESGYPO 360
 DB 301 GYDMRKLTNGTVVSKHPLKSVTFVDNHDTPQGSLSTVQTFKPLAFAFILTRESGYPO 360
 QY 361 VFYGDWYGTGDSQREIPALKKIEBILKARKQYVGAQHDYFDHHDIVGWTREGDSVA 420
 DB 361 VFYGDWYGTGDSQREIPALKKIEBILKARKQYVGAQHDYFDHHDIVGWTREGDSVA 420
 QY 421 NSGLAALITDGPAGAKRMVYGRONAGETWHDITGNRSEPVVINSBGGEFHHVNGGSVSIY 480
 DB 421 NSGLAALITDGPAGAKRMVYGRONAGETWHDITGNRSEPVVINSBGGEFHHVNGGSVSIY 480
 QY 481 VQR 483
 DB 481 VQR 483

RESULT 6
 ID AAY07384 standard; protein; 483 AA.

CC processing of starch, i.e. starch liquefaction and saccharification. They
 CC may also be useful for washing, dishwashing and textile desizing. Hybrid
 CC alpha-amylases comprising partial amino acid sequences derived from two
 CC or more alpha-amylases have also been created in order to increase enzyme
 CC stability

XX Sequence 483 AA:

Query Match 100.0%; Score 2666; DB 3; Length 483;
 Best Local Similarity 100.0%; Pred. No. 1.7e-224;
 Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANNGTLMQYFEMWPNQGHWRRLQNDSDATLAEGHTAWIPPAVYKTSQADVGAYD 60
 DB 1 ANNGTLMQYFEMWPNQGHWRRLQNDSDATLAEGHTAWIPPAVYKTSQADVGAYD 60
 QY 61 LYDGEFHQKGTAVTKYGTGKELQSAIKLSHRDINVGDVVINKGADATEDVAVEV 120
 DB 61 LYDGEFHQKGTAVTKYGTGKELQSAIKLSHRDINVGDVVINKGADATEDVAVEV 120
 QY 121 DPADNRNVTSGEHLIKAWTHFHPFGSGTYSDFKMWYHPDGTWDSRKLNRITYKFGK 180
 DB 121 DPADNRNVTSGEHLIKAWTHFHPFGSGTYSDFKMWYHPDGTWDSRKLNRITYKFGK 180
 QY 181 AMDWEVSNGNNDYLYMADIDYDHPDVAEIKRWGTWYANLQDGFRLDAVHIKFSF 240
 DB 181 AMDWEVSNGNNDYLYMADIDYDHPDVAEIKRWGTWYANLQDGFRLDAVHIKFSF 240
 QY 241 LRDVNVHREKTKGEMFTVAEYQNDLGALENYLNKTNFNHVSVDVLAHQFHAASVTOGG 300
 DB 241 LRDVNVHREKTKGEMFTVAEYQNDLGALENYLNKTNFNHVSVDVLAHQFHAASVTOGG 300
 QY 301 GYDMRKLNGTVVSKHPLKSVTFVNDHDTQPGQSLSTVQTFKPLAVAFILTRSSGYPO 360
 DB 301 GYDMRKLNGTVVSKHPLKSVTFVNDHDTQPGQSLSTVQTFKPLAVAFILTRSSGYPO 360
 QY 361 VFYGDWYGTGDSQREIPALKHIEPIKARKQYVAGQHDYFDHDIIVGWTREGDSVA 420
 DB 361 VFYGDWYGTGDSQREIPALKHIEPIKARKQYVAGQHDYFDHDIIVGWTREGDSVA 420
 QY 421 NSGLAALITDGPAGAKRMVYGRONAGETWHDITGNRSEPVVINSBGMGEFHNQGSVSIT 480
 DB 421 NSGLAALITDGPAGAKRMVYGRONAGETWHDITGNRSEPVVINSBGMGEFHNQGSVSIT 480
 QY 481 VQR 483
 DB 481 VQR 483

RESULT 8
 AAY97545
 ID AAY97545 standard; protein; 483 AA.

XX AAY97545;

DT 12-FEB-2001 (first entry)

XX B. licheniformis termamyl-like alpha amylase.

XX Termamyl-like alpha-amylase; variant; starch liquefaction; fuel;
 XX detergent composition; laundry cleaning composition; ethanol production;
 XX dish washing cleaning composition; hard surface cleaning composition;
 XX industrial ethanol production; textile desizing.

OS Bacillus licheniformis.

XX WO200060059-A2.

XX 12-OCT-2000.

XX 28-MAR-2000; 2000WO-DK000148.

XX 30-MAR-1999; 99DK-00000437.

XX (NOVO) NOVO NORDISK AS.
 PA Andersen C, Jorgensen CT, Bisgard-Frantzen H, Svendsen A;
 PI Kjaerulf S;
 DR WPI: 2001-015656/02.
 XX N-PsDB; AAA37849.

PT New variants of parent Termamyl-like alpha-amylase, useful in starch
 PT liquefaction, in detergent compositions and in ethanol production,
 PT exhibit altered cleavage pattern relative to the parent.

XX Claim 1; Page 60-62; 78pp; English.

CC This sequence represents a termamyl-like alpha amylase. The invention
 CC relates to a variant (1) of parent Termamyl-like alpha-amylase comprising
 CC alteration at one or more of the positions M13, G48, T49, S50, Q51, A52,
 CC D53, V54, G57, G107, G108, A111, S168 and M197. The alterations in (1)
 CC are independently an insertion of an amino acid downstream of the amino
 CC acid which occupies the position of an amino acid substitution of the amino
 CC acid which occupies the position with a different amino acid. The variant
 CC has alpha-amylase activity (1) or compositions containing it are useful
 CC in starch liquefaction, in detergent compositions such as laundry, dish
 CC washing and hard surface cleaning compositions, ethanol production such
 CC as fuel, drinking and industrial ethanol production, desizing of
 CC textiles, fabrics or garments. (1) exhibits a reduced capability of
 CC cleaving a substrate close to the branching point, and further exhibits
 CC improved substrate specificity and/or improved specific activity relative
 CC to the parent alpha-amylase

XX Sequence 483 AA:

Query Match 100.0%; Score 2666; DB 4; Length 483;
 Best Local Similarity 100.0%; Pred. No. 1.7e-224;
 Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANNGTLMQYFEMWPNQGHWRRLQNDSDATLAEGHTAWIPPAVYKTSQADVGAYD 60
 DB 1 ANNGTLMQYFEMWPNQGHWRRLQNDSDATLAEGHTAWIPPAVYKTSQADVGAYD 60
 QY 61 LYDGEFHQKGTAVTKYGTGKELQSAIKLSHRDINVGDVVINKGADATEDVAVEV 120
 DB 61 LYDGEFHQKGTAVTKYGTGKELQSAIKLSHRDINVGDVVINKGADATEDVAVEV 120
 QY 121 DPADNRNVTSGEHLIKAWTHFHPFGSGTYSDFKMWYHPDGTWDSRKLNRITYKFGK 180
 DB 121 DPADNRNVTSGEHLIKAWTHFHPFGSGTYSDFKMWYHPDGTWDSRKLNRITYKFGK 180
 QY 181 AMDWEVSNGNNDYLYMADIDYDHPDVAEIKRWGTWYANLQDGFRLDAVHIKFSF 240
 DB 181 AMDWEVSNGNNDYLYMADIDYDHPDVAEIKRWGTWYANLQDGFRLDAVHIKFSF 240
 QY 241 LRDVNVHREKTKGEMFTVAEYQNDLGALENYLNKTNFNHVSVDVLAHQFHAASVTOGG 300
 DB 241 LRDVNVHREKTKGEMFTVAEYQNDLGALENYLNKTNFNHVSVDVLAHQFHAASVTOGG 300
 QY 301 GYDMRKLNGTVVSKHPLKSVTFVNDHDTQPGQSLSTVQTFKPLAVAFILTRSSGYPO 360
 DB 301 GYDMRKLNGTVVSKHPLKSVTFVNDHDTQPGQSLSTVQTFKPLAVAFILTRSSGYPO 360
 QY 361 VFYGDWYGTGDSQREIPALKHIEPIKARKQYVAGQHDYFDHDIIVGWTREGDSVA 420
 DB 361 VFYGDWYGTGDSQREIPALKHIEPIKARKQYVAGQHDYFDHDIIVGWTREGDSVA 420
 QY 421 NSGLAALITDGPAGAKRMVYGRONAGETWHDITGNRSEPVVINSBGMGEFHNQGSVSIT 480
 DB 421 NSGLAALITDGPAGAKRMVYGRONAGETWHDITGNRSEPVVINSBGMGEFHNQGSVSIT 480
 QY 481 VQR 483
 DB 481 VQR 483

RESULT 9
 ABB06936
 ID ABB06936 standard; protein; 483 AA.
 XX
 AC ABB06936;
 XX
 DT 19-JUN-2002 (first entry)
 XX
 DE B. licheniformis termamyli-like alpha-amylase protein SEQ ID NO:8.
 XX
 KW Bacillus; termamyli-like alpha-amylase; alpha-amylase; EC 3.2.1.1;
 KW variant; mutant; enzyme; protein co-ordinate data; cleaning; detergent;
 KW washing; sweetener; ethanol; starch.
 XX
 OS Bacillus licheniformis.
 XX
 PN W020016712-A2.
 XX
 PD 13-SEP-2001.
 XX
 PF 07-MAR-2001; 2001WO-DK000144.
 XX
 PR 09-MAR-2000; 2000DK-00000376.
 PR 15-MAR-2000; 2000US-0189857P.
 PR 23-FEB-2001; 2001DK-00000303.
 PR 26-FEB-2001; 2001US-0271382P.
 XX
 PA (NOVO) NOVOZYMES AS.
 XX
 PI Andersen C, Borchert TV, Nielsen BR;
 XX
 DR WPI: 2002-239612/29.
 DR N-PSDB; ABL50567.
 XX
 PT Novel variant of parent termamyli-like alpha-amylase useful as a component
 PT in washing and dishwashing compositions, for textile desizing, for starch
 PT liquefaction, and for producing sweeteners and ethanol from starch.
 XX
 PS Claim 8; Page 142-143; 153pp; English.
 XX
 CC The present invention describes a variant of a parent termamyli-like alpha
 CC -amylase (EC 3.2.1.1) (I) comprising an alteration at one or more
 CC positions of a group of 31 possible amino acid positions. The alteration
 CC in (I) may be at Arg28, Arg118, Asn174, Arg181, Gly182, Asp183, Gly184,
 CC Gly186, Trp189, Asn195, Met202, Tyr298, Leu302, Ser303, Asn305,
 CC Arg310, Asn314, Arg320, His324, Glu345, Tyr396, Arg400, Trp439, Arg444,
 CC Asn445, Lys446, Glu448, Arg458, Asn471, or Asn484. (I) can be used for
 CC washing and/or dishwashing, textile desizing, and starch liquefaction.
 CC (I) is useful as a component in hard surface cleaning detergent
 CC composition, and for producing sweeteners and ethanol from starch. (I)
 CC has altered solubility, preferably increased solubility, in particular
 CC under washing, dish washing or hard surface cleaning conditions. The
 CC present sequence represents a Bacillus licheniformis termamyli-like alpha-
 CC amylase which is used in the exemplification of the present invention.
 XX
 SO Sequence 483 AA.
 Query Match 100.0%; Score 2666; DB 5; Length 483;
 Best Local Similarity 100.0%; Pred. No. 1.7e-224;
 Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 181 AMDMEVSNNGNYDYLIMVADIDYDHPDVAAEIKRWGTWYANELQDGRFLDAVGKIKRSF 240
 DB 181 AMDMEVSNNGNYDYLIMVADIDYDHPDVAAEIKRWGTWYANELQDGRFLDAVGKIKRSF 240
 QY 241 LRDVNVHVEKTKGKEMFTVAEYWDNGLALENYLNTKTPNNSVPPVPLHYQFHAASQGG 300
 DB 241 LRDVNVHVEKTKGKEMFTVAEYWDNGLALENYLNTKTPNNSVPPVPLHYQFHAASQGG 300
 QY 301 GYDMRKLINGTVASKPLKSVTFVNNHDTOPQOSLESTVQTFKPLAVAFILTRBSGYPQ 360
 DB 301 GYDMRKLINGTVASKPLKSVTFVNNHDTOPQOSLESTVQTFKPLAVAFILTRBSGYPQ 360
 QY 361 VFYGDWYGTGKDSQREIPALKEKIEPILKARKQVYGAQHDFDHDIVGWTREGDSVA 420
 DB 361 VFYGDWYGTGKDSQREIPALKEKIEPILKARKQVYGAQHDFDHDIVGWTREGDSVA 420
 QY 421 NSGLAALITDGPAGAKRMVYGRONAGETWHDITGNRSEPPVINSGEWGEFVNGSVSIIY 480
 DB 421 NSGLAALITDGPAGAKRMVYGRONAGETWHDITGNRSEPPVINSGEWGEFVNGSVSIIY 480
 QY 481 VQR 483
 DB 481 VQR 483
 RESULT 10
 AAU12152
 ID AAU12152 standard; protein; 483 AA.
 XX
 AC AAU12152;
 XX
 DT 09-APR-2002 (first entry)
 XX
 DE Bacillus TERMAMYLI alpha-amylase.
 XX
 KW TERMAMYLI; alpha-amylase; detergent; dishwashing; textile desizing;
 KW starch liquefaction; ethanol production; hard surface cleaner; sweetener;
 KW amylopectin; limit dextrin; NOVAMYLI.
 XX
 OS Bacillus licheniformis.
 XX
 PN W0200189107-A2.
 XX
 PD 22-NOV-2001.
 XX
 PF 10-MAY-2001; 2001WO-DK000323.
 XX
 PR 12-MAY-2000; 2000DK-00000779.
 XX
 PA (NOVO) NOVOZYMES AS.
 XX
 PI Svendsen A, Jorgensen CT, Nielsen BR;
 XX
 DR WPI: 2002-106123/14.
 DR N-PSDB; AAS20025.
 XX
 PT New variant of parent Termamyli-like alpha-amylase for use as a component
 PT in washing and dishwashing compositions, for textile desizing, for starch
 PT liquefaction, and for producing sweeteners and ethanol from starch.
 XX
 PS Claim 5; Fig 1; 84pp; English.
 XX
 CC The invention relates to a variant of parent TERMAMYLI-like alpha- amylase
 CC comprising an alteration at regions 186-193, 261-276, 283-293 or 334-339,
 CC or at position 234, where the variant has alpha-amylase activity and each
 CC position corresponds to a position of a parent Termamyli-like alpha-
 CC amylase sequence having a Bacillus licheniformis alpha-amylase sequence
 CC of 483 amino acids, given in specification. The variant alpha- amylase, a
 CC detergent additive comprising the variant or a detergent composition
 CC comprising the variant, is useful for washing and/or dishwashing or
 CC textile desizing. The alpha-amylase is useful for starch liquefaction or
 CC ethanol production and as a component in a hard surface cleaning

RESULT 12
 AAB47853
 ID AAB47853 standard; protein; 483 AA.
 XX
 AC AAB47853;
 XX
 DT 02-APR-2002 (first entry)
 XX
 DE Bacillus termamyli alpha amylase.
 XX
 KW Alpha amylase; Bacillus; Termamyli-like; maltodextrin; glucose syrup;
 KW starch; food; feed; pharmaceutical; confectionery; candy; isotonic drink;
 KW bakery; cereal bar; ice cream; coffee whitener; salad dressing;
 KW cured meat; fermented meat; spice.
 XX
 OS Bacillus licheniformis.
 XX
 PN WO200196537-A2.
 XX
 PD 20-DEC-2001.
 XX
 PF 13-JUN-2001; 2001WO-DK000404.
 XX
 PR 14-JUN-2000; 2000DK-00000917.
 XX
 PR 20-JUN-2000; 2000US-0212852P.
 XX
 PA (NOVO) NOVOZYMES AS.
 XX
 PI Nielsen BR, Welbye M;
 XX
 DR WPI; 2002-098064/13.
 XX
 DR N-PSDB; AAI72214.
 XX
 PT New modified alpha-amylase derived from the genus Bacillus and/or is a
 PT Termamyli-like alpha-amylase, which has been pre-oxidized for producing
 PT maltodextrin or glucose syrup.
 XX
 PS Claim 5; Page 36-37; 47pp; English.
 XX
 CC The sequences given in AAB47850-56 show modified alpha-amylases derived
 CC from the genus Bacillus. These alpha amylases are Termamyli-like alpha
 CC amylase and they have been pre-oxidized. The alpha amylase is useful for
 CC producing a maltodextrin or glucose syrup, by treating starch with a pre-
 CC oxidized alpha-amylase until a product with a DE between 5-45 has been
 CC provided and/or until a product with a molecular weight of between 5-30
 CC kDa has been provided. The product comprises a maltodextrin with a DE of
 CC 18.5 and/or a maltodextrin with a molecular weight of 14-16 kDa. The
 CC alpha amylase is useful for producing a maltodextrin or glucose syrup,
 CC where the glucose syrup is useful as an ingredient in food, feed or
 CC pharmaceuticals. Glucose syrup is useful in confectionery such as
 CC candies, beverages such as isotonic drinks, bakery such as cereal bars,
 CC dairy and ice cream such as coffee whiteners, conventional foods such as
 CC salad dressings, and food ingredients and preparations such as cured
 CC meat, fermented meat, spices and seasoning encapsulated flavours
 XX
 SQ Sequence 483 AA;
 XX
 QY Query Match 100.0%; Score 2666; DB 5; Length 483;
 DB Best Local Similarity 100.0%; Pred. No. 1.7e-224;
 DB Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ANNGTMOYFEMMPDQGHMRLODSAYLAHEGTTAWIPPAKYSQADVGYGAND 60
 DB 1 ANNGTMOYFEMMPDQGHMRLODSAYLAHEGTTAWIPPAKYSQADVGYGAND 60
 QY 61 LYDGEFHOKGTVEKTKGTGKGLSALKSLSHRDINVGDVVINKGADATEDVAVEV 120
 DB 61 LYDGEFHOKGTVEKTKGTGKGLSALKSLSHRDINVGDVVINKGADATEDVAVEV 120
 QY 121 DPADNRVYISGEHLIKAWTHFFPPRGSTYSDFRWMYHHDGTDWDSRLNLIYFQCK 180
 DB 121 DPADNRVYISGEHLIKAWTHFFPPRGSTYSDFRWMYHHDGTDWDSRLNLIYFQCK 180
 QY 121 DPADNRVYISGEHLIKAWTHFFPPRGSTYSDFRWMYHHDGTDWDSRLNLIYFQCK 180
 DB 121 DPADNRVYISGEHLIKAWTHFFPPRGSTYSDFRWMYHHDGTDWDSRLNLIYFQCK 180

QY 181 AMDEVSNGENVYDIYMDADIDYDHPDAAEIKRWGTWYANELQDGFELDAVKHIFSF 240
 DB 181 AMDEVSNGENVYDIYMDADIDYDHPDAAEIKRWGTWYANELQDGFELDAVKHIFSF 240
 QY 241 LRDVNVHVEKTEKEMFTVAEYQNDLGALENYLNKTNFNHVSFVDFPLHYQPHAASTOGG 300
 DB 241 LRDVNVHVEKTEKEMFTVAEYQNDLGALENYLNKTNFNHVSFVDFPLHYQPHAASTOGG 300
 QY 301 GYDMRKILNCTVVSKEPLKSVTFVNDHDTQPGQSLESTVQTWFKPLAVAFILTRSGYQ 360
 DB 301 GYDMRKILNCTVVSKEPLKSVTFVNDHDTQPGQSLESTVQTWFKPLAVAFILTRSGYQ 360
 QY 361 VFYGDWYGTGDSQREIPLKKEIPLIKARKQYAGAGHDYFDHDIYGMTREGDSSVA 420
 DB 361 VFYGDWYGTGDSQREIPLKKEIPLIKARKQYAGAGHDYFDHDIYGMTREGDSSVA 420
 QY 421 NSGLAALITDGPAGAKRMVYGRONAGETWHDITGNSEPVVINSBGWGEFHYNGGSVSIY 480
 DB 421 NSGLAALITDGPAGAKRMVYGRONAGETWHDITGNSEPVVINSBGWGEFHYNGGSVSIY 480
 QY 481 VQR 483
 DB 481 VQR 483
 QY 481 VQR 483
 DB 481 VQR 483
 RESULT 13
 ABB76589
 ID ABB76589 standard; protein; 483 AA.
 XX
 AC ABB76589;
 XX
 DT 19-AUG-2002 (first entry)
 XX
 DE Termamyli-like alpha-amylase #4.
 XX
 KW Termamyli; alpha amylase; starch liquefaction; ethanol production;
 KW textile desizing; detergent; enzyme.
 XX
 OS Bacillus licheniformis.
 XX
 PN WO200210355-A2.
 XX
 PD 07-FEB-2002.
 XX
 PF 12-JUL-2001; 2001WO-DK000488.
 XX
 PR 01-AUG-2000; 2000DK-00001160.
 XX
 PR 12-SEP-2000; 2000DK-00001354.
 XX
 PR 10-NOV-2000; 2000DK-00001687.
 XX
 PR 26-APR-2001; 2001DK-00000655.
 XX
 PA (NOVO) NOVOZYMES AS.
 XX
 PI Thisted T, Kjaerulff S, Andersen C, Fuglsang CC;
 XX
 DR WPI; 2002-280633/32-
 XX
 DR N-PSDB; ABI96210.
 XX
 PT Variant of parent Termamyli-like alpha amylase, useful in detergent
 PT compositions, for starch liquefaction, ethanol production, washing and/or
 PT dish washing, and textile desizing.
 XX
 PS Claim 1; Fig 4; 90pp; English.
 XX
 CC This invention relates to variants of a parent Termamyli-like alpha-
 CC amylases. These are used for starch liquefaction, ethanol production,
 CC detergent, and textile desizing. The amylases have altered stability,
 CC particularly at high temperatures from 70-120plusC and low pH in the
 CC range from pH 4.0-6.0. The present sequence is a termamyli-like-alpha-
 CC amylase
 XX
 SQ Sequence 483 AA;
 XX

Query Match 100.0%; Score 2666; DB 5; Length 483;
Best Local Similarity 100.0%; Pred. No. 1.7e-224;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANINGTLMQYFEWYMPNDGQHWRLQNDSDAYLAHEGHTAVWIPPAYKGTSGADVGAYD 60
DB 1 ANINGTLMQYFEWYMPNDGQHWRLQNDSDAYLAHEGHTAVWIPPAYKGTSGADVGAYD 60
QY 61 LYDIGEHOQGTVTRTKYGTGKELQSAIKSLHSRDINVGVDVINNHGGADATEDVAVEV 120
DB 61 LYDIGEHOQGTVTRTKYGTGKELQSAIKSLHSRDINVGVDVINNHGGADATEDVAVEV 120
QY 121 DPADRNKRVISGEHLIKAMTHFHPFGSGTYSDFKHMWHFDGTDWDESRKLNRIYKFGQK 180
DB 121 DPADRNKRVISGEHLIKAMTHFHPFGSGTYSDFKHMWHFDGTDWDESRKLNRIYKFGQK 180
QY 181 AMDWEVSNGNNGYIYLMYADIDYDHPVAAEIKRWGTWYANELQDGFRLDAVKHIFSF 240
DB 181 AMDWEVSNGNNGYIYLMYADIDYDHPVAAEIKRWGTWYANELQDGFRLDAVKHIFSF 240
QY 241 LRDWVNHVRKTKGEMFTVAEYQNDLGALENYLNKTNPNHSDVDFLHYQFHAASTOGG 300
DB 241 LRDWVNHVRKTKGEMFTVAEYQNDLGALENYLNKTNPNHSDVDFLHYQFHAASTOGG 300
QY 301 GYDMRKLTNGTVSKHPLKSVTFVDNHDTPQGSLESTVQTFKPLAYAFILTRSGYPO 360
DB 301 GYDMRKLTNGTVSKHPLKSVTFVDNHDTPQGSLESTVQTFKPLAYAFILTRSGYPO 360
QY 361 VFYGDWYGTGDSOREIPALKHKEIPIIKAKQYAYGAOHDFPHNDIVGWTREGDSVA 420
DB 361 VFYGDWYGTGDSOREIPALKHKEIPIIKAKQYAYGAOHDFPHNDIVGWTREGDSVA 420
QY 421 NSGLAALITDGPAGAKMYVGRONAGETWHDITGNRSEPVVINSBGWGFHNNGSVSIY 480
DB 421 NSGLAALITDGPAGAKMYVGRONAGETWHDITGNRSEPVVINSBGWGFHNNGSVSIY 480
QY 481 VQR 483
DB 481 VQR 483

RESULT 14
AAR98007
ID AAR98007 standard; protein; 531 AA.
XX
AC AAR98007;
XX
DT 27-AUG-2003 (revised)
DT 16-OCT-1996 (first entry)
XX
DE PeB signal-Termamyl-leucine zipper.
XX
KW Allergen; allergy; self-oligomerizing polypeptide; Termamyl;
KW alpha-amylase; leucine zipper; detergent.
XX
OS Synthetic.
OS Chimeric.
OS Chimeric.
XX
FH Key Location/Qualifiers
FH Protein 1..482
FT /label= Termamyl
FT Region 483..489
FT /label= Linker
FT Domain 490..531
FT /label= Leucine_zipper
XX
XX WO9616177-A1.
XX
XX 30-MAY-1996.
XX
XX 23-NOV-1995; 95WO-DK000463.
XX

PR 24-NOV-1994; 94DX-00001343.
XX
XX (NOVO) NOVO-NORDISK AS.
XX
XX Bjornvad ME, Prento A;
XX
XX WPI; 1996-268613/27.
XX
XX N-PeDB; AAT33228.
XX
XX Prodn. of self-oligomerising peptide(s) with reduced allergenicity - used
XX in household and personal cleaning prods., and in food and feeds etc.
XX
XX Disclosure; Page 61-63; 85pp; English.
XX
XX A polypeptide (AAR98007) is composed of Termamyl alpha-amylase, a linker
XX derived from the IgG3 hinge domain and a leucine zipper from the GCN4
XX yeast transcription factor. It was produced by PCR amplification of the
XX Termamyl gene and ligation of synthetic oligonucleotides (see also
XX AAT33228-32) encoding the leucine zipper and linker. Upon expression in
XX E.coli, using a vector including the pelB signal sequence, the Termamyl
XX product self-oligomerised into a dimer that was secreted into the
XX periplasm. The method constitutes an industrially applicable process for
XX producing a biologically active polypeptide that self-oligomerises owing
XX to the presence of leucine zippers, the enlarged size of the resulting
XX polypeptide leading to a reduction in its allergenicity. (Updated on 27-
XX AUG-2003 to correct OS field.)
XX
XX Sequence 531 AA;
SQ

Query Match 100.0%; Score 2666; DB 2; Length 531;
Best Local Similarity 100.0%; Pred. No. 1.9e-224;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANINGTLMQYFEWYMPNDGQHWRLQNDSDAYLAHEGHTAVWIPPAYKGTSGADVGAYD 60
DB 1 ANINGTLMQYFEWYMPNDGQHWRLQNDSDAYLAHEGHTAVWIPPAYKGTSGADVGAYD 60
QY 61 LYDIGEHOQGTVTRTKYGTGKELQSAIKSLHSRDINVGVDVINNHGGADATEDVAVEV 120
DB 61 LYDIGEHOQGTVTRTKYGTGKELQSAIKSLHSRDINVGVDVINNHGGADATEDVAVEV 120
QY 121 DPADRNKRVISGEHLIKAMTHFHPFGSGTYSDFKHMWHFDGTDWDESRKLNRIYKFGQK 180
DB 121 DPADRNKRVISGEHLIKAMTHFHPFGSGTYSDFKHMWHFDGTDWDESRKLNRIYKFGQK 180
QY 181 AMDWEVSNGNNGYIYLMYADIDYDHPVAAEIKRWGTWYANELQDGFRLDAVKHIFSF 240
DB 181 AMDWEVSNGNNGYIYLMYADIDYDHPVAAEIKRWGTWYANELQDGFRLDAVKHIFSF 240
QY 241 LRDWVNHVRKTKGEMFTVAEYQNDLGALENYLNKTNPNHSDVDFLHYQFHAASTOGG 300
DB 241 LRDWVNHVRKTKGEMFTVAEYQNDLGALENYLNKTNPNHSDVDFLHYQFHAASTOGG 300
QY 301 GYDMRKLTNGTVSKHPLKSVTFVDNHDTPQGSLESTVQTFKPLAYAFILTRSGYPO 360
DB 301 GYDMRKLTNGTVSKHPLKSVTFVDNHDTPQGSLESTVQTFKPLAYAFILTRSGYPO 360
QY 361 VFYGDWYGTGDSOREIPALKHKEIPIIKAKQYAYGAOHDFPHNDIVGWTREGDSVA 420
DB 361 VFYGDWYGTGDSOREIPALKHKEIPIIKAKQYAYGAOHDFPHNDIVGWTREGDSVA 420
QY 421 NSGLAALITDGPAGAKMYVGRONAGETWHDITGNRSEPVVINSBGWGFHNNGSVSIY 480
DB 421 NSGLAALITDGPAGAKMYVGRONAGETWHDITGNRSEPVVINSBGWGFHNNGSVSIY 480
QY 481 VQR 483
DB 481 VQR 483

RESULT 15
AAW22523
ID AAW22523 standard; protein; 630 AA.

XX AAM2523;
 AC 17-OCT-2003 (revised)
 DT 08-FEB-1998 (first entry)
 XX
 DE Alpha-amyase-CenA cellulose binding domain hybrid enzyme.
 XX Desizing; cellulose; fabric; enzyme hybrid; Termamyl; alpha-amyase;
 KM cellulose binding domain; CenA; Bacillus licheniformis;
 KM Cellulomonas firm; protein secretion.
 XX
 OS Bacillus licheniformis.
 OS Cellulomonas firm; strain ATCC 484.
 OS Chimeric.
 XX
 PH Key
 FT Peptide
 FT /label= Sig_peptide
 FT /note= "Termamyl signal peptide"
 FT 20..630
 FT /label= Mat protein
 FT /note= "CBD (aa29-147)-Termamyl (aa148-630) hybrid"
 XX
 PN WO9728256-A1.
 PD 07-AUG-1997.
 XX
 XX 29-JAN-1997; 97WO-DK000041.
 PF 29-JAN-1997; 96DK-00000093.
 PR 29-JAN-1997; 96DK-00000093.
 XX
 XX (NOVO) NOVO-NORDISK AS.
 PA
 XX Von Der Osten C, Bjornvad M, Vind J, Rasmussen MD;
 PI MPI, 1997-402610/37.
 DR N-PSDB; AA777063.
 XX
 PT Desizing cellulose-containing fabric or textile using an enzyme hybrid -
 PT which comprises a catalytically active amino acid sequence of a non-
 PT cellulolytic enzyme linked to an amino acid sequence comprising a
 PT cellulose binding domain.
 XX
 XX Example 3; Page 60; 72pp; English.
 PS
 CC This protein sequence comprises a hybrid enzyme in which Bacillus
 CC licheniformis alpha-amyase (Termamyl) signal peptide is linked to the
 CC cellulose binding domain (CBD) of Cellulomonas firm CenA, which is
 CC further linked to mature Termamyl polypeptide. The CBD-Termamyl fusion
 CC has been expressed and secreted as an approx. 85 kDa protein in Bacillus
 CC subtilis p12306 transformants. A claimed process for desizing cellulose-
 CC containing fabric or textile comprises treating the fabric or textile
 CC with a modified enzyme (enzyme hybrid) comprising a non-cellulolytic
 CC enzyme linked to a CBD. The process gives improved enzyme performance by
 CC modifying the enzyme so as to increase its affinity for cellulose
 CC fabric. A desizing composition suitable for use in the process comprises
 CC the enzyme hybrid and a wetting agent. (Updated on 17-OCT-2003 to
 CC standardise OS field)
 CC
 XX
 SQ Sequence 630 AA;

Query Match 100.0%; Score 2666; DB 2; Length 630;
 Best Local Similarity 100.0%; Pred. No. 2,5e-224;
 Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANINGTLMQYFFWYMNPDGQWRLQNDGAYLAHSGITAWIPPAKYGTSGADVGAYD 60
 DB 148 ANINGTLMQYFFWYMNPDGQWRLQNDGAYLAHSGITAWIPPAKYGTSGADVGAYD 207
 QY 61 LYLDFGHQKGVTRTKYGTGKGLQSAIKSLHSRDINVGQVVIHKGADATEDVTAVAV 120
 DB 208 LYLDFGHQKGVTRTKYGTGKGLQSAIKSLHSRDINVGQVVIHKGADATEDVTAVAV 267

QY 121 DPADNRNVIISGEHLIKANTHFFPGRGSTYSDFFKHWTHFPGDTWDESRKLNRIYKRGK 180
 DB 266 DPADNRNVIISGEHLIKANTHFFPGRGSTYSDFFKHWTHFPGDTWDESRKLNRIYKRGK 327
 QY 181 AMDWEVSNENGVYDYLMTADIDYDHPDVAAEIKKRGTYANELQDGRDLDAVKIKFSF 240
 DB 328 AMDWEVSNENGVYDYLMTADIDYDHPDVAAEIKKRGTYANELQDGRDLDAVKIKFSF 387
 QY 241 LRDWVNHVREKTKEMFTVAEYQNDGALBNYLNKTNFNHSDVPDPLHYQFHAASSTGG 300
 DB 388 LRDWVNHVREKTKEMFTVAEYQNDGALBNYLNKTNFNHSDVPDPLHYQFHAASSTGG 447
 QY 301 GYDMRLTLNGTVASHPPLKSVTFVNNHTOPQOSLESTVQTMFKFLAYAFILTRSGYPO 360
 DB 448 GYDMRLTLNGTVASHPPLKSVTFVNNHTOPQOSLESTVQTMFKFLAYAFILTRSGYPO 507
 QY 361 VFYGDWYGTGKDSOREIPALKEIPILKARKQYAYGAQHDYFDRHDIVGWTRGDSVA 420
 DB 508 VFYGDWYGTGKDSOREIPALKEIPILKARKQYAYGAQHDYFDRHDIVGWTRGDSVA 567
 QY 421 NSGLAALITDGPQAKRMVYRGQNGETWHDITGNRSEPVVINSQMGSEFHNQGSVSILY 480
 DB 568 NSGLAALITDGPQAKRMVYRGQNGETWHDITGNRSEPVVINSQMGSEFHNQGSVSILY 627
 QY 481 VQR 483
 DB 628 VQR 630

Search completed: May 3, 2004, 20:50:29
 Job time : 53.0521 secs

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OM protein - protein search, using sw model

Run on: May 3, 2004, 20:44:58 ; Search time 34.1233 Seconds
(without alignments)
4435.289 Million cell updates/sec

Title: US-10-644-187-4
Perfect score: 2624
Sequence: 1 VNGTLMQYEWYTPNDGQHM.....KIGSDQWGEFHNDSVSTY 480

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SP archaea:*
2: SP bacteria:*
3: SP fungi:*
4: SP human:*
5: SP invertebrate:*
6: SP mammal:*
7: SP_mmc:*
8: SP_organelle:*
9: SP_phage:*
10: SP_plant:*
11: SP_rodent:*
12: SP_virus:*
13: SP_vertebrate:*
14: SP_unclassified:*
15: SP_virus:*
16: SP_bacteriap:*
17: SP_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2061	78.5	519	2 Q9ROT8	Q9ROT8 cytophaga s
2	1947	74.2	513	16 Q81A54	Q81A54 bacillus ce
3	1946	74.2	533	2 Q9A054	Q9A054 bacillus me
4	1914	72.9	513	16 Q81YJ4	Q81YJ4 bacillus an
5	1836	70.0	516	2 Q82839	Q82839 bacillus sp
6	1767.5	67.4	549	2 Q31193	Q31193 bacillus st
7	1766.5	67.3	549	2 Q9KXV6	Q9KXV6 bacillus st
8	1762.5	67.2	521	2 P71034	P71034 bacillus sp
9	1749.5	66.7	613	2 Q59222	Q59222 bacillus sp
10	1614.5	61.5	501	2 Q93148	Q93148 bacillus sp
11	1474.5	56.2	507	16 Q87H66	Q87H66 vibrio para
12	1359	51.8	481	16 Q89YPI	Q89YPI bacteroides
13	1253	47.8	493	2 Q03657	Q03657 bacillus ci
14	1217	46.4	484	16 Q97049	Q97049 streptococc
15	1212	46.2	484	16 Q8DPC8	Q8DPC8 streptococc
16	1206.5	46.0	488	16 Q8E966	Q8E966 streptococc

17	1206.5	46.0	488	16 Q8E0M2	Q8E0M2 streptococc
18	1205.5	45.9	486	16 Q8DPT08	Q8DPT08 streptococc
19	1197	45.6	492	16 Q8YTU21	Q8YTU21 anabaena sp
20	1190.5	45.4	484	2 Q50583	Q50583 streptococc
21	1182.5	45.1	486	2 Q68875	Q68875 streptococc
22	1177.5	44.9	485	2 Q53786	Q53786 streptococc
23	1127	42.9	491	16 Q9CG59	Q9CG59 lactococc
24	1057.5	40.3	529	3 Q877B1	Q877B1 aspergillus
25	1050	40.0	506	16 Q8U916	Q8U916 aspergilli
26	1006	38.3	494	16 Q8Z555	Q8Z555 salmonella
27	1000	38.1	495	16 Q8F6L8	Q8F6L8 escherichia
28	999	38.1	495	16 Q8XB66	Q8XB66 escherichia
29	989	37.7	495	16 Q7UAB0	Q7UAB0 shigella fl
30	987	37.6	495	16 Q83R40	Q83R40 shigella fl
31	496	18.9	469	1 Q50200	Q50200 thermococc
32	494.5	18.8	461	1 Q8NKR5	Q8NKR5 thermococc
33	480.5	18.3	461	1 Q33476	Q33476 pyrococcus
34	480	18.3	457	1 Q93647	Q93647 thermococc
35	476.5	18.2	460	1 Q08452	Q08452 pyrococcus
36	476.5	18.2	460	1 Q08452	Q08452 pyrococcus
37	476.5	18.2	461	1 Q8NKR4	Q8NKR4 thermococc
38	476.5	18.2	473	17 Q8U319	Q8U319 uncultured
39	464.5	17.7	432	14 Q8JTK3	Q8JTK3 uncultured
40	351.5	13.4	826	10 Q9CAR6	Q9CAR6 arabidopsis
41	351.5	13.4	887	10 Q94A41	Q94A41 arabidopsis
42	334.5	12.7	906	10 Q8LQK4	Q8LQK4 oryza sativ
43	326	12.4	420	10 Q9ZP43	Q9ZP43 phaseolus v
44	324.5	12.4	421	10 Q7X9T1	Q7X9T1 phaseolus a
45	322	12.3	416	10 Q8LJQ6	Q8LJQ6 musa acumina

ALIGNMENTS

RESULT 1
Q9ROT8 PRELIMINARY; PRT; 519 AA.

AC Q9ROT8 01-MAY-2000 (TRENBLREL.13, Created)
DT 01-MAY-2000 (TRENBLREL.13, Last sequence update)
DR 01-JUN-2003 (TRENBLREL.24, Last annotation update)
DE Raw starch digesting amylase precursor.
OS Cytophaga sp.
OC Bacteria; Bacteroidetes; Sphingobacteriales; Sphingobacteriales;
OC Flexibacteraceae; Cytophaga.
OX NCBI_TaxID=29535;
RN [1]
RP SEQUENCE FROM N.A.
RA Jeang C.L., Chen L.S., Chen M.Y.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF067653; AAF00567.1; -.
DR HSBP; P06278; IVOS.
DR GO; GO:0004556; P:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha amyl cat.
DR InterPro; IPR006589; Alp amyl cat. sub.
DR InterPro; IPR006046; Glyco hydro_13.
DR Pfam; PF00128; alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Amy; 1.
DR SIGNAL.
FT CHAIN.
SQ SEQUENCE 519 AA; 58337 MW; 356888AADF98B163 CRC64;
1 57 POTENTIAL.
58 519 RAW STARCH DIGESTING AMYLASE.
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QY 62 LGFEQKGTVRTKTKGTSELODAIGSLHSRNVGVYVNLNKAAGADATEDYTAVERNPA 121
DB 98 LGFENQGTVRTKTKGTSELODAIGSLHSRNVGVYVNLNKAAGADATEDYTAVERNPA 157
QY 122 NRNOETSEBYOIKAWTDFRPPRGNTYSDFKWMEYHFDGADWDESKISRIEFGREGKA 181
DB 158 NRNOETSEBYOIKAWTDFRPPRGNTYSDFKWMEYHFDGADWDESKISRIEFGREGKA 217
QY 182 WMEVSESENANVYIMADVDYDHPDVVAETKMGWYANELSLDGFRIIDAAKHIFESFL 241
DB 218 WMEVSESENANVYIMADVDYDHPDVVAETKMGWYANELSLDGFRIIDAAKHIFESFL 277
QY 242 RDWQAVROATGKEMFTVAEYWMONNAGKLENTKTSFNOSVDFVPLHFNLOAASSQGG 301
DB 278 RDWQAVROATGKEMFTVAEYWMONNAGKLENTKTSFNOSVDFVPLHFNLOAASSQGG 337
QY 302 YDMRRLIDGTIVSRHPEKATFVENHDTQPGSLESTVQWPKPLAYAFILTRBSGYPOV 361
DB 338 YDMRRLIDGTIVSRHPEKATFVENHDTQPGSLESTVQWPKPLAYAFILTRBSGYPOV 397
QY 362 FYGDMYGTGKTSPEKIPSLKDNIEPIIKARKEYAYGPOHDYIDHPVIGMTRBSGSAK 421
DB 398 FYGDMYGTGKTSPEKIPSLKDNIEPIIKARKEYAYGPOHDYIDHPVIGMTRBSGSAK 457
QY 422 SGLAALITDGPQSGKMYAGLKNAGETWYDITGNREDYKISDGMGEFHVNDGSVSIY 480
DB 458 SGLAALITDGPQSGKMYAGLKNAGETWYDITGNREDYKISDGMGEFHVNDGSVSIY 516

RESULT 2

ID 081AS4 PRELIMINARY; PRT; 513 AA.
AC 081AS4;
DT 01-JUN-2003 (Tremblrel. 24, Created)
DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Glucan 1,4-alpha-maltohexaoseidase (EC 3.2.1.98).
GN BC3482.
OS Bacillus cereus (strain ATCC 14579 / DSM 31).
OC Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus.
NCBI_TaxID=226900;
RX MEDLINE=22608415; PubMed=12721630;
RA Ivanova N., Sorokin A., Anderson I., Galleron N., Candellon B.,
Kapural V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A.,
Chu L., Mazur M., Goldstein E., Larsen N., D'Souza M., Walunas T.,
Greckin Y., Pusch G., Haselkorn R., Fongstein M., Ehrlich S.D.,
Overbeek R., Kyrpides N.,
RT "Genome sequence of Bacillus cereus and comparative analysis with
Bacillus anthracis".
RT Nature 423:87-91(2003).
RL EMBL: A017809; AAP10417.1; -
DR GO; GO:0004556; F:alpha-amylose activity; IEA.
DR GO; GO:0016758; F:hydrolase activity; acting on glycosyl bonds; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha amyl cat.
DR InterPro; IPR006589; Alp amyl_cat_sub.
DR Pfam; PF00128; alpha-amylose; 1.
DR SMART; SM00642; Amy, 1.
KW Glycosidase; Hydrolase; Complete proteome.
SQ SEQUENCE 513 AA; 58306 MW; 05C4611C4BF9F6 CRC64;

Query Match

Best Local Similarity 74.2%; Score 1947; DB 16; Length 513;
Matches 344; Conservative 47; Mismatches 88; Indels 0; Gaps 0;

QY 2 NGTLMQYFENYTPNDGCHWRLONDAEHLSDITLWVMPAYKAGISQSDNGYGPYDLYD 61
DB 32 NGTLMQYFENYTPNDGCHWRLONDAEHLSDITLWVMPAYKAGISQSDNGYGPYDLYD 91
QY 62 LGFEQKGTVRTKTKGTSELODAIGSLHSRNVGVYVNLNKAAGADATEDYTAVERNPA 121

DB 92 LGFENQGTVRTKTKGTSELODAIGSLHSRNVGVYVNLNKAAGADATEDYTAVERNPA 151
QY 122 NRNOETSEBYOIKAWTDFRPPRGNTYSDFKWMEYHFDGADWDESKISRIEFGREGKA 181
DB 152 NRNOETSEBYOIKAWTDFRPPRGNTYSDFKWMEYHFDGADWDESKISRIEFGREGKA 211
QY 182 WMEVSESENANVYIMADVDYDHPDVVAETKMGWYANELSLDGFRIIDAAKHIFESFL 241
DB 212 WMEVSESENANVYIMADVDYDHPDVVAETKMGWYANELSLDGFRIIDAAKHIFESFL 271
QY 242 RDWQAVROATGKEMFTVAEYWMONNAGKLENTKTSFNOSVDFVPLHFNLOAASSQGG 301
DB 272 RDWQAVROATGKEMFTVAEYWMONNAGKLENTKTSFNOSVDFVPLHFNLOAASSQGG 331
QY 302 YDMRRLIDGTIVSRHPEKATFVENHDTQPGSLESTVQWPKPLAYAFILTRBSGYPOV 361
DB 332 YDMRRLIDGTIVSRHPEKATFVENHDTQPGSLESTVQWPKPLAYAFILTRBSGYPOV 391
QY 362 FYGDMYGTGKTSPEKIPSLKDNIEPIIKARKEYAYGPOHDYIDHPVIGMTRBSGSAK 421
DB 392 FYGDMYGTGKTSPEKIPSLKDNIEPIIKARKEYAYGPOHDYIDHPVIGMTRBSGSAK 451
QY 422 SGLAALITDGPQSGKMYAGLKNAGETWYDITGNREDYKISDGMGEFHVNDGSVSIY 480
DB 452 SGLAALITDGPQSGKMYAGLKNAGETWYDITGNREDYKISDGMGEFHVNDGSVSIY 510

RESULT 3

ID 09A054 PRELIMINARY; PRT; 533 AA.
AC 09A054;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Alpha-amylose.
OS Bacillus megaterium.
OC Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus.
NCBI_TaxID=1404;
RX MEDLINE=1404;
RA Kim Y.B., Lee B.N., Son H.J., Lee J.W., Kim B.J., Kim Y.-W.,
Park K.-H.,
RT "Cloning of maltopentose-producing amylose from Bacillus megaterium
RT KSM B-404".
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF220440; AAK00598.1; -
DR HSSP; P06278; IVUS.
DR GO; GO:0004556; F:alpha-amylose activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha amyl cat.
DR InterPro; IPR006589; Alp amyl_cat_sub.
DR Pfam; PF00128; alpha-amylose; 1.
DR SMART; SM00642; Amy, 1.
SQ SEQUENCE 533 AA; 60557 MW; 789CECD6A19C7DDE CRC64;

Query Match

Best Local Similarity 72.0%; Score 1946; DB 2; Length 533;
Matches 345; Conservative 44; Mismatches 90; Indels 0; Gaps 0;

QY 2 NGTLMQYFENYTPNDGCHWRLONDAEHLSDITLWVMPAYKAGISQSDNGYGPYDLYD 61
DB 52 NGTLMQYFENYTPNDGCHWRLONDAEHLSDITLWVMPAYKAGISQSDNGYGPYDLYD 111
QY 62 LGFEQKGTVRTKTKGTSELODAIGSLHSRNVGVYVNLNKAAGADATEDYTAVERNPA 121
DB 112 LGFENQGTVRTKTKGTSELODAIGSLHSRNVGVYVNLNKAAGADATEDYTAVERNPA 171
QY 122 NRNOETSEBYOIKAWTDFRPPRGNTYSDFKWMEYHFDGADWDESKISRIEFGREGKA 181
DB 172 NRNOETSEBYOIKAWTDFRPPRGNTYSDFKWMEYHFDGADWDESKISRIEFGREGKA 231
QY 182 WMEVSESENANVYIMADVDYDHPDVVAETKMGWYANELSLDGFRIIDAAKHIFESFL 241

Db 232 WDEVSESENGNVDYLYADLDFDHPDVANEMKKMGWYANELNDLDFDLAVKHTDHEYL 291
QY 242 RWMVOAATGATGEMFTVAEYQNNAGKLENTYLNKTSFNQSVFDPVPLHFNLOAASQGGG 301
Db 292 RDMVNHVRQOTGKEMFAVAEYQNDIQTLNNYLAKNVQSVFDPALPHNFHYASKNGN 351
QY 302 YDMRRLDGTGVSRRPEKAVTFVENHNDTOPQGSLESTVQTFKPLAAYAFILTRRESGPOV 361
Db 352 YDMRNLKGTVAANHPTLAVTLVENHDSQGSLSVSPWFKPLAAYAFILTRAGYPSV 411
QY 362 FYGDMYGTGTSPEKIPSLKDNIEPLIKRKEYAVGPOHDYIDHPDVIGMTEGDSAAK 421
Db 412 FYGDYGTGTSNYSYEIPALKDKIDPILITARKNVAAYGTQGDYIDHPDVIGMTEGDSVHAN 471
QY 422 SGLAALITDGPQGSKMYAGLKNAGETWYDITGNRSQDYGKSDGGEFHVNDGSVSY 480
Db 472 SGLATLISDGPQGSKMYAGLKNAGETWYDITGNRSQDYGKSDGGEFHVNDGSVSY 530

RESULT 4

Q81YJ4 PRELIMINARY; PRT; 513 AA.
AC 081YJ4
DT 01-JUN-2003 (Tremblrel. 24, Created)
DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Alpha-amylose.
GN AMY5 OR BA3551.
OS Bacillus anthracis (strain Ames).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=198094;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22608414; PubMed=12721629;
RA Read T.D., Peterson S.N., Tourasse N., Baillye L.W., Paulsen I.T.,
RA Nelson K.E., Tettelin H., Fouts D.B., Eisen J.A., Gill S.R.,
RA Holtzapple E.K., Oksstad O.A., Helgason E., Ralston J., Wu M.,
RA Kolonay J.F., Beaman M.J., Dodson R.J., Brinkac L.M., Gwinn M.,
RA DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Hatt D.H.,
RA Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
RA Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,
RA Berry K.J., Plant R.D., Wolf A.M., Watkins K.L., Nierman W.C.,
RA Hazen A., Cline R., Redmond C., Thwaite J.E., White O., Salzberg S.L.,
RA Thomason B., Friedlander A.M., Koehler T.M., Hanna P.C., Kolsto A.B.,
RA Fraser C.M.;
RT "The genome sequence of Bacillus anthracis Ames and comparison to
RT closely related bacteria."
RL Nature 423:81-86(2003).
DR EMBL; AEO17035; AAP27311.1; -.
DR TIGR; BA3551; -.
DR GO; GO:0004556; F:alpha-amylose activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amy1_cat.
DR InterPro; IPR006589; Alp_amy1_cat_sub.
DR Pfam; PF00128; alpha-amylose; 1.
DR SMART; SM00642; Amy; 1.
KM Complete proteome.
SQ SEQUENCE 513 AA; 58445 MW; 55806EF282FD159B CRC64;

Query Match 72.8%; Score 1914; DB 16; Length 513;
Best Local Similarity 70.8%; Pred. No. 5.3e-124;
Matches 339; Conservative 47; Mismatches 93; Indels 0; Gaps 0;

QY 2 NGTLMQYFEMWTPRNDGQHMRLQNDAEHLSDIGITAWVTPPAKYGLSQSDNGYGPDIYD 61
Db 32 NGTLMQYFEMWTPRNDGQHMRLQNDAEHLSDIGITAWVTPPAKYGLSQSDNGYGPDIYD 91
QY 62 LGFPOKGTATKTKGTSKSEIQAIGSLHSHRNQVGVYDVLNHAAGADATEDYAVEVNP 121
Db 92 LGFPOKGTATKTKGTSKSEIQAIGSLHSHRNQVGVYDVLNHAAGADATEDYAVEVNP 151
QY 122 NRNOETSEBYQIAKAWDFRPPGKNTYSDPKMWHYFDGADWDESKIRIKFGECKA 181

Db 152 NRNAVESGDYEISAMTGPNPGRGDNYSNFKMWHYFDGTDWDEGRKLNRIYKFRIGICKA 211
QY 182 WDEVSESENGNVDYLYADLDFDHPDVANEMKKMGWYANELNDLDFDLAVKHTDHEYL 241
Db 212 WDEVSESENGNVDYLYADLDFDHPDVANEMKKMGWYANELNDLDFDLAVKHTDHEYL 271
QY 242 RWMVOAATGATGEMFTVAEYQNNAGKLENTYLNKTSFNQSVFDPVPLHFNLOAASQGGG 301
Db 272 RDMVNHVRQOTGKEMFAVAEYQNDIQTLNNYLAKNVQSVFDPALPHNFHYASKNGN 331
QY 302 YDMRRLDGTGVSRRPEKAVTFVENHNDTOPQGSLESTVQTFKPLAAYAFILTRRESGPOV 361
Db 352 YDMRNLKGTVAANHPTLAVTLVENHDSQGSLSVSPWFKPLAAYAFILTRAGYPSV 411
QY 362 FYGDMYGTGTSPEKIPSLKDNIEPLIKRKEYAVGPOHDYIDHPDVIGMTEGDSAAK 421
Db 412 FYGDYGTGTSNYSYEIPALKDKIDPILITARKNVAAYGTQGDYIDHPDVIGMTEGDSVHAN 451
QY 422 SGLAALITDGPQGSKMYAGLKNAGETWYDITGNRSQDYGKSDGGEFHVNDGSVSY 480
Db 452 SGLATLISDGPQGSKMYAGLKNAGETWYDITGNRSQDYGKSDGGEFHVNDGSVSY 510

RESULT 5

Q82839 PRELIMINARY; PRT; 516 AA.
AC 082839
DT 01-NOV-1998 (Tremblrel. 08, Created)
DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Amylose.
GN Amylose sp.
OS Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1409;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=KSM-1378;
RA Igarashi K., Hatada Y., Ikawa K., Araki H., Ozawa T., Kobayashi T.,
RA Ozaki K., Ito S.;
RT "Improved thermostability of a Bacillus alpha-amylose by deletion of
RT an arginine-glycine residue is caused by enhanced calcium binding."
RL Biochem. Biophys. Res. Commun. 248:372-377(1998).
DR EMBL; AB008763; BA32431.1; -.
DR HSSP; P06278; IVUS.
DR GO; GO:0004556; F:alpha-amylose activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amy1_cat.
DR InterPro; IPR006589; Alp_amy1_cat_sub.
DR Pfam; PF00128; alpha-amylose; 1.
DR PRINTS; PR00110; ALPHAMYLASE.
DR SMART; SM00642; Amy; 1.
SQ SEQUENCE 516 AA; 58841 MW; D90A8C90ECC182P8 CRC64;

Query Match 70.0%; Score 1836; DB 2; Length 516;
Best Local Similarity 67.0%; Pred. No. 1.3e-118;
Matches 323; Conservative 65; Mismatches 86; Indels 8; Gaps 3;

QY 2 NGTLMQYFEMWTPRNDGQHMRLQNDAEHLSDIGITAWVTPPAKYGLSQSDNGYGPDIYD 61
Db 37 NGTLMQYFEMWTPRNDGQHMRLQNDAEHLSDIGITAWVTPPAKYGLSQSDNGYGPDIYD 96
QY 62 LGFPOKGTATKTKGTSKSEIQAIGSLHSHRNQVGVYDVLNHAAGADATEDYAVEVNP 121
Db 97 LGFPOKGTATKTKGTSKSEIQAIGSLHSHRNQVGVYDVLNHAAGADATEDYAVEVNP 156
QY 122 NRNOETSEBYQIAKAWDFRPPGKNTYSDPKMWHYFDGADWDESKIRIKFGECKA 180
Db 157 NRNOETSEBYQIAKAWDFRPPGKNTYSDPKMWHYFDGADWDESKIRIKFGECKA 216
QY 181 AMDVEVSENGNVDYLYADLDFDHPDVANEMKKMGWYANELNDLDFDLAVKHTDHEYL 240

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Db 217 AMDWEVDIENGYDLYADIDMDHPREVINELRMGVWYNTLNLGFRIDAVKHIXSY 276
Qy 241 LRDWQAVROATGKEMFTVAEYWNAGKLENTYLNKTSFNOSVDFPHNLQAASSQGG 300
Db 277 TRDWLTHRNTTGKMFVAEYFNKNDLAIENYLNKTSFNOSVDFPHNLQAASSQGG 336
Qy 301 GYDWRLLDGVTVSRHPEKAVTFVENHDTQPGQSLSTVQTFKPLAVAFILTRREGYPO 360
Db 337 YEDMKNILNGSVYQGHPIHATVFVNNDHSDQGEALLESFVQSWFKPLAVAFILTRREGYPS 396
Qy 361 VYEGMYG--TKGTSPEKEIPSLKDNIEPLIKARKEAYAGPOHDYIDHEDVIGWTRREGDS 418
Db 397 VFYGYGYYGTPHG-----VPSKSKIDPLQARQYVAGTGHDFDHDHDIIGWTRREGDS 451
Qy 419 AAKSGLAALITDGPQSGKMYVAGLKNAGETWYDITGNRSPTVKIGSDGGEFHNVDGSVS 478
Db 452 HENSGLATIMSDGPGANKMYVAGKAKAGQVWREDITGNRSPTVITINADGNGFTVNGAVS 511
Qy 479 IY 480
Db 512 VM 513

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RESULT 6

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O31193 PRELIMINARY; PRT; 549 AA.
ID O31193
AC 031193: 01-JAN-1998 (TEMBLrel. 05, Created)
DT 01-JAN-1998 (TEMBLrel. 05, Last sequence update)
DB 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
DE Alpha amylase.
OS Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.
OX NCBI_TaxID=1422;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 31195;
RA da Silva A.C.R., Fernandes E., Pueyo M.T.;
RT Submitted (NOV-1997) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF003864; AAB6961.1; -.
DR PIR: A54541; A54541.
DR HSP: P06278; IVUS.
DR GO: GO:0004556; F:alpha-amylase activity; IEA.
DR GO: GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro: IPR006047; Alpha amyl cat.
DR InterPro: IPR006046; Glyco_hydro_13.
DR Pfam: PF00128; alpha-amylase; 1.
DR PRINTS: PR00110; ALPHAAMYLASE.
DR SMART: SM00642; Amy; 1.
SQ SEQUENCE 549 AA; 62651 MW; 2CA689EDACC4D262 CRC64;

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Query Match

Best Local Similarity 67.4%; Score 1767.5; DB 2; Length 549;
 Pred. No. 7.8e-114; Matches 315; Conservative 57; Mismatches 103; Indels 5; Gaps 2;

```

Qy 2 NGTLMQFEWYTPNDQHWKRLQNDAEHLSDIGITAWIPPAVKGLSOSDNGYGPYDLYD 61
Db 39 NGTLMQFEWYTPNDQHWKRLQNDAEHLSDIGITAWIPPAVKGLSOSDNGYGPYDLYD 98
Qy 62 LGEPQCKGTVRTKYGKSELQDAIGSLHRSNVOYGVYVFNHKAAGADATEDVTAAYENPA 121
Db 99 LGEPQCKGTVRTKYGKSELQDAIGSLHRSNVOYGVYVFNHKAAGADATEDVTAAYENPA 158
Qy 122 NKNQETSEBYQIKAMTDFRPPRGNTYSDFKMWHYHFDGADWDESRKISRIFKRGEGKA 181
Db 159 DNROEISGTYQIQAMTKFDFPGKNTYSSFKMWHYHFDGADWDESRKISRIFKRGEGKA 218
Qy 182 MDWEVSEKNGNDYLYADVDYDHPVVAETKKMGIVYANELSLDGFRIIDAKHITKFSFL 241
Db 219 MDWEVTEKNGNDYLYADVDYDHPVVAETKKMGIVYANELSLDGFRIIDAKHITKFSFL 278

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Qy 242 RDWQAVROATGKEMFTVAEYWNAGKLENTYLNKTSFNOSVDFPHNLQAASSQGG 301
Db 279 PDWLSYVSQGTGKPLFTVGEYWSYDINKLHNITKNGTMSLFDAPLNKFEYTAASKGGA 338
Qy 302 YDWRLLDGVTVSRHPEKAVTFVENHDTQPGQSLSTVQTFKPLAVAFILTRREGYPO 361
Db 339 YEDMKNILNGSVYQGHPIHATVFVNNDHSDQGEALLESFVQSWFKPLAVAFILTRREGYPS 398
Qy 362 FYGDMYGTGTSPEK-EIPSLKDNIEPLIKARKEAYAGPOHDYIDHEDVIGWTRREGDS 420
Db 399 FYGDMYGTGTSPEK-EIPSLKDNIEPLIKARKEAYAGPOHDYIDHEDVIGWTRREGDS 454
Qy 421 KSGLAALITDGPQSGKMYVAGLKNAGETWYDITGNRSPTVKIGSDGGEFHNVDGSVS 480
Db 455 GSGLAALITDGPQSGKMYVAGLKNAGETWYDITGNRSPTVKIGSDGGEFHNVDGSVS 514

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RESULT 7

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O9KMY6 PRELIMINARY; PRT; 549 AA.
ID O9KMY6
AC O9KMY6: 01-OCT-2000 (TEMBLrel. 15, Created)
DT 01-OCT-2000 (TEMBLrel. 15, Last sequence update)
DB 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
DE Alpha-amylase (EC 3.2.1.1).
OS Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.
OX NCBI_TaxID=1422;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=US100;
RA Betar S.;
RT Submitted (JUN-1998) to the EMBL/Genbank/DBJ databases.
DR EMBL: Y17557; CAB93517.1; -.
DR PIR: A54541; A54541.
DR HSP: P06278; IVUS.
DR GO: GO:0004556; F:alpha-amylase activity; IEA.
DR GO: GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO: GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro: IPR006047; Alpha amyl cat.
DR InterPro: IPR006046; Glyco_hydro_13.
DR InterPro: IPR006045; Alp amyl cat sub.
DR Pfam: PF00128; alpha-amylase; 1.
DR PRINTS: PR00110; ALPHAAMYLASE.
DR SMART: SM00642; Amy; 1.
DR GlycoSite: Hydrolase.
SQ SEQUENCE 549 AA; 62582 MW; 8DA3E6DF9120BCE CRC64;

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Query Match

Best Local Similarity 67.3%; Score 1766.5; DB 2; Length 549;
 Pred. No. 9.2e-114; Matches 315; Conservative 57; Mismatches 103; Indels 5; Gaps 2;

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Qy 2 NGTLMQFEWYTPNDQHWKRLQNDAEHLSDIGITAWIPPAVKGLSOSDNGYGPYDLYD 61
Db 39 NGTLMQFEWYTPNDQHWKRLQNDAEHLSDIGITAWIPPAVKGLSOSDNGYGPYDLYD 98
Qy 62 LGEPQCKGTVRTKYGKSELQDAIGSLHRSNVOYGVYVFNHKAAGADATEDVTAAYENPA 121
Db 99 LGEPQCKGTVRTKYGKSELQDAIGSLHRSNVOYGVYVFNHKAAGADATEDVTAAYENPA 158
Qy 122 NKNQETSEBYQIKAMTDFRPPRGNTYSDFKMWHYHFDGADWDESRKISRIFKRGEGKA 181
Db 159 DNROEISGTYQIQAMTKFDFPGKNTYSSFKMWHYHFDGADWDESRKISRIFKRGEGKA 218
Qy 182 MDWEVSEKNGNDYLYADVDYDHPVVAETKKMGIVYANELSLDGFRIIDAKHITKFSFL 241
Db 219 MDWEVTEKNGNDYLYADVDYDHPVVAETKKMGIVYANELSLDGFRIIDAKHITKFSFL 278
Qy 242 RDWQAVROATGKEMFTVAEYWNAGKLENTYLNKTSFNOSVDFPHNLQAASSQGG 301
Db 279 PDWLSYVSQGTGKPLFTVGEYWSYDINKLHNITKNGTMSLFDAPLNKFEYTAASKGGA 338
Qy 302 YDWRLLDGVTVSRHPEKAVTFVENHDTQPGQSLSTVQTFKPLAVAFILTRREGYPO 361

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Db      339  FDMKTLMTNTLMKDOPLAVATFVNDHDTBPGALQSVWDPWFKPLAYAFILITQEGYPCV 398
      362  FYGDMYGTGKTSRK-ETPSLKDNIEPLIKARKEYAYGPHDYIDHPVIGMTRGDSAA 420
      399  FYGQYVGI-----PQYNIPSLKSKIDPLIARRDYAYGTQHDYDHSIIIGMTRGVEKRP 454
Qy      421  KSGLAALITDPGSGSKMYAGLKNAGETWYITGNRSPTYKISDGMGEFNVDSVSIY 480
      455  GSGLAALITDPGSGSKMYAGLKNAGETWYITGNRSPTYKISDGMGEFNVDSVSIY 514

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RESULT 8
ID      P71034      PRELIMINARY;      PRT;      521 AA.
AC      P71034;
DT      01-FEB-1997 (TREMBLrel. 02, Created)
DT      01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DT      01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE      Alpha-amylose precursor.
OS      Bacillus sp. MK 716.
OC      Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX      NCBI_TaxID=54116;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=MK 716;
RA      Sidhu G.S., Chakrabarti T.;
RT      "Molecular cloning and expression of the gene encoding for
RT      thermostable alpha-amylose of a thermophilic bacterial isolate.";
RL      Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
DR      EMBL; U07445; AB18785.1; -.
DR      HSSP; P06278; 1VUS.
DR      GO; GO:0004556; F:alpha-amylose activity; IEA.
DR      GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR      InterPro; IPR006047; Alpha_amy1_cat.
DR      InterPro; IPR006589; Alp_amy1_cat_sub.
DR      InterPro; IPR006046; Glyco_hydro_13.
DR      Pfam; PF00128; alpha-amylose; 1.
DR      PRINTS; PR00110; ALPHAMYLASE.
DR      SMART; SM00642; Amy; 1.
KW      Signal.
FT      CHAIN
FT      SIGNAL
SQ      SEQUENCE      521 AA; 59311 MW; 5612A88596D922E1 CRC64;

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Query Match 67.2%; Score 1762.5; DB 2; Length 521;
 Best Local Similarity 65.4%; Pred. No. 1.6e-113;
 Matches 314; Conservative 57; Mismatches 104; Indels 5; Gaps 2;

```

Qy      2  NGTLMQVFEMVTPRDGQHWKRLQNDALHLSDIGITAVMIPPAKYGISQSDNGYGPYDLY 61
      39  NGTLMQVFEMVTPRDGQHWKRLQNDALHLSDIGITAVMIPPAKYGISQSDNGYGPYDLY 98
Qy      62  LGEFOQKGTIRTKYKGTSELDQAIQSLHSHNVQYGVVYLNHKAADATEDVAVAVENPA 121
      99  LGEFNQGAIRTKYKGTGTAQYLAQAIQAHAAGQVAVDVVDHKGADGTEFVDAVAVENPS 158
Db      122  NRRQETSEEEYQIAKWDFFRFGNGNTYSDPKMHWYHFDGADWDESKRISIRFRRGEQA 181
      159  DRNQEISGTQIAQAMTKFDFRFGNGNTYSDPKMHWYHFDGADWDESKRISIRFRRIGRA 218
Qy      182  WDNVESSSENGYVLYMADVDYDHPDVAVATKKGWYANELSLDGFRIIDAAGIKFSPL 241
      219  WDNVEVDENENYIYIMADIDMDHPEVYTELKMGWYVNTTNIIDGFRIDAAGIKFSF 278
Db      242  RDVQVQVQATGKEMFVAEYQWNAKLENTYLNKTSFNOSVDFVPLHFNLAQASSQGG 301
      279  PDWLSYVRSQTKRFLFVGEYSYDINKLHNTYITKNGTWSLDPADLHNNFYAASKGGA 338
Qy      302  YDMRRLDGTIVSRHPKAVTFVENHDTOPGQSLSTVQWTFKPLAYAFILITRESGYPC 361
      339  FDMKTLMTNTLMKDOPLAVATFVNDHDTBPGALQSVWDPWFKPLAYAFILITQEGYPC 398

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Qy      362  FYGDMYGTGKTSRK-ETPSLKDNIEPLIKARKEYAYGPHDYIDHPVIGMTRGDSAA 420
      399  FYGQYVGI-----PQYNIPSLKSKIDPLIARRDYAYGTQHDYDHSIIIGMTRGVEKRP 454
Qy      421  KSGLAALITDPGSGSKMYAGLKNAGETWYITGNRSPTYKISDGMGEFNVDSVSIY 480
      455  GSGLAALITDPGSGSKMYAGLKNAGETWYITGNRSPTYKISDGMGEFNVDSVSIY 514

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RESULT 9
ID      O59222      PRELIMINARY;      PRT;      613 AA.
AC      O59222;
DT      01-NOV-1996 (TREMBLrel. 01, Created)
DT      01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT      01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE      Alpha-amylose (EC 3.2.2.1).
GN      AMY.
OS      Bacillus sp. TS-23.
OC      Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX      NCBI_TaxID=38441;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=TS-23;
RA      Lin L.-L., Chu W.-S., Hsu W.-H.;
RT      Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
DR      EMBL; U22045; AAA63900.1; -.
DR      HSSP; P06278; 1VUS.
DR      GO; GO:0004556; F:alpha-amylose activity; IEA.
DR      GO; GO:0016798; F:hydrolyase activity, acting on glycosyl bonds; IEA.
DR      GO; GO:0008477; F:purine nucleosidase activity; IEA.
DR      GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR      InterPro; IPR006047; Alpha_amy1_cat.
DR      InterPro; IPR006589; Alp_amy1_cat_sub.
DR      InterPro; IPR002044; CBD_4.
DR      InterPro; IPR006046; Glyco_hydro_13.
DR      InterPro; IPR006046; Glyco_hydro_13.
DR      Pfam; PF00128; alpha-amylose; 1.
DR      Pfam; PF00686; CBM 20; 1.
DR      PRINTS; PR00110; ALPHAMYLASE.
DR      ProDom; PD001568; CBD 4; 1.
DR      SMART; SM00642; Amy; 1.
KW      Glycosidase; Hydrolyase.
FT      CHAIN
FT      SIGNAL
SQ      SEQUENCE      613 AA; 69537 MW; 14684A30FC2895E8 CRC64;

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Query Match 66.7%; Score 1749.5; DB 2; Length 613;
 Best Local Similarity 65.1%; Pred. No. 1.6e-112;
 Matches 313; Conservative 58; Mismatches 105; Indels 5; Gaps 2;

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Qy      1  VNGTLMQVFEMVTPRDGQHWKRLQNDALHLSDIGITAVMIPPAKYGISQSDNGYGPYDLY 60
      35  INETMQVFEMVTPRDGQHWKRLQNDALHLSDIGITAVMIPPAKYGISQSDNGYGPYDLY 94
Qy      61  DLGEFOQKGTIRTKYKGTSELDQAIQSLHSHNVQYGVVYLNHKAADATEDVAVAVENP 120
      95  DLGEFNQGAIRTKYKGTGTAQYLAQAIQAHAAGQVAVDVVDHKGADGTEFVDAVAVENP 154
Db      121  ANRQETSEEEYQIAKWDFFRFGNGNTYSDPKMHWYHFDGADWDESKRISIRFRRGEQA 180
      155  SNRQETSGTQIAQAMTKFDFRFGNGNTYSDPKMHWYHFDGADWDESKRISIRFRRIGTK 214
Qy      181  WDNVESSSENGYVLYMADVDYDHPDVAVATKKGWYANELSLDGFRIIDAAGIKFSF 240
      215  WDNVEVDENENYIYIMADIDMDHPEVYTELKMGWYVNTTNIIDGFRIDAAGIKFSF 274
Db      241  LDVQVQVQATGKEMFVAEYQWNAKLENTYLNKTSFNOSVDFVPLHFNLAQASSQGG 300
      275  FPDWLSYVRSQTKRFLFVGEYSYDINKLHNTYITKNGTWSLDPADLHNNFYAASKGGA 334
Qy      301  YDMRRLDGTIVSRHPKAVTFVENHDTOPGQSLSTVQWTFKPLAYAFILITRESGYPC 360
      335  YDMRRLDGTIVSRHPKAVTFVENHDTOPGQSLSTVQWTFKPLAYAFILITQEGYPC 394
Qy      361  VFDKRLYIANTLMKDOPLAVATFVNDHDTBPGALQSVWDPWFKPLAYAFILITQEGYPC 394
      361  VFDKRLYIANTLMKDOPLAVATFVNDHDTBPGALQSVWDPWFKPLAYAFILITQEGYPC 419

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Db 395 VFYGDYGI----PKNYFGLKSKIDPLLIARDYVYGRDYIDHQDITGWTREGIDPK 450
Qy 420 AKSGLAALITDGGGSKRWYAGLKNAGLFWYDITGRTDPTWYIGSGWGEFFHNDGSYSI 479
Db 451 PMSGALALITDGGGSKRWYAGLKNAGLFWYDITGRTDPTWYIGSGWGEFFHNDGSYSI 510
Qy 480 Y 480
Db 511 W 511

RESULT 10
Q93148 PRELIMINARY; PRT; 501 AA.
ID Q93148
AC Q93148
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Amylase.
GN AmyK39.
OS Bacillus sp. KSM-K38.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_Taxid=129736;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KSM-K38;
RA Hayashi Y.;
RL "Isolation of a new Bacillus alpha-amylase."
RT Submitted (NOV-2000) to the EMBL/GenBank/DBD databases.
DR EMBL; AB051102; BAB71820.1; -.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR InterPro; IPR006047; P:carbohydrate metabolism; IEA.
DR Pfam; PF00128; alpha-amylase; 1.
SQ SEQUENCE 501 AA; 57485 MW; 1240F46739A5CC11 CRC64;

Query Match 61.5%; Score 1614.5; DB 2; Length 501;
Best Local Similarity 59.8%; Pred. No. 2,6e-103;
Matches 287; Conservative 67; Mismatches 121; Indels 5; Gaps 2;

Qy 1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAWTIPPAKGLSGSDNGYGYDY 60
Db 24 LNTGMMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAWTIPPAKGLSGSDNGYGYDY 83
Qy 61 DLGEFOOKGTVRTKYGKSELQDAIGLSHRVQYGVVYLNHKAGADATEDVTAVERN 120
Db 84 DLGEFOOKGTVRTKYGKSELQDAIGLSHRVQYGVVYLNHKAGADATEDVTAVERN 143
Qy 121 ANRQETSEBYQIKAWTDFRPPGRNTYSDFKHMYHPDGAWDSESRKISRIFKRGEGK 180
Db 144 TNMWDJISGAYTIDAWTGFSGSRNNAYSDFKRMHFHFGVMDQRYQENHIFRPANTN- 202
Qy 181 AMDWEVSSENGNDYLMYADVDYDHPDVAETKKGWIYANELSLDGEFIDAKHKKSF 240
Db 203 -KMRDRDENGNIDYLGSIIDPSHEVQDELKDMGSMFTDELDGIRLDAIKHIFRY 261
Qy 241 LRDVQAVROATGKEMPTVAEYQNNAGKLENTLNTSFNSQVFDVPLHFNILQAASQGG 300
Db 262 TSDMVAHROHREADQDFVVGGEYWKDVGALFEFLIDEMWESLFDVPLHFNIFYRASQGG 321
Qy 301 GYDMRRLDGTIVVSRPEKAVTFVENHDTOPGQSLSTVQTWKPLAVALFILLREGGYPO 360
Db 322 SYMKRILKLSGLVLEAPMAVTFYVDNHDTPQGESLESWYADMFKPLAVALFILLREGGYPO 381
Qy 361 VFYGDYGIKTSPEKIPSLKDNIEPLKARKKAYVPOHDYIDHPDVIWGTREGDSSAA 420
Db 382 VFYGDYGIKTSPEKIPSLKDNIEPLKARKKAYVPOHDYIDHPDVIWGTREGDSSAA 438
Qy 421 KSGLAALITDGGGSKRWYAGLKNAGLFWYDITGRTDPTWYIGSGWGEFFHNDGSYSI 480
Db 439 NSGLAALITDGGGSKRWYAGLKNAGLFWYDITGRTDPTWYIGSGWGEFFHNDGSYSI 498
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RESULT 11
Q87H6 PRELIMINARY; PRT; 507 AA.
ID Q87H6
AC Q87H6
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Alpha-amylase.
GN VPA0999.
OS Vibrio parahaemolyticus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales.
OC Vibrionaceae; Vibrio.
OX NCBI_Taxid=670;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RIMD 221063 / Serotype O3:K6;
RX MEDLINE=22508454; Pubmed=12620739;
RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
RA Iijima Y., Naito M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
RA Yasunaga T., Honda T., Saitohawa H., Hattori M., Iida T.;
RT "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
RT distinct from that of V. cholerae."
RL Lancet 361:743-749(2003).
DR EMBL; AP005087; BAC62342.1; -.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR InterPro; IPR006047; P:carbohydrate metabolism; IEA.
DR Pfam; PF00128; alpha-amylase; 1.
DR Complete proteome.
SQ SEQUENCE 507 AA; 58428 MW; 91B549E2B0700BD CRC64;

Query Match 56.2%; Score 1474.5; DB 16; Length 507;
Best Local Similarity 54.9%; Pred. No. 1,2e-93;
Matches 267; Conservative 76; Mismatches 128; Indels 15; Gaps 6;

Qy 2 NGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAWTIPPAKGLSGSDNGYGYDY 60
Db 26 NGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAWTIPPAKGLSGSDNGYGYDY 85
Qy 61 DLGEFOOKGTVRTKYGKSELQDAIGLSHRVQYGVVYLNHKAGADATEDVTAVERN 120
Db 86 DLGEFOOKGTVRTKYGKSELQDAIGLSHRVQYGVVYLNHKAGADATEDVTAVERN 145
Qy 121 ANRQETSEBYQIKAWTDFRPPGRNTYSDFKHMYHPDGAWDSESRKISRIFKRGEGK 180
Db 146 DNRIEIDGKM-LEAWEFNFPGRNDKYSNFWHTWYHFGVDMDAGKEKALFKFGECK 204
Qy 181 AMDWEVSSENGNDYLMYADVDYDHPDVAETKKGWIYANELSLDGEFIDAKHKKSF 240
Db 205 AMDWEVSSENGNDYLMYADVDYDHPDVAETKKGWIYANELSLDGEFIDAKHKKSF 264
Qy 241 LRDVQAVROATGKEMPTVAEYQNNAGKLENTLNTSFNSQVFDVPLHFNILQAASQGG 300
Db 265 LQEWIDILRKTKGELFTVGEYVYVQNLNITTSQSMSEFDAPLHNNFPAKSKSG 324
Qy 301 GYDMRRLDGTIVVSRPEKAVTFVENHDTOPGQSLSTVQTWKPLAVALFILLREGGYPO 360
Db 325 NYDMRQIMNGTILKMDNVKAVTFVENHDTOPGQSLSTVQTWKPLAVALFILLREGGYPO 384
Qy 361 VFYGDYGIKTSPEKIPSLKDNIEPLKARKKAYVPOHDYIDHPDVIWGTREGDSSAA 420
Db 385 VFYADYGIKTSPEKIPSLKDNIEPLKARKKAYVPOHDYIDHPDVIWGTREGDSSAA 440
Qy 415 GDSGAASGLAALITDGGGSKRWYAGLKNAGLFWYDITGRTDPTWYIGSGWGEFFHNDGSYSI 474
Db 441 GDAHPNS-MAVIMSDPGGKMWYTG--KPSRYVDKIGIRTEWYDANGWAEFPVNG 497
Qy 475 GSYSIY 480
Db 498 GSYSIY 503
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RESULT 12
Q89YPI PRELIMINARY; PRT; 481 AA.
AC Q89YPI;
DT 01-JUN-2003 (TReMBrel. 24, Created)
DT 01-JUN-2003 (TReMBrel. 24, Last sequence update)
DT 01-OCT-2003 (TReMBrel. 25, Last annotation update)
DE Alpha-amylose precursor.
GN BT4630.
OS Bacteroides thetaiotaomicron.
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=818;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VPI-5482 / ATCC 29148;
RX MEDLINE=22550858; PubMed=1263928;
RA Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,
  Chiang H.C., Hooper L.V., Gordon J.I.;
  "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.";
  Science 299:2074-2076(2003).
RT Science 299:2074-2076(2003).
RL EMBL: AB016846; AAC07925.1;
DR GO: GO:0004556; F:alpha-amylose activity; IEA.
DR GO: GO:000575; P:carbohydrate metabolism; IEA.
DR InterPro: IPR006047; Alpha_amy1_cat.
DR InterPro: IPR006589; Alp_amy1_cat_sub.
DR Pfam: PF00128; alpha-amylose; 1.
DR SMART: SM00642; Amy; 1.
DR Complete proteome.
SQ SEQUENCE 481 AA; 55343 MW; B6BF237011F5EE1A CRC64;

Query Match 51.8%; Score 1359; DB 16; Length 481;
Best Local Similarity 50.8%; Pred. No. 1.1e-85;
Matches 244; Conservative 82; Mismatches 149; Indels 4; Gaps 2;

QY 2 NGTLMQFEWYTPNDGQHWRLQNDAEHLSDIGITAVWIPPAKYGLSQSDNGGYPDLYD 61
DB 3 NGWMMQFEWHLADGDHMKRLAMAPDELKAKGIDITWVPVTKAVSAEDTGIGVVDLYD 62
QY 62 LGDFQOKGTATKTKYGTQKSELQDAIGSLHSRNVOYGVVTLNKAQADATEDVTAVEVNP 121
DB 63 LGDFDQKGTATKTKYGTQKSELQDAIGSLHSRNVOYGVVTLNKAQADATEDVTAVEVNP 122
QY 122 NRQETSEVOIKAWTDFRPPRGNTYSDPKMWHYFDGADWDESKISRIFFRGGKA 181
DB 123 ERTKALGEPPEIGQWGYSPHGRKXSDPKMWHYSGTGFDAQKRGSGVFOIQEGKA 182
QY 182 WDWVSESENGNYDYIMTADVDYDHPDVAETKMGWYANELSLDGRIDAAHRIKFSFL 241
DB 183 WSGVSESENGNYDYFILCNDIDLDHPEVSELNRNGKWSNELDGMRLDAIKHMDQGV 242
QY 242 RDMVQAVRQATGKEMFTVAEYWNQNAKLENYLNKTSFNOSVDPVPLHFNLOAASQGG 301
DB 243 ACGLDAVRSRGNDFAVVGEYVNGDLEALDAYIEAVGHKNLDPVPLHNMFOASQGGD 302
QY 302 YDMRRLDGTAVSHHPEKATVFNENHDTPQGSLESTVQTFWFKPLAAYAFILTRSGYPOV 361
DB 303 YDLRDLIKDTLVENHPPLATVIVNDHTQGSLSLESTVQTFWFKPLAAYAFILTRSGYPOV 362
QY 362 FYGDMYGTGTSPEKIPSLKDNIEPIIKAREYAYGQHDYIDHPDVIQWTRBSSAAK 421
DB 363 FYGDIYGIQG--EKSPPTR-IIDILDAARKYAVGQOLEYFHPSTIGIFRTGDEHNH 418
QY 422 SGLAALITDGPGGSKRYAGLKNAGETWYDITGNRSPTVIGSGDGEFFVNDGSVSIY 480
DB 419 SGLVFLMSNDPAGSKIMSLGKHKGEYWHETISISEITLDBEGNGEFVESRNLAIV 477

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RESULT 13
Q03657 PRELIMINARY; PRT; 493 AA.
AC Q03657;
DT 01-NOV-1996 (TReMBrel. 01, Created)

Query Match 47.8%; Score 1253; DB 2; Length 493;
Best Local Similarity 47.2%; Pred. No. 2.4e-78;
Matches 226; Conservative 74; Mismatches 177; Indels 2; Gaps 1;

QY 2 NGTLMQFEWYTPNDGQHWRLQNDAEHLSDIGITAVWIPPAKYGLSQSDNGGYPDLYD 61
DB 4 NHTMMQFEWHLADGDHMKRLAMAPDELKAKGIDITWVPVTKAVSAEDTGIGVVDLYD 63
QY 62 LGDFQOKGTATKTKYGTQKSELQDAIGSLHSRNVOYGVVTLNKAQADATEDVTAVEVNP 121
DB 64 LGDFDQKGTATKTKYGTQKSELQDAIGSLHSRNVOYGVVTLNKAQADATEDVTAVEVNP 123
QY 122 NRQETSEVOIKAWTDFRPPRGNTYSDPKMWHYFDGADWDESKISRIFFRGGKA 181
DB 124 DRTKEISEPPEIGQWGYSPHGRKXSDPKMWHYSGTGFDAQKRGSGVFOIQEGKA 183
QY 182 WDWVSESENGNYDYIMTADVDYDHPDVAETKMGWYANELSLDGRIDAAHRIKFSFL 241
DB 184 WNVNVDDEFNGYDILMFANIDYNHDPVREXIDWGMKILDTLQCGGRLDAIKHINEFI 243
QY 242 RDMVQAVRQATGKEMFTVAEYWNQNAKLENYLNKTSFNOSVDPVPLHFNLOAASQGG 301
DB 244 KEFAEMIRKRGQDFYIVGEFVNSNLDACREFLDTVDYQIDLFPVSLHYKLHNSLGRD 303
QY 302 YDMRRLDGTAVSHHPEKATVFNENHDTPQGSLESTVQTFWFKPLAAYAFILTRSGYPOV 361
DB 304 FDLSKIPTDITLVQNHPTAVIVFVNDHSQPHALESNIGWFKSAVALTLRLRDGYFV 363
QY 362 FYGDMYGTGTSPEKIPSLKDNIEPIIKAREYAYGQHDYIDHPDVIQWTRBSSAAK 421
DB 364 FYGDIYGIQG--PEPVQKKEILDILLSARCNKAYGQDEYFDANITGWRARVEIEG 421
QY 422 SGLAALITDGPGGSKRYAGLKNAGETWYDITGNRSPTVIGSGDGEFFVNDGSVSIY 480
DB 422 SGLAVVINSNDGGEKRYAGLKNAGETWYDITGNRSPTVIGSGDGEFFVNDGSVSIY 480

RESULT 14
Q97049 PRELIMINARY; PRT; 484 AA.
AC Q97049;
DT 01-OCT-2001 (TReMBrel. 18, Created)
DT 01-OCT-2001 (TReMBrel. 18, Last sequence update)
DT 01-JUN-2003 (TReMBrel. 24, Last annotation update)
DE Alpha-amylose.
GN SP1382.
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.

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NCBI_TaxID=1313;
 OX [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN-ATCC BAA-334 / TIGR4;
 RX MEDLINE=21357209; PubMed=11463916;
 RA Tettein H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,
 RA Peterson S., Heidelberg J., Deboy R.T., Haft D.H., Dodson R.J.,
 RA Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,
 RA Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,
 RA Holtapple E., Khouri H., Wolf A.M., Uterback T.R., Hansen C.L.,
 RA McDonald L.A., Feldblyum T.V., Angioli S., Dickinson T., Hickey E.K.,
 RA Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,
 RA Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.,
 RT "Complete genome sequence of a virulent isolate of Streptococcus
 pneumoniae";
 RL Science 293:498-506(2001).
 DR EMBL; AE007435; AAK75480.1; -
 DR PIR; G95160; G95160.
 DR TIGR; S81382;
 DR GO; GO:0004556; F:alpha-amylase activity; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro; IPR006047; Alpha_amyl_cat.
 DR InterPro; IPR006589; Alp_amyl_cat_sub.
 DR InterPro; IPR006046; Glyco_hydro_13.
 DR Pfam; PF00128; alpha-amylase; 1.
 DR PRINTS; PR00110; ALPHAAMYLASE.
 DR SMART; SM00642; Amy; 1.
 KW Complete proteome.
 SQ SEQUENCE 484 AA; 55918 MW; 4E90A450A90EFB8C CRC64;

Query Match 46.4%; Score 1217; DB 16; Length 484;
 Best local similarity 47.0%; Pred. No. 7, 3e-76;
 Matches 226; Conservative 81; Mismatches 168; Indels 6; Gaps 3;

QY 2 NGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPAYKGLSGDNGYGYDLYD 61
 DB 3 NOTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPAYKGLSGDNGYGYDLYD 62
 QY 62 LGFPOQKGYRTYKTKSELDALIGSLHSRNQVQDVVNLNKAADATADYTAVERNPA 121
 DB 63 LGFPOQKGYRTYKTKSELDALIGSLHSRNQVQDVVNLNKAADATADYTAVERNPA 122
 QY 122 NNRQETSEYQIKAWTDPRFPGRGNTYSDFKMWHYFDGADWDESKRISRIKFRGEKGA 181
 DB 123 DRTVELGEPTLNGWTSFTFDGRQDTYNGFHHMWHYFTGTDYDAKSKSGIYLIOQDNKG 182
 QY 182 WDME--VSSENGNDYLMVADVDYDHPDYVAETKKKGIYANELSLDGRIDAAKIKFS 239
 DB 183 WANEELVDNNGNDYLMVADVDYDHPDYVAETKKKGIYANELSLDGRIDAAKIKFS 242
 QY 240 FLRDVQAVROATGKEMFTVAEYQWONNAGLENYLNKTSFNQSVDPVPHFNLOAASQ 299
 DB 243 FMRNFIRDMKEKGGDDPYVGEFNNPDKEANDYLEKTEHPDLVDVRLHQNLFEASQ 302
 QY 300 GGYDMRLDGYVSRPEKAVTFVENHDTOPQOSLESTYQTFKRLAFAFITRESGTP 359
 DB 303 ANYDLRGIFTDSVLEKPDCAVTFVNDHDTORQALSTVEEFKPAVALIILRODGLP 362
 QY 360 QVFYGMVGTGTSPEIKIPILKARKEVAYGPQHDYIDHPVIGWTRGDSGA 419
 DB 363 CVFYGYGYSQYAGQ--DFKEILDRLLAIRKDLAVGQNDYFDHANCIGWRSQAEV 419
 QY 420 AKSGLAALITDGGGSKRMVAGIKNAGETWYDITGRSDTYKIGSGMGEFHYNDGSYSI 479
 DB 420 -QSPIAVLLISNDGSKSMFVQGEWNTQTFVDLLGNHQQVITIDEGYQGFVSASVS 478
 QY 480 Y 480
 DB 479 W 479

RESULT 15
 Q8DPC8

ID Q8DPC8 PRELIMINARY; PRT; 484 AA.
 AC Q8DPC8;
 DT 01-MAR-2003 (T-EMBLrel. 23, Created)
 DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
 DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
 DE Alpha-amylase (EC 3.2.1.1).
 GN ANY OR SPRI239.
 OS Streptococcus pneumoniae (strain ATCC BAA-255 / R6).
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=171101;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21429245; PubMed=11544234;
 RA Hoskins J., Alborn W.E. Jr., Arnold J., Blaszcak L.C., Burgett S.,
 RA Dehoff B.S., Estrem S.T., Fritz L., Fu D.-J., Fuller W., Geringer C.,
 RA Gilmour R., Glas J.S., Khoja H., Kraft A.R., Lagace R.E.,
 RA Leblanc D.J., Lee L.N., Lefkowitz B.J., Lu J., Matsushima P.,
 RA McHenry S.M., McHenry M., Mclester K., Mundy C.W., Nicot T.I.,
 RA Norris F.H., O'Gara M., Peery R.B., Robertson G.T., Rocky P.,
 RA Sun P.-X., Winkler M.E., Yang Y., Young-Bellido M., Zhao G.,
 RA Zook C.A., Baltz R.H., Jaskunas S.R., Rostock P.R. Jr., Skatrud P.L.,
 RA Glas J.T.;
 RT "Genome of the bacterium Streptococcus pneumoniae strain R6";
 RL J. Bacteriol. 183:5709-5717(2001).
 DR EMBL; AE008495; AAI00043.1; -
 DR PIR; F98026; F98026.
 DR GO; GO:0004556; F:alpha-amylase activity; IEA.
 DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro; IPR006047; Alpha_amyl_cat.
 DR InterPro; IPR006589; Alp_amyl_cat_sub.
 DR InterPro; IPR006046; Glyco_hydro_13.
 DR Pfam; PF00128; alpha-amylase; 1.
 DR PRINTS; PR00110; ALPHAAMYLASE.
 DR SMART; SM00642; Amy; 1.
 KW Glycosidase; Hydrolase; Complete proteome.
 SQ SEQUENCE 484 AA; 55880 MW; DA511868187A0FFC CRC64;

Query Match 46.2%; Score 1212; DB 16; Length 484;
 Best local similarity 46.6%; Pred. No. 1, 6e-75;
 Matches 224; Conservative 84; Mismatches 167; Indels 6; Gaps 3;

QY 2 NGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPAYKGLSGDNGYGYDLYD 61
 DB 3 NOTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPAYKGLSGDNGYGYDLYD 62
 QY 62 LGFPOQKGYRTYKTKSELDALIGSLHSRNQVQDVVNLNKAADATADYTAVERNPA 121
 DB 63 LGFPOQKGYRTYKTKSELDALIGSLHSRNQVQDVVNLNKAADATADYTAVERNPA 122
 QY 122 NNRQETSEYQIKAWTDPRFPGRGNTYSDFKMWHYFDGADWDESKRISRIKFRGEKGA 181
 DB 123 DRTVELGEPTLNGWTSFTFDGRQDTYNGFHHMWHYFTGTDYDAKSKSGIYLIOQDNKG 182
 QY 182 WDME--VSSENGNDYLMVADVDYDHPDYVAETKKKGIYANELSLDGRIDAAKIKFS 239
 DB 183 WANEELVDNNGNDYLMVADVDYDHPDYVAETKKKGIYANELSLDGRIDAAKIKFS 242
 QY 240 FLRDVQAVROATGKEMFTVAEYQWONNAGLENYLNKTSFNQSVDPVPHFNLOAASQ 299
 DB 243 FMRNFIRDMKEKGGDDPYVGEFNNPDKEANDYLEKTEHPDLVDVRLHQNLFEASQ 302
 QY 300 GGYDMRLDGYVSRPEKAVTFVENHDTOPQOSLESTYQTFKRLAFAFITRESGTP 359
 DB 303 ANYDLRGIFTDSVLEKPDCAVTFVNDHDTORQALSTVEEFKPAVALIILRODGLP 362
 QY 360 QVFYGMVGTGTSPEIKIPILKARKEVAYGPQHDYIDHPVIGWTRGDSGA 419
 DB 363 CVFYGYGYSQYAGQ--DFKEILDRLLAIRKDLAVGQNDYFDHANCIGWRSQAEV 419
 QY 420 AKSGLAALITDGGGSKRMVAGIKNAGETWYDITGRSDTYKIGSGMGEFHYNDGSYSI 479

Tue May 4 14:34:48 2004

us-10-644-187-4.rpt

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Db 420 -QSP1AVLISNDQENSKMFWGQEWNTQTFVDLIGSHQGVITIDEGYGQFPVSARSYSV 478

Qy 480 Y 480

Db 479 W 479

Search completed: May 3, 2004, 20:53:13
Job time : 35.1232 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 3, 2004, 20:36:03 ; Search time 10.4645 Seconds
(without alignments)
2403.363 Million cell updates/sec

Title: US-10-644-187-2

Sequence: 1 ANNGTLMQFEWYMPNDGQ.....SEGMBEFHNGSVSTYVOR 483
2666

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2648	99.3	512	1	AMY_BACLI
2	2184	81.9	514	1	AMY_BACAM
3	1879	70.5	518	1	AMY6_BACST
4	1776.5	66.6	549	1	AMY_BACST
5	1058	39.7	494	1	AMY2_SALTY
6	1047	39.3	495	1	AMY2_ECOTI
7	340	12.8	1196	1	AMYB_PAEPO
8	311.5	11.7	421	1	AMVA_VIGMU
9	304	11.4	440	1	AM3A_ORYSA
10	300	11.3	437	1	AM3C_ORYSA
11	298	11.2	713	1	CDGT_BAC8
12	294	11.0	713	1	CDGT_BAC8
13	292.5	11.0	413	1	AMY3_WHEAT
14	292	11.0	718	1	CDGT_BACCI
15	291.5	10.9	718	1	CDGT_BACCS
16	290	10.9	437	1	AM3E_ORYSA
17	289	10.8	438	1	AM3B_ORYSA
18	288	10.7	712	1	CDGT_BAC3
19	286	10.7	713	1	CDGT_BACCI
20	281	10.5	435	1	AM3D_ORYSA
21	279	10.5	713	1	CDGT_BACSP
22	277.5	10.4	710	1	CDGT_THERTU
23	276.5	10.4	718	1	CDGT_BACLI
24	271.5	10.2	528	1	AMY_BACCI
25	262	9.8	494	1	AMY3_SACFI
26	259	9.7	368	1	AMY3_HORVU
27	259	9.7	427	1	AMY2_HORVU
28	259	9.7	429	1	AMY6_HORVU
29	257	9.6	428	1	AMY1_ORYSA
30	252.5	9.5	438	1	AMY1_HORVU
31	247	9.3	441	1	MGTA_THENA
32	245.5	9.2	719	1	AMCM_BACST
33	242.5	9.1	443	1	AM2A_ORYSA

34	242.5	9.1	445	1	AMC2_ORYSA	P27941 oryza sativ
35	237.5	8.9	713	1	CDG2_PAEPA	P31835 paenibacill
36	236.5	8.9	676	1	AMY1_ECOTI	P25718 escherichia
37	234.5	8.8	581	1	AMY1_SCHPO	O09840 schizosacch
38	233.5	8.8	919	1	AMY1_STRTI	O05884 streptomyce
39	231.5	8.7	442	1	MGTA_THENA	O86956 thermotoga
40	231.5	8.7	711	1	CDGT_BACST	P31787 bacillus st
41	226	8.5	498	1	AMY3_DICTH	P14899 dictyoglomu
42	218	8.2	478	1	YQ29_SCHPO	Q10427 schizosacch
43	215.5	8.1	564	1	AMY4_SCHPO	Q97769 schizosacch
44	211	7.9	704	1	CDGT_BACCO	P27036 bacillus oh
45	211	7.9	1476	1	GPFB_STMMU	P08987 streptococc

ALIGNMENTS

RESULT 1	AMY_BACLI	STANDARD;	PRT;	512 AA.
ID	AMY_BACLI			
AC	P06278.084112;			
DT	01-JAN-1988 (Rel. 06, Created)			
DT	01-JAN-1988 (Rel. 06, Last sequence update)			
DT	15-MAR-2004 (Rel. 43, Last annotation update)			
DE	Alpha-amylase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan			
DE	glucanohydrolase) (BLA).			
GN	AMYS OR AMYL.			
OS	Bacillus licheniformis.			
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.			
OX	NCBI_Taxid=1402;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=ATCC 27811.			
RX	MEDLINE=86111694; PubMed=2418011;			
RA	Yukki T., Nomura T., Teruka H., Tsuboi A., Yamagata H.,			
RA	Teukagoshi N., Ueda S.;			
RT	"Complete nucleotide sequence of a gene coding for heat- and			
RT	pH-stable alpha-amylase of Bacillus licheniformis: comparison of the			
RT	amino acid sequences of three bacterial liquefying alpha-amylases			
RT	deduced from the DNA sequences."			
RL	J. Biochem. 98:1147-1156(1985).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=86195857; PubMed=3009417;			
RA	Gray G.L., Mainzer S.E., Rey M.W., Lamsa M.H., Kindle K.L.,			
RA	Cermone C., Reguadt C.;			
RT	"Structural genes encoding the thermophilic alpha-amylases of			
RT	Bacillus stearothermophilus and Bacillus licheniformis."			
RL	J. Bacteriol. 166:635-645(1986).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RA	Shahosseini M., Ziaei A.A., Ghaemi N., Pourabaei A.A.;			
RT	"An unusual DNA sequence encoded a hyperthermostable alpha-amylase."			
RT	Submitted (OCT-2001) to the EMBL/Genbank/DBS databases.			
RN	[4]			
RP	SEQUENCE OF 1-104 FROM N.A.			
RX	MEDLINE=84185455; PubMed=6609154;			
RA	Stephens M.A., Orlepp S.A., Ollington J.F., McConnell D.J.;			
RT	"Nucleotide sequence of the 5' region of the Bacillus licheniformis			
RT	alpha-amylase gene: comparison with the B. amyloliquefaciens gene."			
RL	J. Bacteriol. 158:369-372(1984).			
RN	[5]			
RP	SEQUENCE OF 1-29 FROM N.A.			
RX	MEDLINE=89213924; PubMed=2540150;			
RA	Isoide B.M., Chambliss G.H., McConnell D.J.;			
RT	"Bacillus licheniformis alpha-amylase gene, amyL, is subject to			
RT	promoter-independent catabolite repression in Bacillus subtilis."			
RL	J. Bacteriol. 171:2435-2442(1989).			
RN	[6]			
RP	SEQUENCE OF 30-47.			
RX	MEDLINE=82098050; PubMed=6172418;			
RA	Kuhn H., Fietzek P.P., Lampen U.O.;			
RT	"N-terminal amino acid sequence of Bacillus licheniformis			

RT alpha-amylase: comparison with *Bacillus amyloliquefaciens* and
 RT *Bacillus subtilis* enzymes.";
 RL J. Bacteriol. 149:372-373(1982).
 RN [7]
 RN MAPPING OF SUBSTRATE-BINDING SITE.
 RX MEDLINE=2192788; PubMed=11997021.
 RA Kanda U., Gyemant G., Remenyik J., Hovanszki G., Lipak A.
 RT "Action pattern and substrate mapping of *Bacillus licheniformis*
 RT alpha-amylase (BLA) with modified maltotriogalactoside substrates.";
 RL FEBS Lett. 518:79-82(2002).
 RN [8]
 RN MUTAGENESIS OF HIS-64; HIS-162; HIS-276; HIS-322; HIS-435 AND HIS-479.
 RP STRAIN=ATCC 6598;
 RX MEDLINE=90368748; PubMed=2394736;
 RA Declercq N., Joyet P., Galliardin C., Maeson J.M.,
 RT "Use of amber suppressors to investigate the thermostability of
 RT *Bacillus licheniformis* alpha-amylase. Amino acid replacements at 6
 RT histidine residues reveal a critical position at His-133.";
 RL J. Biol. Chem. 265:15481-15488(1990).
 RN [9]
 RN MUTAGENESIS OF ALA-238.
 RP STRAIN=ATCC 6598;
 RX MEDLINE=96367070; PubMed=8771184;
 RA Declercq N., Joyet P., Trosset J.Y., Garnier J., Galliardin C.,
 RT "Hyperthermostable mutants of *Bacillus licheniformis* alpha-amylase:
 RT multiple amino acid replacements and molecular modelling.";
 RL Protein Eng. 8:1029-1037(1995).
 RN [10]
 RN MUTAGENESIS OF ASP-150; ASN-155; ARG-175; ASP-193; ASN-201; GLN-207;
 RP ASN-217; ASN-219; ASN-221; ASP-229; ASP-233; ALA-258; GLU-300; GLN-359
 RP AND GLU-365.
 RX STRAIN=ATCC 6598;
 RX MEDLINE=20425100; PubMed=10968904;
 RA Declercq N., Machus M., Wiegand G., Huber R., Galliardin C.,
 RT "Probing structural determinants specifying high thermostability in
 RT *Bacillus licheniformis* alpha-amylase.";
 RL J. Mol. Biol. 301:1041-1057(2000).
 RN [11]
 RN MUTAGENESIS OF GLN-293 AND ASN-294.
 RP STRAIN=ATCC 6598;
 RX MEDLINE=22622182; PubMed=12736372;
 RA Declercq N., Machus M., Joyet P., Wiegand G., Huber R.,
 RT "Hyperthermostabilization of *Bacillus licheniformis* alpha-amylase and
 RT modulation of its stability over a 50 degrees C temperature range.";
 RL Protein Eng. 16:287-293(2003).
 RN [12]
 RN MUTAGENESIS OF TRP-292 AND VAL-315.
 RP STRAIN=ATCC 27811;
 RX MEDLINE=22797417; PubMed=12915728;
 RA Rivera M.H., Lopez-Munguia A., Sobeyon X., Saab-Rincon G.,
 RT "Alpha-amylase from *Bacillus licheniformis* mutants near to the
 RT catalytic site: effects on hydrolytic and transglycosylation
 RT activity.";
 RL Protein Eng. 16:505-514(2003).
 RN [13]
 RN X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
 RP STRAIN=ATCC 27811;
 RX MEDLINE=95182462; PubMed=7877175;
 RA Machus M., Wiegand G., Huber R.,
 RT "Crystal structure of calcium-depleted *Bacillus licheniformis* alpha-
 RT amylase at 2.2-A resolution.";
 RL J. Mol. Biol. 246:545-559(1995).
 RN [14]
 RN X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RP MEDLINE=98212915; PubMed=9551551.
 RX Machus M., Declercq N., Huber R., Wiegand G.,
 RT "Activation of *Bacillus licheniformis* alpha-amylase through a
 RT disorder-->order transition of the substrate-binding site mediated
 RT by a calcium-sodium-calcium metal triad.";
 RL Structure 6:281-292(1998).
 RN [15]
 RN X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 320-512.

RX MEDLINE=20384196; PubMed=10924103;
 RA Brzozowski A.M., Lawson D.M., Turkemburg J.P., Bisgaard-Frantzen H.,
 RA Svendsen A., Borcherdt T.V., Dauter Z., Wilson K.S., Davies G.J.,
 RT "Structural analysis of a chimeric bacterial alpha-amylase.
 RT High-resolution analysis of native and ligand complexes.";
 RL Biochemistry 39:9099-9107(2000).
 RN [16]
 RN X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF MUTANT
 RP H162V/N219F/A238V/Q293S/N294Y.
 RP STRAIN=ATCC 6598;
 RX MEDLINE=22538505; PubMed=12540849;
 RA Machus M., Declercq N., Huber R., Wiegand G.,
 RT "Kinetic stabilization of *Bacillus licheniformis* alpha-amylase through
 RT introduction of hydrophobic residues at the surface.";
 RL J. Biol. Chem. 278:11546-11553(2003).
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
 CC linkages in oligosaccharides and polysaccharides.
 CC -1- COFACTOR: Binds 3 calcium ions and 1 sodium ion per subunit.
 CC -1- SUBUNIT: Monomer.
 CC -1- BIOTECHNOLOGY: Used in the food industry for high temperature
 CC liquefaction of starch-containing mashes and in the detergent
 CC industry to remove starch. Sold under the name Termamy1 by
 CC Novozymes.
 CC -1- MISCELLANEOUS: Able to work at relatively high (alkaline) pH
 CC values (up to pH 11) and at high temperatures (up to 100 degrees
 CC Celsius).
 CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
 CC
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 CC
 CC EMBL; X03336; CAA26981.1; -
 CC EMBL; M38570; AAA22226.1; -
 CC EMBL; M13556; AAA22240.1; -
 CC EMBL; K01984; AAA22193.1; -
 CC EMBL; AF438149; AAO26743.1; -
 CC EMBL; M26412; AAA22237.1; -
 CC EMBL; A17930; CAA01355.1; -
 CC PIR; A91997; ALBSL.
 CC PDB; 1BFL; 23-MAR-99.
 CC PDB; 1BFL; 17-AUG-96.
 CC PDB; 1E3X; 21-JUN-01.
 CC PDB; 1E3Z; 24-JUN-03.
 CC PDB; 1E40; 24-JUN-03.
 CC PDB; 1E43; 21-JUN-01.
 CC PDB; 1O80; 03-APR-03.
 CC PDB; 1YGS; 13-MAR-97.
 CC InterPro; IPR006589; Alp_aml_cat_sub.
 CC InterPro; IPR006047; Alpha_aml_cat.
 CC InterPro; IPR006046; Glyco_hydro_13.
 CC Pfam; PF00128; alpha-amylase; 1.
 CC PRINTS; PR00110; ALPHAMYLASE.
 CC SMART; SM00642; Aamy; 1.
 CC Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
 CC Signal; 3d-structure.
 CC CHAIN
 CC FT 1 512
 CC FT 260 260
 CC FT ACT SITE 264 264
 CC FT ACT SITE 357 357
 CC FT METAL 133 133
 CC FT METAL 190 190
 CC FT METAL 210 210
 CC FT METAL 212 212
 CC FT METAL 223 223
 CC FT METAL 229 229
 CC FT METAL 231 231
 CC FT METAL 233 233
 CC
 CC ALPHA-AMYLASE.
 CC
 CC CALCIUM 1.
 CC CALCIUM 2 (VIA CARBOXYL OXYGEN).
 CC CALCIUM 2 AND SODIUM.
 CC CALCIUM 1 AND SODIUM.
 CC CALCIUM 1 AND SODIUM.
 CC CALCIUM 2.
 CC CALCIUM 2.

SQ SEQUENCE 514 AA; 58403 MW; 3DB66B3FB5CCE7E CRC64;
 Query Match 81.9%; Score 2184; DB 1; Length 514;
 Best Local Similarity 80.3%; Pred. No. 9,8e-153;
 Matches 388; Conservative 44; Mismatches 49; Indels 2; Gaps 1;

QY 3 LNSTLMQYFEMWMPNDGQHRRLONDSAYLAHGITAWIPRAYKGTSGQADVGAYVLY 62
 DB 32 VAGTLMQYFEMWTPDNGQHRRLONDSAYLAHGITAWIPRAYKGTSGQADVGAYVLY 91
 QY 63 DLGEFQKGTAVTKYGTGKELOSAIKSLHSRDINYGVDVINHGKADATEDVTAVEVP 122
 DB 92 DLGEFQKGTAVTKYGTGKELODAIGSLSRNVQYGVVLNKGADATEDVTAVEVP 151
 QY 123 AARNVISEGHLIKMTHEHPFGSTGSDGKMHYHEDGDMDSRLNLYKFE--QK 180
 DB 152 AARNQTSSEYQIKATWDFRFGKGTYSDFKMHYHEDGDMDSRLNLYKFEKRGK 211
 QY 181 AMDWEVSENGVNDYLMYADIDYDHPVAEIKRWGTAYANLQDGFRLDAVKIKESF 240
 DB 212 AMDWEVSENGVNDYLMYADVDDYDHPVAEIKRWGTAYANLQDGFRLDAVKIKESF 271
 QY 241 LDDVYVAREKTKEMFTYAEWQNDLALNTYLNKTNPNHSEVPVPLHYQPHASTGG 300
 DB 272 LDDVYVAREKTKEMFTYAEWQNDLALNTYLNKTNPNHSEVPVPLHYQPHASTGG 331
 QY 301 GYDMKRLNGTVSKPLKSTVTVFVNDHDTQPGQSLSTQVTFKFLAYAFILTRREGYPQ 360
 DB 332 GYDMKRLNGTVSKPLKSTVTVFVNDHDTQPGQSLSTQVTFKFLAYAFILTRREGYPQ 391
 QY 361 VYEGDMYGTGDSQREIPALKEKIEPILKAKQYAYGAQHDYFDDHIVGTREBDSVA 420
 DB 392 VYEGDMYGTGDSQREIPALKEKIEPILKAKQYAYGAQHDYFDDHIVGTREBDSVA 451
 QY 421 NSGLALITDGPAGKMYVGRONAGETWHDITGNRSEPVVNSGGEFHNAGSVAISY 480
 DB 452 NSGLALITDGPAGKMYVGRONAGETWHDITGNRSEPVVNSGGEFHNAGSVAISY 511
 QY 481 VQR 483
 DB 512 VQR 514

RESULT 3
 AMT6_BACS7
 ID AMT6_BACS7 STANDARD; PRT; 518 AA.
 AC P19571;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Glucan 1,4-alpha-maltohexaosidase precursor (EC 3.2.1.98) (66-amyase)
 OS (Maltotetraose-producing amylase) (Exo-maltohexaohydrolase).
 OC Bacillus sp. (strain 707).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1416;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 34-36.
 RX MEDLINE=88162814; Pubmed=3258152;
 RA Tsukamoto A., Kimura K., Ishii Y., Takano T., Yamane K.;
 RT "Nucleotide sequence of the maltotetraose-producing amylase gene from
 RT an alkalophilic Bacillus sp. #707 and structural similarity to
 RT liquefying type alpha-amyloses.";
 RL Biochem. Biophys. Res. Commun. 151:25-31(1988).
 CC -1- CATALYTIC ACTIVITY: Hydrolysis of 1,4-alpha-D-glucosidic linkages
 CC in amylose polysaccharides so as to remove successive
 CC maltotetraose residues from the non-reducing chain ends.
 CC -1- COFACTOR: Binds 2 calcium ions and 1 sodium ion per subunit (by
 CC similarity).
 CC -1- PATHWAY: Starch degradation.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
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 CC or send an email to license@sdb.ch).
 CC EMBL: M18862; AAA2231.1;
 DR PIR: A27705; A27705.
 DR HSP: P06278; 1V08.
 DR InterPro: IPR006589; Alp_amy1_cat_sub.
 DR InterPro: IPR006047; Alp_amy1_cat.
 DR InterPro: IPR006046; Glyco_hydro_13.
 DR Pfam: PF00128; alpha-amyase; 1.
 DR PRINTS: PR00110; ALPHAAMYLASE.
 DR SMART: SM00542; Amyy; 1.
 KM Hydroxylase; Glycosidase; Carbohydrate metabolism; signal.
 FT SIGNAL 1 33
 FT CHAIN 34 518
 FT ACT_SITE 269 269 BY SIMILARITY.
 FT ACT_SITE 273 273 BY SIMILARITY.
 FT ACT_SITE 366 366 BY SIMILARITY.
 FT METAL 139 139 CALCIUM 1 (BY SIMILARITY).
 FT METAL 196 196 CALCIUM 2 (BY SIMILARITY).
 FT METAL 219 219 CALCIUM 2 (VIA CARBOXYL OXYGEN) (BY
 FT SIMILARITY).
 FT METAL 221 221 CALCIUM 2 AND SODIUM (BY SIMILARITY).
 FT METAL 232 232 CALCIUM 1 AND SODIUM (BY SIMILARITY).
 FT METAL 238 238 CALCIUM 1 AND SODIUM (BY SIMILARITY).
 FT METAL 240 240 CALCIUM 2 (BY SIMILARITY).
 FT METAL 242 242 CALCIUM 2 (BY SIMILARITY).
 FT METAL 273 273 CALCIUM 1 (VIA CARBOXYL OXYGEN) (BY
 FT SIMILARITY).
 SQ SEQUENCE 518 AA; 59009 MW; 3A961E21612682C4 CRC64;
 Query Match 70.5%; Score 1879; DB 1; Length 518;
 Best Local Similarity 67.8%; Pred. No. 2,3e-130;
 Matches 329; Conservative 67; Mismatches 79; Indels 10; Gaps 4;

QY 4 NGTLMQYFEMWMPNDGQHRRLONDSAYLAHGITAWIPRAYKGTSGQADVGAYVLY 63
 DB 39 NGTLMQYFEMWTPDNGQHRRLONDSAYLAHGITAWIPRAYKGTSGQADVGAYVLY 98
 QY 64 LGSEHOKGTAVTKYGTGKELOSAIKSLHSRDINVGVDVINHGKADATEDVTAVEVPA 123
 DB 99 LGSEHOKGTAVTKYGTGKELOSAIKSLHSRDINVGVDVINHGKADATEDVTAVEVPA 158
 QY 124 DNRNVISEHLIKAMTHFHPFGSTGSDGKMHYHEDGDMDSRLNLYKFEKRGK 180
 DB 159 DNRNVISEHLIKAMTHFHPFGSTGSDGKMHYHEDGDMDSRLNLYKFEKRGK 218
 QY 181 AMDWEVSENGVNDYLMYADIDYDHPVAEIKRWGTAYANLQDGFRLDAVKIKESF 240
 DB 219 AMDWEVSENGVNDYLMYADIDYDHPVAEIKRWGTAYANLQDGFRLDAVKIKESF 278
 QY 241 LDDVYVAREKTKEMFTYAEWQNDLALNTYLNKTNPNHSEVPVPLHYQPHASTGG 300
 DB 272 LDDVYVAREKTKEMFTYAEWQNDLALNTYLNKTNPNHSEVPVPLHYQPHASTGG 338
 QY 301 GYDMKRLNGTVSKPLKSTVTVFVNDHDTQPGQSLSTQVTFKFLAYAFILTRREGYPQ 360
 DB 332 GYDMKRLNGTVSKPLKSTVTVFVNDHDTQPGQSLSTQVTFKFLAYAFILTRREGYPQ 398
 QY 361 VYEGDMYGTGDSQREIPALKEKIEPILKAKQYAYGAQHDYFDDHIVGTREBDSVA 428
 DB 399 VYEGDMYGTGDSQREIPALKEKIEPILKAKQYAYGAQHDYFDDHIVGTREBDSVA 453
 QY 419 VANSGLALITDGPAGKMYVGRONAGETWHDITGNRSEPVVNSGGEFHNAGSVAISY 478
 DB 454 VANSGLALITDGPAGKMYVGRONAGETWHDITGNRSEPVVNSGGEFHNAGSVAISY 513
 QY 479 IYVQR 483

Db 514 IWMNK 518

RESULT 4

AMY_BACST STANDARD; PRT; 549 AA.

AC P06279; Q45519; 01-JAN-1988 (Rel. 06, Created)

DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Alpha-amylase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan glucanohydrolase).

GN AMYS.

OS Bacillus stearothermophilus.

OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.

OX NCBI_TaxID=1422;

NP SEQUENCE FROM N.A., AND SEQUENCE OF 35-39.

RP MEDLINE=85234394; Pubmed=3924897;

RA Nakajima R., Imanaka T., Alba S.;

RT "Nucleotide sequence of the Bacillus stearothermophilus alpha-amylase gene.";

RL J. Bacteriol. 163:401-406(1985).

RN [2]

RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RC STRAIN=DYS/PHI300;

RX MEDLINE=86008166; Pubmed=3876333;

RA Ihara H., Sasaki T., Tsuboi A., Yamagata H., Tsukagoshi N., Ueda S.;

RT "Complete nucleotide sequence of a thermophilic alpha-amylase gene: homology between prokaryotic and eukaryotic alpha-amylases at the active sites.";

RL J. Biochem. 98:95-103(1985).

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=NZ-3;

RX MEDLINE=86195957; Pubmed=3009417;

RA Gray G.L., Mainzer S.E., Key M.W., Lamea M.H., Kindle K.L., Carmona C., Reigada C.;

RT "Structural genes encoding the thermophilic alpha-amylases of Bacillus stearothermophilus and Bacillus licheniformis.";

RL J. Bacteriol. 166:635-643(1986).

RN [4]

RP SEQUENCE FROM N.A.

RA Smolinen I., Karp M., Lautamo J., Marttela P.;

RT "Thermotable alpha amylase of Bacillus stearothermophilus: cloning, expression, and secretion by Escherichia coli.";

RL (in) Chaloupka J., Krumphanz V. (eds.);

RT Extracellular enzymes of microorganisms, pp.129-137, Plenum Press, New York (1987).

RN [5]

RP SEQUENCE OF 1-122 FROM N.A., AND SEQUENCE OF 35-48.

RC STRAIN=DY-5;

RX MEDLINE=60592211; Pubmed=2999073;

RA Tsukagoshi N., Iritani S., Sasaki T., Takemura T., Ihara H., Ito Y., Yamagata H., Ueda S.;

RT "Efficient synthesis and secretion of a thermophilic alpha-amylase by protein-producing Bacillus brevis 47 carrying the Bacillus stearothermophilus amylase gene.";

RL J. Bacteriol. 164:1182-1187(1985).

RN [6]

RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).

RX MEDLINE=2115602; Pubmed=1126887;

RA Svud D., Fujimoto Z., Takase K., Matsumura M., Mizuno H.;

RT "Crystal structure of Bacillus stearothermophilus alpha-amylase: possible factors determining the thermostability.";

RL J. Biochem. 129:461-468(2001).

CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic linkages in oligosaccharides and polysaccharides.

CC -1- COFACTOR: Binds 3 calcium ions and 1 sodium ion per subunit.

CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.

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CC -----

CC EMBL; M1450; AA22235.2; -

CC EMBL; X02769; CA26547.1; -

CC EMBL; M57457; AA22227.1; -

CC EMBL; M13255; AA22241.1; -

CC PIR; A2436; A2436.

CC PIR; A91999; ALBSF.

CC PDB; 1HVX; 05-AUG-03.

CC InterPro; IPR006589; Alp_amyl_cat_sub.

CC InterPro; IPR006047; Alpha_amyl_cat.

CC InterPro; IPR006046; Glyco_hydro_13.

CC Pfam; PF00126; alpha-amylase; 1.

CC PRINTS; PR00110; ALPHAMYLASE.

CC SMART; SM00642; Amy; 1.

CC Carbohydrate metabolism; Hydrolyase; Glycosidase; Calcium-binding;

CC Signal; 3D-structure.

CC SIGNAL 1 34

CC FT CHAIN 35 549

CC FT ACT SITE 268 268

CC FT ACT SITE 272 272

CC FT ACT SITE 365 365

CC FT METAL 139 139

CC FT METAL 196 196

CC FT METAL 218 218

CC FT METAL 220 220

CC FT METAL 231 231

CC FT METAL 237 237

CC FT METAL 238 238

CC FT METAL 239 239

CC FT METAL 272 272

CC FT METAL 337 337

CC FT METAL 339 339

CC FT METAL 440 440

CC FT METAL 441 441

CC FT METAL 464 464

CC FT METAL 13 13

CC FT CONFLICT 13 13

CC FT CONFLICT 23 23

CC FT CONFLICT 31 31

CC FT CONFLICT 107 107

CC FT CONFLICT 167 167

CC FT CONFLICT 179 179

CC FT CONFLICT 251 251

CC FT CONFLICT 260 260

CC FT CONFLICT 284 284

CC FT CONFLICT 312 312

CC FT CONFLICT 338 338

CC FT CONFLICT 342 342

CC FT CONFLICT 346 346

CC FT CONFLICT 376 376

CC FT CONFLICT 526 527

CC FT CONFLICT 527 527

CC FT CONFLICT 535 535

CC SQ SEQUENCE 549 AA; 62670 MW; 3A2DD93A955E79D3 CRC64;

Qy 1 ANLNGTLMQYFEMTPNDGQWRRLQNDASVLAHGGITAVWIPAYKGTSGADVGAYD 60

Qy 36 APFNGTMMQYFEMTLPDGLTMTVANEANNLSLGITLMLPRAYKGTSGADVGAYD 95

Qy 61 LYDGEFQKGTATKTKGTGELDSATKSHSDINYYGVVNHKGGADATEQVTAVEV 120

Qy 96 LYDGEFQKGTATKTKGTGELDSATKSHSDINYYGVVNHKGGADATEQVTAVEV 155

Db 96 LYDGEFQKGTATKTKGTGELDSATKSHSDINYYGVVNHKGGADATEQVTAVEV 155

Qy 61 LYDGEFQKGTATKTKGTGELDSATKSHSDINYYGVVNHKGGADATEQVTAVEV 120

Qy 36 APFNGTMMQYFEMTLPDGLTMTVANEANNLSLGITLMLPRAYKGTSGADVGAYD 95

Qy 1 ANLNGTLMQYFEMTPNDGQWRRLQNDASVLAHGGITAVWIPAYKGTSGADVGAYD 60

Qy 96 LYDGEFQKGTATKTKGTGELDSATKSHSDINYYGVVNHKGGADATEQVTAVEV 155

Db 96 LYDGEFQKGTATKTKGTGELDSATKSHSDINYYGVVNHKGGADATEQVTAVEV 155

Qy 61 LYDGEFQKGTATKTKGTGELDSATKSHSDINYYGVVNHKGGADATEQVTAVEV 120

Qy 36 APFNGTMMQYFEMTLPDGLTMTVANEANNLSLGITLMLPRAYKGTSGADVGAYD 95

Qy 1 ANLNGTLMQYFEMTPNDGQWRRLQNDASVLAHGGITAVWIPAYKGTSGADVGAYD 60

Qy 96 LYDGEFQKGTATKTKGTGELDSATKSHSDINYYGVVNHKGGADATEQVTAVEV 155

Db 96 LYDGEFQKGTATKTKGTGELDSATKSHSDINYYGVVNHKGGADATEQVTAVEV 155

Qy 61 LYDGEFQKGTATKTKGTGELDSATKSHSDINYYGVVNHKGGADATEQVTAVEV 120

Qy 36 APFNGTMMQYFEMTLPDGLTMTVANEANNLSLGITLMLPRAYKGTSGADVGAYD 95

Qy 1 ANLNGTLMQYFEMTPNDGQWRRLQNDASVLAHGGITAVWIPAYKGTSGADVGAYD 60

Qy 96 LYDGEFQKGTATKTKGTGELDSATKSHSDINYYGVVNHKGGADATEQVTAVEV 155

Db 96 LYDGEFQKGTATKTKGTGELDSATKSHSDINYYGVVNHKGGADATEQVTAVEV 155

Qy 61 LYDGEFQKGTATKTKGTGELDSATKSHSDINYYGVVNHKGGADATEQVTAVEV 120

Qy 36 APFNGTMMQYFEMTLPDGLTMTVANEANNLSLGITLMLPRAYKGTSGADVGAYD 95

Qy 1 ANLNGTLMQYFEMTPNDGQWRRLQNDASVLAHGGITAVWIPAYKGTSGADVGAYD 60

Qy 96 LYDGEFQKGTATKTKGTGELDSATKSHSDINYYGVVNHKGGADATEQVTAVEV 155

Db 96 LYDGEFQKGTATKTKGTGELDSATKSHSDINYYGVVNHKGGADATEQVTAVEV 155

Qy 61 LYDGEFQKGTATKTKGTGELDSATKSHSDINYYGVVNHKGGADATEQVTAVEV 120

Qy 36 APFNGTMMQYFEMTLPDGLTMTVANEANNLSLGITLMLPRAYKGTSGADVGAYD 95

Qy 1 ANLNGTLMQYFEMTPNDGQWRRLQNDASVLAHGGITAVWIPAYKGTSGADVGAYD 60

Qy 96 LYDGEFQKGTATKTKGTGELDSATKSHSDINYYGVVNHKGGADATEQVTAVEV 155

Db 96 LYDGEFQKGTATKTKGTGELDSATKSHSDINYYGVVNHKGGADATEQVTAVEV 155

Qy 61 LYDGEFQKGTATKTKGTGELDSATKSHSDINYYGVVNHKGGADATEQVTAVEV 120

Qy 36 APFNGTMMQYFEMTLPDGLTMTVANEANNLSLGITLMLPRAYKGTSGADVGAYD 95

Qy 1 ANLNGTLMQYFEMTPNDGQWRRLQNDASVLAHGGITAVWIPAYKGTSGADVGAYD 60

Qy 96 LYDGEFQKGTATKTKGTGELDSATKSHSDINYYGVVNHKGGADATEQVTAVEV 155

Db 96 LYDGEFQKGTATKTKGTGELDSATKSHSDINYYGVVNHKGGADATEQVTAVEV 155

Qy 61 LYDGEFQKGTATKTKGTGELDSATKSHSDINYYGVVNHKGGADATEQVTAVEV 120

Qy 36 APFNGTMMQYFEMTLPDGLTMTVANEANNLSLGITLMLPRAYKGTSGADVGAYD 95

Qy 1 ANLNGTLMQYFEMTPNDGQWRRLQNDASVLAHGGITAVWIPAYKGTSGADVGAYD 60

Qy 96 LYDGEFQKGTATKTKGTGELDSATKSHSDINYYGVVNHKGGADATEQVTAVEV 155

Db 96 LYDGEFQKGTATKTKGTGELDSATKSHSDINYYGVVNHKGGADATEQVTAVEV 155

Qy 61 LYDGEFQKGTATKTKGTGELDSATKSHSDINYYGVVNHKGGADATEQVTAVEV 120

Qy 36 APFNGTMMQYFEMTLPDGLTMTVANEANNLSLGITLMLPRAYKGTSGADVGAYD 95

Qy 1 ANLNGTLMQYFEMTPNDGQWRRLQNDASVLAHGGITAVWIPAYKGTSGADVGAYD 60

Qy 96 LYDGEFQKGTATKTKGTGELDSATKSHSDINYYGVVNHKGGADATEQVTAVEV 155

Db 96 LYDGEFQKGTATKTKGTGELDSATKSHSDINYYGVVNHKGGADATEQVTAVEV 155

Qy 61 LYDGEFQKGTATKTKGTGELDSATKSHSDINYYGVVNHKGGADATEQVTAVEV 120

Qy 36 APFNGTMMQYFEMTLPDGLTMTVANEANNLSLGITLMLPRAYKGTSGADVGAYD 95

Qy 1 ANLNGTLMQYFEMTPNDGQWRRLQNDASVLAHGGITAVWIPAYKGTSGADVGAYD 60

Qy 96 LYDGEFQKGTATKTKGTGELDSATKSHSDINYYGVVNHKGGADATEQVTAVEV 155

Db 96 LYDGEFQKGTATKTKGTGELDSATKSHSDINYYGVVNHKGGADATEQVTAVEV 155

Qy 61 LYDGEFQKGTATKTKGTGELDSATKSHSDINYYGVVNHKGGADATEQVTAVEV 120

Qy 36 APFNGTMMQYFEMTLPDGLTMTVANEANNLSLGITLMLPRAYKGTSGADVGAYD 95

Qy 1 ANLNGTLMQYFEMTPNDGQWRRLQNDASVLAHGGITAVWIPAYKGTSGADVGAYD 60

Qy 96 LYDGEFQKGTATKTKGTGELDSATKSHSDINYYGVVNHKGGADATEQVTAVEV 155

Db 96 LYDGEFQKGTATKTKGTGELDSATKSHSDINYYGVVNHKGGADATEQVTAVEV 155

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AMV2_SALTY STANDARD; PRT; 494 AA.
AC P26613;
DT 01-AUG-1992 (Rel. 23, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cytoplasmic alpha-amylase (EC 3.2.1.1) (1,4-alpha-D-glucan
  glucanohydrolase).
GN AMYA OR STM1963.
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OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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RC STRAIN=SCW1103;
RX MEDLINE=93015717; PubMed=1400215;
  RA Rata M., Kawagishi I., Mueller V., Kihara M., Macnab R.M.;
  RT "Escherichia coli produces a cytoplasmic alpha-amylase, AmyA.";
  RL J. Bacteriol. 174:6644-6652 (1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=L72 / SCSCL412 / ATCC 700720;
RX MEDLINE=21534948; PubMed=11677609;
  RA McLelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
  RA Courtney L., Portolillo S., Ali J., Dante M., Du F., Hou S., Layman D.,
  RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
  RA Ryan E., Sun H., Flores L., Miller W., Stoneking T., Nian M.,
  RA Waterston R., Wilson R.K.;
  RT "Complete genome sequence of Salmomella enterica serovar Typhimurium
  RT L72.";
  RL Nature 413:852-856 (2001).
RN [3]
RP SEQUENCE OF 1-6 FROM N.A.
RC STRAIN=STM1103;
RX MEDLINE=92407478; PubMed=1527488;
  RA Kawagishi I., Mueller V., Williams A.W., Irikura V.M., Macnab R.M.;
  RT "Subdivision of flagellar region III of the Escherichia coli and
  RT Salmomella typhimurium chromosomes and identification of two
  RT additional flagellar genes.";
  RL J. Gen. Microbiol. 138:1051-1065 (1992).
RN [4]
RP SEQUENCE OF 476-494 FROM N.A.

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RX MEDLINE=9381452; PubMed=8371104;
  RA Rata M., Kihara M., Kawagishi I., Macnab R.M.;
  RT "Organization of the Escherichia coli and Salmomella typhimurium
  RT chromosomes between flagellar regions IIIa and IIId, including a
  RT large non-coding region.";
  RL J. Gen. Microbiol. 139:1401-1407 (1993).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
  CC linkages in oligosaccharides and polysaccharides.
CC -1- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
  CC between the Swiss Institute of Bioinformatics and the EMBL outstation
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  CC use by non-profit institutions as long as its content is in no way
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  CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
  CC or send an email to license@isb-sib.ch).
CC -----
DB EMBL, L01643; AAA27110.1; -
DB EMBL, AB008787; AAL20875.1; -
DB EMBL, M85241; AAA27079.1; -
DB EMBL, L13280; AAA71970.1; -
DB PIR, B45738; B45738.
DB HSSP, P06278; IVS3.
DB StyGene; SG10011; amyA.
DR InterPro; IPR006589; Alp_ami1_cat_sub.
DR InterPro; IPR006047; Alpha_ami1_cat.
DR Pfam; PF00128; Alpha-amylase; 1.
DR SMART; SM00642; AmyA; 1.
KW Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
  KW Complete proteome.
FT ACT_SITE 235 BY SIMILARITY.
FT ACT_SITE 265 BY SIMILARITY.
FT ACT_SITE 332 BY SIMILARITY.
FT METAL 104 CALCIUM (BY SIMILARITY).
FT METAL 239 CALCIUM (VIA CARBONYL OXYGEN) (BY
  FT SIMILARITY).
FT FT
FT CONFLICT 462 462 L -> S (IN REF. 1).
SQ SEQUENCE 494 AA; 56522 MW; SC1F862FED5E47C CRC64;

Query Match 39.7%; Score 1058; DB 1; Length 494;
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QY 4 NGTLMQYEFWTPNDQGHWRRLQNSAYLAHEGITA VWPAYKQTSQA-DVYGAYDLY 62
DB 3 NPTLQYFHWYPPGGLKMSFLARADGLNDIGINWVLPACGAGSGVSGDYDLDF 62
QY 63 DLGEFHQKGYRTKYGKELQSAIKSLHSRDINVDYVINKGADAFEDVAVAVDP 122
DB 63 DLGEFDQKGTATYGRKRLTALIDALKNNIAVLIDVAVNHMGADDEKRLIVQREVQ 122
QY 123 ADRNRVIGEHLIKANTHFFPPRGSTYSDFKWHYFDGTDMDSEKLNRIYK----FQ 178
DB 123 DDKRQIDNINIEEGGWIRYTFPARAGQYNSFINWYHFGSDIHENDEDEGIFIVADYT 182
QY 179 GKMDWEVSNENGVYLYMADIDYHPVAAEIKRWGTYANELOLDFRLDAVKHKE 238
DB 183 GDGNWDDQYVDEMGNFDYLMGENIDFRHNAVYEEIKYARAWMEGTQDGRLLAVKIIIPA 242
QY 239 SFLRDVNVHREKTKGEMFTVAEYQNDLGALNNYLNKNFNHVSFVDFVLIHQPHASTQ 298
DB 243 WFKYEMIHVQAVAPKPLFTVAETHSHVDKLCYTIIDQVDGKMTLFPAPLOMKHESRQ 302
QY 299 GGGYDMRLKNGTVVSGHPLKSTVTFVNDHTOPGQSLBSTVQWTFKPLVAFILTRBSGY 358
DB 303 GAEYDMRHI FTGLVLEADPFHNAVTLVANHDTPQLALAEVPEVFKPLAVALILRENGV 362
QY 359 POFYFGDMVGTGKDSQREIPALKHKEPIIKARKQYAYGAQHDYFDHDI VGMTEG 410

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Db 363 PSVFPDYGYAGSYDSENGEETCRVDMPI-NQLDLILARQFAHGIOTLFEDHNCIA 421
 QY 411 WTRBGSSVANSGLAITDGPAGAKMYGRONAGETHTDITGNSEPVINSEWGEF 470
 Db 422 FSHSGTBE--NPGCVVVLNSGDDGEKTLILDVNYANKTRWDFLGNDEYVTVNDQGEATF 479
 QY 471 HVGNGSVISIV 481
 Db 480 FCNAGSVSVWV 490

RESULT 6
 AMY2_ECOLI
 ID AMY2_ECOLI STANDARD; PRT; 495 AA.
 AC P26612; P78072; Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Cytoplasmic alpha-amylase (EC 3.2.1.1) (1,4-alpha-D-glucan
 glucanohydrolase).
 OS AMYA OR B1927.
 GN Escherichia coli.
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 CC Enterobacteriaceae; Escherichia.
 CC NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Jall;
 RA MEDLINE=93015717; PubMed=1400215;
 RA Raha M., Kawagishi I., Mueller V., Kihara M., Macnab R.M.,
 RT "Escherichia coli produces a cytoplasmic alpha-amylase, AmyA.",
 RL J. Bacteriol. 174:6644-6652 (1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RA MEDLINE=97426617; PubMed=9278503;
 RA Blactner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-VIDES J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden W.A., Rose D.C.,
 RA Mau B., Shao Y.,
 RT "The complete genome sequence of Escherichia coli K-12.",
 RL Science 277:1453-1474 (1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RA MEDLINE=97251158; PubMed=9097040;
 RA Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T.,
 RA Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M.,
 RA Makino K., Maki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
 RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T.,
 RA Saito N., Sampei G., Seki Y., Sivasubram S., Tagami H.,
 RA Takeda U., Takemoto K., Wada C., Yamamoto Y., Horikuchi I.,
 RA "A 460-kb DNA sequence of the Escherichia coli K-12 genome
 RT corresponding to the 40.1-50.0 min region on the linkage map.",
 RL DNA Res. 3:379-392 (1996).
 RN [4]
 RP SEQUENCE OF 1-5 FROM N.A.
 RC STRAIN=Jall;
 RA MEDLINE=92407478; PubMed=1527488;
 RA Kawagishi I., Mueller V., Williams A.W., Irikura V.M., Macnab R.M.,
 RT "Subdivision of flagellar region III of the Escherichia coli and
 RT Salmonella typhimurium chromosomes and identification of two
 RT additional flagellar genes.",
 RL J. Gen. Microbiol. 138:1051-1065 (1992).
 RN [5]
 RP SEQUENCE OF 475-495 FROM N.A.
 RC STRAIN=Jall;
 RA MEDLINE=93381452; PubMed=8371104;
 RA Raha M., Kihara M., Kawagishi I., Macnab R.M.,
 RT "Organization of the Escherichia coli and Salmonella typhimurium
 RT chromosomes between flagellar regions Itra and IIb, including a
 RT large non-coding region.",
 RL J. Gen. Microbiol. 139:1401-1407 (1993).

CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
 CC linkages in oligosaccharides and polysaccharides.
 CC -1- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
 CC -1- SUBUNIT: Monomer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
 CC -----
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 CC or send an email to license@ebi.ac.uk).
 CC -----
 DR EMBL, L01642; AAA3810.1; -
 DR EMBL, AE000285; AAC74994.1; -
 DR EMBL, D90833; BA15755.1; -
 DR EMBL, M85240; -; NOT ANNOTATED_CDS.
 DR EMBL, U13279; AA482575.1; -
 DR PIR, D64956; A45738.
 DR HSP, P06278; IVUS.
 DR Ecogene; Egl1387; amyA.
 DR InterPro; IPR005689; Alp_amy1_cat_sub.
 DR InterPro; IPR005047; Alpha_amy1_cat.
 DR Pfam; PF00128; alpha-amylase; 1.
 DR SMART; SM00642; Amy; 1.
 DR KEGG; K00642; alpha-amylase; 1.
 DR Complete proteome.
 KM Carbohydrate metabolism; Hydrolyase; Glycosidase; Calcium-binding;
 FT ACT_SITE 235 BY SIMILARITY.
 FT ACT_SITE 265 BY SIMILARITY.
 FT ACT_SITE 332 BY SIMILARITY.
 FT METAL 104 CALCIUM (BY SIMILARITY).
 FT METAL 239 CALCIUM (VIA CARBOXYL OXYGEN) (BY
 FT SIMILARITY).
 FT CONFLICT 19 KL -> SS (IN REF. 1).
 FT CONFLICT 109 A -> V (IN REF. 1).
 FT CONFLICT 149 Q -> E (IN REF. 1).
 FT CONFLICT 234 L -> I (IN REF. 1).
 SQ SEQUENCE 495 AA; 56639 MW; 26AF679DDA54D6 CRC64;

Query Match 39.3%; Score 1047; DB 1; Length 495;
 Best Local Similarity 42.2%; Pred. No. 2,1e-69;
 Matches 208; Conservative 86; Mismatches 179; Indels 20; Gaps 8;

QY 4 NGTLMYFEMWMPNNGOHRLQNDASVLAHGIYAWIPPAKGTSGA-DVYGAYDLY 62
 DB 3 NPTLQCFHWYTBEGKLMPELAERADGENDGIMWMLPRAKASGYSVGIDSLDF 62
 QY 63 DLGEFHQKTVKTKYGTKELOSATKSLHSRDINYGDVVNHKGDATEDVAVYDP 122
 DB 63 DLGEFHQKSIPTKQDKQALAAIDALRENDIAVLVVVNHKGADEKEAIRVQRYNA 122
 QY 123 ADNRKRISEHLI-KAWTHFHPGSGTSPFKHWHVPGDTPWDESKRIKRYK--- 176
 DB 123 DDRTOI--DEILIECGATRYTPPAAGYSQFINDPKFSSIDHLENDEGIRKYND 180
 QY 177 FQGAWDMEVSNENGNVYLTADIDYHPDVAAEIKRWGTYVANELQDGFRLDAVKHI 236
 DB 181 YTBEGMNDQVDELGNFYLMGENIDFRNHAVTBEIKYARWAWMGQTCDDGFRLLAVKXI 240
 QY 237 KEFLFDWVNHVREKRGKMFVAEYQWDDALENYKTNPNNSVFPVPIHYOPHAAS 296
 DB 241 PANFYKEMHEHVOEVAKPLFTVAEYWSHEVDLQTYIDQVGKTMFLPAPLOMKFHEAS 300
 QY 297 TQGGYDMKRLNGTVVSKPLSKVTFVNHDPQSGSLSTVQVTFKPLAVALFITRES 356
 DB 301 RMGRDDYDMQIFGTGLVEADPFHAATLVANHTDPLQALEAPVEPFKPLAVALILREN 360
 QY 357 GYFQVRYGDMYGYK-----GDSGR--EFPALKHKEFLPKARKQVAYGAQNDYFDHNDI 408
 DB 361 GVPSVFPDYGYAGHYEDVGGDGTYPIDWFIIE-QDLDELILARQFAHGIOTLFEDHNC 419

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QY 409 VGMREDDSSVANSGLALITPGGAKMYGRONAGETWHDITGNSEPVVINSBGWG 468
DB 420 IAFSRSGTDER--PGCVVMSNGDDGDEKTHIGENYGNKWTMDPLGNROERVVDENGEA 477
QY 469 EFHVGSGYSIYV 481
DB 478 TFCNGSGYSVWV 490

RESULT 7
AMB PAEPO STANDARD; PRT; 1196 AA.
ID AMB PAEPO
AC P21543;
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 15-MAY-2004 (Rel. 43, Last annotation update)
DE Beta/alpha-amyase precursor [includes: Beta-amyase (EC 3.2.1.2);
DE Alpha-amyase (EC 3.2.1.1)].
OS Paenibacillus polymyxa (Bacillus polymyxa).
OC Bacteria; Firmicutes; Bacillales; Paenibacillaceae; Paenibacillus.
OX NCBI_TaxID=1406;
RN [1]
RP SEQUENCE OF 1-936 FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=72;
RX MEDLINE=87165765; PubMed=2435707;
RA Kawazu T., Nakanishi Y., Uozumi N., Sasaki T., Yamagata H.,
RA Tsukagoshi N., Uda S.;
RT "Cloning and nucleotide sequence of the gene coding for enzymatically
RT active fragments of the Bacillus polymyxa beta-amyase."
RL J. Bacteriol. 169:1564-1570(1987).
RN [2]
RP SEQUENCE OF 689-1196 FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=72;
RX MEDLINE=8913046; PubMed=2464578;
RA Uozumi N., Sakurai K., Sasaki T., Takekawa S., Yamagata H.,
RA Tsukagoshi N., Uda S.;
RT "A single gene directs synthesis of a precursor protein with beta-
RT and alpha-amyase activities in Bacillus polymyxa."
RL J. Bacteriol. 171:375-382(1989).
RN [3]
RP SEQUENCE OF 1-776 FROM N.A.
RC STRAIN=ATCC 8523;
RX MEDLINE=87231094; PubMed=2438660;
RA Rhodes C., Strasser J., Friedberg P.;
RT "Sequence of an active fragment of B. polymyxa beta amyase."
RL Nucleic Acids Res. 15:3934-3934(1987).
RN [4]
RP DISULFIDE BOND, AND MUTAGENESIS OF CYSTEINE RESIDUES.
RX MEDLINE=91215008; PubMed=1827035;
RA Uozumi N., Matsuda T., Tsukagoshi N., Uda S.;
RT "Structural and functional roles of cysteine residues of Bacillus
RT polymyxa beta-amyase."
RL Biochemistry 30:4454-4459(1991).
CC -1- FUNCTION: THE PRECURSOR PROTEIN IS PROTEOLYTICALLY CLEAVED TO
CC PRODUCE MULTIFORM BETA-AMYLASES AND A 48 KDA ALPHA-AMYLASE AFTER
CC SECRETION.
CC -1- CATALYTIC ACTIVITY: Hydrolysis of 1,4-alpha-glucosidic linkages in
CC polysaccharides so as to remove successive maltose units from the
CC non-reducing ends of the chains.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: In the N-terminal section; belongs to family 14 of
CC glycosyl hydrolases.
CC -1- SIMILARITY: In the C-terminal section; belongs to family 13 of
CC glycosyl hydrolases.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
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CC -----
CC EMBL: M15817; AA85446.1; -
CC EMBL: Y00150; CA66344.1; -
CC FIR; A29130; A29130.
CC HSP; P36924; 1892.
CC InterPro: IPR006589; Alp_amy1_cat_sub.
CC InterPro: IPR006048; Alpha_amy1_C.
CC InterPro: IPR006047; Alpha_amy1_cat.
CC InterPro: IPR005085; CBM_25.
CC InterPro: IPR006046; Glyco_hydro_13.
CC InterPro: IPR00554; Glyco_hydro_14.
CC Pfam: PF00128; alpha-amyase; 1.
CC Pfam: PF03423; CBM_25; 2.
CC Pfam: PF01373; Glyco_hydro_14; 1.
CC PRINTS: PR00110; ALPHAMYLASE.
CC PRINTS: PR00750; BETAMYLASE.
CC SMART: SM00642; Amy; 1.
CC SMART: SM00632; Amy; C; 1.
CC PROSITE: PS00506; BETA_AMYLASE_1; 1.
CC PROSITE: PS00679; BETA_AMYLASE_2; 1.
CC KW Multifunctional enzyme; Hydrolase; Glycosidase; signal;
CC Polyasaccharide degradation; Repeat.
CC FT SIGNAL 1 35
CC FT CHAIN 36 1196
CC FT DOMAIN 36 454
CC FT REPEAT 455 558
CC FT REPEAT 565 668
CC FT DOMAIN 669 1196
CC FT DISULFID 118 126
CC FT ACT_SITE 198 198
CC FT ACT_SITE 394 394
CC FT MUTAGEN 118 118
CC FT MUTAGEN 126 126
CC FT MUTAGEN 358 358
CC FT CONFLICT 1 1
CC FT CONFLICT 67 67
CC FT CONFLICT 100 100
CC FT CONFLICT 154 154
CC FT CONFLICT 177 177
CC FT CONFLICT 227 228
CC FT CONFLICT 330 330
CC FT CONFLICT 425 425
CC FT CONFLICT 493 493
CC FT CONFLICT 532 532
CC FT CONFLICT 552 552
CC FT CONFLICT 665 665
CC FT CONFLICT 681 681
CC FT CONFLICT 686 686
CC FT CONFLICT 725 728
CC FT CONFLICT 736 736
CC FT CONFLICT 741 741
CC FT CONFLICT 758 758
CC FT CONFLICT 1196 AA; 130893 MM; A41EA68708257064 CRC64;
CC SQ SEQUENCE

Query Match 12.8%; Score 340; DB 1; Length 1196;
Best Local Similarity 23.1%; Pred. No. 4.2e-17;
Matches 119; Conservative 64; Mismatches 175; Indels 158; Gaps 22;

QY 12 EWMYNDGQHRRLNDGSAVLAEGITAVWIPPAVKGSQ-ADVGAGVLDYLDGEFHQK 70
DB 779 KWH-----GDFQGITLNDKDYIKMGFTLWTPYTMQSEYAHYGHYDY----- 826
QY 71 GTVRTKYTGKGLGSAIKLSHRDINVGADVIVNHKGGADATBEDVTAVEVDPRNRVIS 130
DB 827 -AVDGLGTMDKLGELVKAKDKXNIAVWVDVYVNHNTGTFQ----- 865
QY 131 GEHLIKAWHHFHPGRGSYSDF-KWHYHEDGTQWDSRLNRIYKFGKAMWEVSNE 189
DB 866 -----FGNGFAKAFEDADWYHNGDITDGDYNN-----QWKI--E 901
QY 190 NGNYDLYMTADIDYDHPVAAEIKKGTWYANEQLDGFRLDAYVGHIFSLRDVNHVR 249
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DB 902 NG--DVAGLDDLNENPATNELKMLNTGTGIDGLDVKVPGFKDP----- 954
QY 250 EKTGKEMFTVAEYQNDLGALENYLNKTNHNSVFVPLHYOPFAASTOGGYDMRKL-- 307
DB 955 -DQANFTWGEIFHGGPAYVDY---TRYLAALDFPMYTL--KDVFGHDSMRKID 1008
QY 308 -----LNGTVASGHPKLSVTFVNDHTOGGSLSEVQYWFEPFLAFLITRE 355
DB 1009 RYSDRDYRPAQNTNGVFINHDK--RFLNDASGRKQANDKWPOL--KALGFTLT-S 1062
QY 356 SGYPQVEYGMVYGTGDSQREIPALKXLEPILKARKOYAGAHDPDHDIVGWTREG 415
DB 1063 RGIPIIYQGTGGGSGDD--PA-----NENMNFANHDLVQYIAKLVYRN 1109
QY 416 DSSVANGSLALITDGGGAKRMVYGRNGNGETMHD-----ITGNREPVVINSRG- 467
DB 1110 HPALON-----GSQR-----EKWVDSFYSPORSKNGDEALVFINNSVN 1148
QY 468 -----GEF-----HVNGGSVSI 479
DB 1149 SQTRTIGNFDNLNGTRLTNQLNSDSVQINNGSITV 1184

RESULT 8
ID AMYA_VIGMU STANDARD; PRT; 421 AA.
AC P17859;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Alpha-amy-lase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
  glucanohydrolase).
GN AMY1.1.
OS Vigna mungo (Rice bean) (Black gram).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseolaeae; Vigna.
OX NCBI_TaxID=3915;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cotyledon;
RX MEDLINE=90332425; PubMed=2377468;
RA Yamauchi D., Minamikawa T.;
RT "Nucleotide sequence of cDNA for alpha-amy-lase from cotyledons of
  germinating Vigna mungo seeds."
RL Nucleic Acids Res. 18:4250-4250(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94120017; PubMed=8290640;
RA Takeuchi H., Yamauchi D., Wada S., Minamikawa T.;
RT "Nucleotide sequence of the alpha-amy-lase gene from Vigna mungo."
RL Plant Physiol. 103:1459-1459(1993).
CC -1 CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
  linkages in oligosaccharides and polysaccharides.
CC -1 COFACTOR: Binds 3 calcium ions per subunit (by similarity).
CC -1 SUBUNIT: Monomer (by similarity).
CC -1 SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
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  or send an email to license@isb-sib.ch).
CC EMBL; X53049; CAA37217.1; -
DR EMBL; X73301; CAA51734.1; -
DR PIR; P04063; IAVA.
DR HSP; P04063; IAVA.
DR InterPro; IPR006589; Alp_amy1_cat_sub.
DR InterPro; IPR006047; Alpha_amy1_cat.

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DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; alpha-amy-lase.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Amyy; 1.
KW Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
KW Signal.
KW SIGNAL.
FT CHAIN 1 23 PROBABLE.
FT ACT_SITE 24 421 ALPHA-AMYLASE.
FT ACT_SITE 201 202 BY SIMILARITY.
FT ACT_SITE 309 309 BY SIMILARITY.
FT METAL 113 113 CALCIUM 1 (BY SIMILARITY).
FT METAL 130 130 CALCIUM 2 (BY SIMILARITY).
FT METAL 133 133 CALCIUM 2 (BY SIMILARITY).
FT METAL 135 135 CALCIUM 2 (BY SIMILARITY).
FT METAL 139 139 CALCIUM 2 (BY SIMILARITY).
FT METAL 145 145 CALCIUM 2 (BY SIMILARITY).
FT METAL 160 160 CALCIUM 3 (BY SIMILARITY).
FT METAL 168 168 CALCIUM 3 (VIA CARBONYL OXYGEN) (BY
  SIMILARITY).
SQ SEQUENCE 421 AA; 46888 MW; 15CA0DABA3DBA656 CRC64;
  Query Match 11.7%; Score 311.5; DB 1; Length 421;
  Best Local Similarity 27.2%; Pred. No. 1,4e-15;
  Matches 126; Conservative 48; Mismatches 159; Indels 131; Gaps 22;
QY 7 LMOYFEMWPNDDQWRRRLQNDASVLAERGITAWIPPAKYGTSGADYVGAAYLDYDGE 66
DB 26 LFGGFWSESKKGGWNSLKNSIPDLANAGITHWLPPSGVSPE--GYLPGRLYDD- 82
QY 67 FHQKGVTRTKYGGKGLQSAIKLSHRDINVDVYVNHKGADATETVETVENDPADRN 126
DB 83 -----ASKTSGKNEKSLIAFHEKGIKCLADVINNR-----TAKRD----- 121
QY 127 RVISGELIKAWTHFHPGRGSGTYSDFKWHYHFDGT-----DMDSRKLRIRYKFOGKA 181
DB 122 -----DWEVSNGNDV-----VLMVADIDYDHPDVAALIKRGWYANELDQGRDLAY 233
QY 182 W-----DWEVSNGNDV-----VLMVADIDYDHPDVAALIKRGWYANELDQGRDLAY 233
DB 144 FICRDDTASDGGANDSGEGYDAAPDIDLHPQVQRELSRWMLKTEIGFDGWRPFPV 203
QY 234 KHKFSPFLDWNVNHVREKTGKEMFTVAEY-----QNDLGALENYLNKTN 278
DB 204 KGYAPSIKTYM-----EGT--KPDFAVGEKWDISYQDQKRYVNDGSHRGALVWVESAG 258
QY 279 FHNISVDVPLHYOPFAASTOGGYDMRKL--NGT---VSKHPLKSVTFVNDHTOPGQ 333
DB 259 GAITAFDFTTKGILQHA-VQS---ELWRILDPNGRPPGKVENAVTFIDNHT----- 310
QY 334 SLESTVQWTFKP-----LVAFLITRESGYPCVFGDMYGTGDSQREIPALKXLEPIL 388
DB 311 --GSTRLMPFPEDKMGQVAYILT--HPTSPISFYDHFDDW-----GLKEQIALKS 358
QY 389 KARKOYAGAGHDYFEDHDIVGWTREGDSVANSGLAALLIDGP 432
DB 359 SIR-----LRNGINKSTVKTIMASEGLIVAKINKIMVTKGP 396

RESULT 9
ID AMYA_ORYA STANDARD; PRT; 440 AA.
AC P27932;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Alpha-amy-lase isozyme 3A precursor (EC 3.2.1.1) (1,4-alpha-D-
  glucan glucanohydrolase).
GN AMY1.2 OR AMY3A.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzae; Oryza.

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OY 181 AMWMEVSENGN-----YDLMVADIDYDHEDVAAIKRWGTWYANELQDGFELDAVKHI 236
Db 153 CDDTQYSDGTGHRDTCGADFAAADIIDLHNPVQRELSDWLRMLRRDVCGEDGWLDPKAGY 212
OY 237 KFEFLBPMVHVHVEKNGKEMFTAAEYQNDLG-----ALENTAKTNFN 280
Db 213 SAAARVYVONARPS-----FVAELTN-NSLSDGCGKPRANODGGROELVYMWKVGGR 266
OY 261 HSVEDVELHYOFHAASDTGGGYDMRKLNGT---VWSKPELKVTFVNDHDTPGOSLES 337
Db 267 ATAFDFTTKGILQSA-VQGLMELMRD-KDGKADGMIGWPEKATVEDVNDT-----GS 318
OY 338 TWQWMEFP-----LAVAFILTRSGYQGVYGMGYGKGSQSEIPALFKHIEPILKARK 392
Db 319 TORMEPPSDKVLIGVAYILT-HPGVPCITYDQVPMN-----LKEINALALATRK 368
OY 393 QYAYGA 398
Db 369 RINGINA 374

RESULT 10
AM3C_ORISA STANDARD; PRT; 437 AA.
ID AM3C_ORISA AC
AC P27939;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Alpha-amylase isozyme 3C precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
  glucanohydrolase).
DE AMY1.7 OR AMY3B.
OS Oryza sativa (Rice).
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eriocaridaceae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Japonica M202; TISSUE=Etiolated leaf;
RC MEDLINE=91329692; PubMed=1714318;
RA Suttillif T.D., Huang N., Lites J.C., Rodriguez R.U.;
RT "Characterization of an alpha-amylase multigene cluster in rice.";
RL Plant Mol. Biol. 16:579-591(1991).
CC -1- FUNCTION: Important for breakdown of endosperm starch during
  germination.
CC -1- CATABOLIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
  linkages in oligosaccharides and polysaccharides.
CC -1- COFACTOR: Binds 3 calcium ions per subunit (By similarity).
CC -1- SUBUNIT: Monomer.
CC -1- TISSUE SPECIFICITY: Germinating seeds.
CC -1- DEVELOPMENTAL STAGE: Expressed at a high level during germination
  in the aleurone cells under the control of the plant hormone
  gibberellic acid and in the developing grains at a low level.
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
CC -----
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  or send an email to license@isb-sib.ch).
CC -----
DR EMBL, X56338, CAA39778.1; .
DR PIR, S14956, S14956.
DR HSSP, P04063, IAVA.
DR Gramene, P27939; .
DR InterPro, IPR006589; Alp_amy1_cat_sub.
DR InterPro, IPR006047; Alpha_amy1_cat.
DR InterPro, IPR006046; Glyco_hydro_13.
DR Pfam, PF00128; alpha-amylase; 1.
DR PRINTS, PRO0110; ALPHAAMYLASE.

```

DR SMART; SM00642; Amy; 1.
 KM Carbohydrate metabolism; Hydrolyase; Glycosidase; Calcium-binding;
 FT SIGNAL; Multigene family.
 FT CHAIN 1 26
 FT ACT_SITE 205 437
 FT ACT_SITE 313 313
 FT METAL 117 117
 FT METAL 117 117
 FT METAL 134 134
 FT METAL 137 137
 FT METAL 139 139
 FT METAL 143 143
 FT METAL 153 153
 FT METAL 164 164
 FT METAL 167 167
 FT METAL 168 168
 FT METAL 169 169
 FT METAL 172 172
 FT METAL 174 174
 FT METAL 174 174
 SQ SEQUENCE 437 AA; 48637 MW; BD304250840C7A8B CRC64;

Query Match 11.3%; Score 300; DB 1; Length 437;
 Best Local Similarity 25.8%; Pred. No. 1e-14;
 Matches 109; Conservative 48; Mismatches 146; Indels 120; Gaps 16;

7 LMOYFETWMPNDQGHRR-LQNDASVLAHGTAVMTTPAYKTSQADVGYGAYDLYDLG 65
 29 LFGQNNHSMNKKQGWVNFHSHVDYIAATGVTHWLP--PSHVAAPQGMPCRLDLD 86
 66 EFHOKGVTRTKYKGSLSAISKLSHSDINVGDVYINHKGADATEDVTAWEVDADR 125
 87 -----ASKYGTGAELRLIAFHSHSKIKCVADIVNH----- 118
 126 NRVISGEHLKAMTHFHPGRSTYSPDKMWHFDG-----TDMDESKLNRYKFG 179
 119 -----RCALYKDSRGICYCFEGTTPSRDMDKPMICSD----- 152
 180 KAMDEVENENGN---YDYLMVADIDYDHPVAAEIKKGTWYANELQDGFPLDAVKA 235
 153 ---DYOVSNGRGRHDTGADFGAARDIDHINTRVOTELSDWMLKSVGVGPMRLDPAKG 209
 236 IKFSPFLRWVNHVEKTEKMEFTVAEYWN-----DICALENYLNKTNFN 280
 210 YSAITAKTYVNT-----DPSFYVAEISMNRKYDNGEPRSNQDGDQELVMAQAVGPR 264
 281 HSVEDVPLHYQFHAASVGGGYDMRKLTNGT-----VSKKPLKSVTPVDNHDTPQOSL 335
 265 ASAFDFTTKGELQAA-VQG---ELMRKDKNGKAPGMGLPEKAVFIFIDNHD----- 314
 336 ESTVGTWPKP-----LAVAFILTRSGYPOVEYGDWGTCKDSQREIPALCHKKEPLKA 390
 315 GSTQNSWPPSPDKMQRVAVILT-HPGVFCIFIDHVFDMN-----LKQRISTAAV 364
 391 RKO 393
 365 RSR 367

RESULT 11
 CCGT_BACS8 STANDARD; PRT; 713 AA.
 ID CDGT_BACS8 STANDARD; PRT; 713 AA.
 AC P17692;
 DT 01-AUG-1990 (Rel. 15; Created)
 DT 01-AUG-1990 (Rel. 15; Last sequence update)
 DT 10-OCT-2003 (Rel. 42; Last annotation update)
 DE Cyclomaltohextrin glucanotransferase precursor (EC 2.4.1.19)
 DE (Cyclodextrin-glycosyltransferase) (CGTase) (Raw-starch-digesting
 DE amylase).
 OS Bacillus sp. (strain B1018).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

OX NCBI_TaxID=1417;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 28-47.
 RX MEDLINE=90147765; Pubmed=1689153;
 RA Itokor P., Tsukagoshi N., Uda S.;
 RT "Nucleotide sequence of the raw-starch-digesting amylase gene from
 RT Bacillus sp. B1018 and its strong homology to the cyclodextrin
 RT glucanotransferase genes."
 RL Biochem. Biophys. Res. Commun. 166:630-636(1990).
 CC -1- FUNCTION: This endo-type adsorbable amylase is capable to
 CC digest raw starch.
 CC -1- CATALYTIC ACTIVITY: Degrades starch to cyclodextrins by formation
 CC of a 1,4-alpha-D-glucosidic bond.
 CC -1- CORFACTOR: Binds 2 calcium ions per subunit (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
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DR EMBL; M3302; AAA22239.1; -
 DR EMBL; D90112; BAA14140.1; -
 DR FIR; S09196; S09196.
 DR HSSP; P43379; 1CDG.
 DR InterPro; IPR006589; Alp_amy1_cat_sub.
 DR InterPro; IPR006048; Alpha_amy1_C.
 DR InterPro; IPR006047; Alpha_amy1_cat.
 DR InterPro; IPR002044; CSD_4.
 DR InterPro; IPR006046; Glyco_hydro_13.
 DR InterPro; IPR007110; IG_1like.
 DR InterPro; IPR002909; IPT_TIG.
 DR Pfam; PFC0128; alpha-amy1ase; 1.
 DR Pfam; PFC02806; alpha-amy1ase_C; 1.
 DR Pfam; PFC0686; CBM_20; 1.
 DR PRINTS; PR01833; TIG; 1.
 DR PRODOM; PD001568; CSD_4; 1.
 DR SMART; SM00642; Amy; 1.
 DR SMART; SM00632; Amy; C; 1.
 KM Transferase; Glycosyltransferase; Calcium-binding; Signal.
 FT SIGNAL 1 27
 FT CHAIN 28 713
 FT ACT_SITE 256 256
 FT ACT_SITE 284 284
 FT ACT_SITE 355 355
 FT METAL 54 54
 FT METAL 56 56
 FT METAL 59 59
 FT METAL 60 60
 FT METAL 80 80
 FT METAL 166 166
 FT METAL 217 217
 FT METAL 226 226
 FT METAL 260 260
 SQ SEQUENCE 713 AA; 77420 MW; 85PB61DA687B88 CRC64;

Query Match 11.2%; Score 298; DB 1; Length 713;
 Best Local Similarity 23.8%; Pred. No. 2.6e-14;
 Matches 113; Conservative 86; Mismatches 175; Indels 100; Gaps 20;

19 GCHWRRLQ--DSAYLAHGTAVMTTP-----AYKTSQADVGYGAYDLYDGEFFHOKGT 72
 78 GSDWQGLINKINGVLTGKGVTRVIMSGVEVNIYSTINSGVNNRHYHGMARDPK--- 134
 73 VTRKGTGKELQSAIKLSHSDINVGDVYINHKGADATEDVTAWEVDADRNRVYSGE 132

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Cc 135 TNPAVGTIADPQTLIAAAKXIKVILDPAPNH-----TSRASSQSPFALNGSLYDNG 188
Cc 133 HLIIKANTHPPHFGSGSTSDPFKMHMYHPGDTMDSEKLNRLRYKFGKAMDEVSNNEN 192
Cc 189 TLGGGT-----NDTONLFPHNGTDFP-----TTENGI 217
Cc 193 YDYLYAWADIDYDHPDVAE-----IKRWGTWANELQDGRFLDAVKIIFSLRDWN 246
Cc 218 YKRL-YDLADLNANNSTSDVYLKDAIKM-----LDLGDIGIRMDAYKMPGKQKSTFA 271
Cc 247 HVREKTKEMFTVAEYV-ONDIGALENYLNTKNHVSFVDFVLAHYQHPAATQ----- 298
Cc 272 AVANNY-KPVFTGEWFLGNEVGP-ENHKEFANESGMSILD-----FRFAQKRVQVFRDNT 324
Cc 299 GGGYDNKRLNGVIVGKHP-KSVTEVDNHDQPGQSLSTQVTKPKPLAAYFILTREG 357
Cc 325 DNNYGLKAMDEGSAADYAOVDVDTIDNDMERFPHSNRNKLEQALAFILLAR--- 381
Cc 358 YPQVFTG-DNY---GTGKDSQREIPALK-----HKIEPLTKARKQVAYGAQHDYED 404
Cc 382 VPAIYVGTQYMGSGCDPDRARIPSFSTSTAYQVIOKLAPLRKSNPAIAYGSTQERWI 441
Cc 405 HHDIWGTREGDSV-----ANSGLAALITDGPQAKRMVGRQNAGET 448
Cc 442 NNDVLIYERKFGSNVAVVANNRNLPASISGLVSLPGQSYNDVGLNGNT 495

RESULT 12
CDGT_BACSO STANDARD; PRT; 713 AA.
AC POS678;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cyclomaltoextrin glucanotransferase precursor (EC 2.4.1.19)
DE (Cyclodextrin-glycosyltransferase) (Cgrase).
GN CGT
OS Bacillus sp. (strain 1011).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1410;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=67308036; Pubmed=2957361;
RA Kiyama K., Katoka S., Ishii Y., Takano T., Yamane K.;
RT "Nucleotide sequence of the beta-cyclodextrin glucanotransferase gene
RT of alkalophilic Bacillus sp. strain 1011 and similarity of its amino
RT acid sequence to those of alpha-amylases."
RL J. Bacteriol. 169:4399-4402(1987).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
RA Harata K., Haga K., Nakamura A., Aoyagi M., Yamane K.;
RT "X-ray structure of cyclodextrin glucanotransferase from alkalophilic
RT Bacillus Sp. 1011. Comparison of two independent molecules at 1.8-A
RT resolution."
RL Acta Crystallogr. D 52:1136-1145(1996).
CC -1- CATALYTIC ACTIVITY: Degrades starch to cyclodextrins by formation
CC of a 1,4-alpha-D-glucosidic bond.
CC -1- COFACTOR: Binds 2 calcium ions per subunit.
CC -1- SUBUNIT: Monomer.
CC -1- MISCELLANEOUS: CGTASE MAY CONSIST OF TWO PROTEIN DOMAINS: THE ONE
CC IN THE AMINO-TERMINAL SIDE CLEAVES THE ALPHA-1,4-GLUCOSIDIC BOND
CC IN STARCH, AND THE OTHER IN THE C-TERMINAL SIDE CATALYZES OTHER
CC ACTIVITIES, INCLUDING THE RECONSTITUTION OF AN
CC ALPHA-1,4-GLUCOSIDIC LINKAGE FOR CYCLIZING THE
CC MALTOOLIGOSACCHARIDE PRODUCED.
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
CC -----
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Cc or send an email to license@isb-sib.ch).
Cc -----
Cc EMBL; M17366; AAA22308.1; -.
Cc PIR; A26678; ALBSG1.
Cc PDB; 1D7E; 17-MAR-00.
Cc PDB; 1DED; 07-APR-00.
Cc PDB; 1I75; 11-APR-01.
Cc PDB; 1PAM; 11-JAN-97.
Cc InterPro; IPR006589; Alp_amy1_cat_sub.
Cc InterPro; IPR006048; Alpha_amy1_C.
Cc InterPro; IPR006047; Alpha_amy1_cat.
Cc InterPro; IPR02044; CBD_4.
Cc InterPro; IPR006046; Glyco_hydro_13.
Cc InterPro; IPR007110; IG_1like.
Cc InterPro; IPR002909; IPT_TIG.
Cc Pfam; PF00128; alpha-amylase; 1.
Cc Pfam; PF02806; alpha-amylase_C; 1.
Cc Pfam; PF00686; CBM_20; 1.
Cc Pfam; PF01833; TIG; 1.
Cc PRINTS; PR00110; ALPHAMYLASE.
Cc PRODOM; PD001568; CBD_4; 1.
Cc SMART; SMO0642; Amyy; 1.
Cc SMART; SMO0632; Amyy; C; 1.
Cc Transferase; Glycosyltransferase; Calcium-binding; Signal;
Cc 3D-structure.
Cc SIGNAL 1
Cc CHAIN 27
Cc FT 28 713 CYCLOMALTODEXTRIN GLUCANOTRANSFERASE.
Cc FT 28 165 A1.
Cc FT 229 166 B.
Cc FT 230 433 A2.
Cc FT 434 522 C.
Cc FT 523 609 D.
Cc FT 610 713 E.
Cc FT 256 284
Cc FT ACT_SITE 284 256
Cc FT ACT_SITE 355 355
Cc FT METAL 54 54
Cc FT METAL 55 54
Cc FT METAL 56 56
Cc FT METAL 59 59
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Cc FT METAL 80 80
Cc FT METAL 166 166
Cc FT METAL 217 217
Cc FT METAL 226 226
Cc FT METAL 260 260
Cc FT METAL 70 77
Cc FT DISULFID 70 77
Cc FT TURN 30 31
Cc FT TURN 33 34
Cc FT TURN 40 41
Cc FT STRAND 44 46
Cc FT HELIX 49 51
Cc FT TURN 52 52
Cc FT TURN 52 52
Cc FT HELIX 57 59
Cc FT HELIX 63 65
Cc FT STRAND 66 66
Cc FT TURN 68 69
Cc FT TURN 73 74
Cc FT STRAND 76 76
Cc FT HELIX 81 89
Cc FT TURN 90 93
Cc FT TURN 94 96
Cc FT TURN 97 97
Cc STRAND 100 103
Cc STRAND 107 109
Cc STRAND 114 116
Cc FT TURN 117 118
Cc FT STRAND 119 121
Cc FT TURN 124 125
Cc STRAND 129 135
Cc FT TURN 137 139
Cc FT HELIX 142 154
Cc FT TURN 155 156

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FT STRAND 158 163
FT TURN 165 166
FT STRAND 167 170
FT TURN 176 177
FT TURN 179 182
FT STRAND 184 186
FT TURN 187 188
FT STRAND 189 192
FT TURN 195 196
FT TURN 198 199
FT STRAND 202 202
FT STRAND 207 207
FT HELIX 213 218
FT STRAND 220 220
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FT STRAND 224 227
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FT HELIX 232 247
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FT STRAND 252 255
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FT HELIX 258 260
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FT STRAND 280 283
FT TURN 289 290
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FT TURN 387 388
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FT TURN 396 399
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FT HELIX 413 421
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FT HELIX 424 427
FT HELIX 429 433
FT STRAND 435 441
FT STRAND 445 452
FT TURN 453 454
FT STRAND 455 462
FT STRAND 469 471
FT STRAND 475 475
FT STRAND 481 483
FT TURN 486 491
FT STRAND 496 498
FT HELIX 500 502
FT STRAND 503 504
FT STRAND 507 509
FT TURN 511 512
FT STRAND 514 519
FT STRAND 527 536
FT TURN 538 539
FT STRAND 541 547
FT STRAND 555 558
FT TURN 559 560
FT STRAND 561 563
FT HELIX 565 567
FT STRAND 568 571
FT STRAND 575 579
FT STRAND 586 593
FT TURN 595 596
FT STRAND 599 599

Query Match 11.0%; Score 294; DB 1; Length 713;
Best Local Similarity 23.0%; Pred. No. 5.2e-14;
Matches 127; Conservative 89; Mismatches 173; Indels 164; Gaps 29;

FT STRAND 603 608
FT STRAND 613 621
FT TURN 627 628
FT STRAND 630 635
FT HELIX 638 640
FT TURN 641 643
FT HELIX 645 647
FT STRAND 649 649
FT STRAND 653 653
FT TURN 660 661
FT STRAND 663 670

19 GCHWRRLQN--DSAYLAHEGTTAVWIPP-----AYKTSQADVGAGADLYDLDBEFHOKGT 72
78 GGDWQGIINKINDGYLTGMGITAIWISQPVENIYSVINYSGVNNTAVHGWADFFK--- 134
73 VRTKYGTEGELQSAIKLSHSDINVGDVVINHEKGADATEDVAVZVDP--ADRNKRVIS 130
135 TNPAVGTWQDFKALIDTTHANIKVILDFAPNHSPPSSD-----DSPFANGRLYD 186
131 GEHLIKAWTHFHPGRGSTYSDFKWHYHFDGTDWDSRKLNRLYKQCGKAMDVEYANEN 190
187 NGNLLGGYT-----NDTONLFPHYGTDFS-----TIEN 215
191 GNYDYLM-YADIDYDHPVAA-----ETKRWGTWYANELODGFRLDAVKIKFSLRDWV 245
216 GYKXNLYDLADLNHNNSVDVYLKDAIKM-----LDGVDGIRVDAVKMPPGQKSM 270
246 NHVREKTEKEMFTVAEYWQNDLGAL-----NYLNTKTFNHSVFDVPLHYQFHAATQ- 298
271 ATINNY--KPVFTGEWF--LGVNEISPEYHQFANESGMS-----LDFRFAOKAROV 319
299 -----GGGYDMRKLINGVYVSKHPK-SYTFVNDH-----TQPG--QSLESTVQWTFKP 345
320 FRDNTDNNYGLKAMLEGSVDYAQVNDQVTFIDHDMERFHTSGDRKLEQ----- 371
346 LAVAFILTRSGYPOVFYQ-DMY--GTGDSOREIPALK-----HKIEILARK 392
372 -ALATFLT-SRCVPAIYVGSQYMSGNDPDRPARLPFSFTTAYGVIOKLAPLRKSNP 429
393 QYAGAQHDYEDHDIVGWTREBDSVA-----NSGLAA 426
430 ALAYGSTERWINDVILYERKFGNNVAVVAINRNMNTPASITGLVLSLRASYNDVLDG 489
427 L-----ITDGGGAKRMVVRQNAGETWH-----DITGN-----RSEP--VVINSEGM 467
490 ILANGTILTYAGAGASNPFLABGTAIVAQYITTDATPTIIGVGPMMARPGVITIIDGGGF 549
468 GEHVNQGSVSIX 480
550 G-----SGKGVY 557

RESULT 13
AMY3_WHEAT STANDARD; PRT; 413 AA.
ID AMY3_WHEAT
AC P08117;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Alpha-amylase AMY3 precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
DE glucanohydrolase).
GN AMY1.1 OR ALPHA-AMY3.
OS Triticum aestivum (wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
OC Triticaceae; Triticum.
OX NCBI_TaxID=4565;
RN [1]

```

RP SEQUENCE FROM N.A.
 RC STRAIN=CV, Chinese Spring;
 RA Baulcombe D.C., Huttly A.K., Martienssen R.A., Barker R.F.,
 RA Jarvis M.G.;
 RL "A novel wheat alpha-amylase gene (alpha-Amy3).";
 RL Mol. Genet. 209:33-40(1987).
 CC -1- FUNCTION: Important for breakdown of endosperm starch during
 CC germination.
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
 CC linkages in oligosaccharides and polysaccharides.
 CC -1- COFACTOR: Binds 3 calcium ions per subunit (By similarity).
 CC -1- SUBUNIT: Monomer (By similarity).
 CC -1- DEVELOPMENTAL STAGE: Expressed at a high level during germination
 CC in the aleurone cells under the control of the plant hormone
 CC gibberellic acid and in the developing grains at a low level.
 CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
 CC -----
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 CC -----
 CC EMBL: X05809; CAA28252.1; -;
 CC EMBL: M16991; AAA34259.1; -;
 CC PIR: S06357; ALMT3.
 CC HSP: P04063; IAVA.
 CC InterPro: IPR006589; Alp amyl cat sub.
 CC InterPro: IPR006047; Alpha amyl cat.
 CC InterPro: IPR006046; Glyco_hydro_13.
 CC Pfam: PF00128; alpha-amylase; 1.
 CC PRINTS: PR00110; ALPHAMYLASE.
 CC SMART: SM00642; Amy; 1.
 CC Germination; Carbohydrate metabolism; Hydrolase; Glycosidase; Seed;
 CC Calcium-binding; Signal; Multimeric family.
 CC FT CHAIN 1 24 POTENTIAL.
 FT ACT_SITE 25 413 ALPHA-AMYLASE AMT3.
 FT METAL 203 203 BY SIMILARITY.
 FT METAL 115 115 CALCIUM 1 (BY SIMILARITY).
 FT METAL 132 132 CALCIUM 2 (BY SIMILARITY).
 FT METAL 135 135 CALCIUM 2 (BY SIMILARITY).
 FT METAL 137 137 CALCIUM 2 (BY SIMILARITY).
 FT METAL 141 141 CALCIUM 2 (BY SIMILARITY).
 FT METAL 151 151 CALCIUM 3 (BY SIMILARITY).
 FT METAL 162 162 CALCIUM 3 (BY SIMILARITY).
 FT METAL 167 167 CALCIUM 1 (VIA CARBONYL OXYGEN) (BY
 FT SIMILARITY).
 FT METAL 170 170 CALCIUM 3 (VIA CARBONYL OXYGEN) (BY
 FT SIMILARITY).
 FT METAL 172 172 CALCIUM 1 AND 3 (BY SIMILARITY).
 SQ SEQUENCE 413 AA; 45370 MW; C262BCALC54FCC4 CRC64;
 Query Match 11.0%; Score 292.5; DB 1; Length 413;
 Best Local Similarity 25.7%; Pred. No. 3.4e-15;
 Matches 121; Conservative 56; Mismatches 155; Indels 139; Gaps 22;
 QY 7 LMYFFEN-YMENDCGWRRLONDSAYLAERGITAVWTPPAVKGSQADVGYGVADYDLDG 65
 DB 28 LFGQFMESWKTQSGWKFKPMQKKEBELASGATHWVLPSPQSQSP-GLYGGQLYNL- 84
 QY 66 EFHQKGVIRYKYGKELQSAIKSLHSRDINVGDIYVNHKGADATEDVTAVEVDPADR 125
 DB 85 -----NSKYGSGADLKSLIQAFKRNKISCVADIYINHR-----CADK 121
 QY 126 NRVISGEHLIKAWTHFHPGRGSGTYSPFKMHWYFDDG-----DMDESKLNRIYKQK 180
 DB 122 K-----DGRG-YVCFE-----GGSNDRLDWGDDELCS----- 150
 QY 181 AMDVENSNGNVD-----YLMYADIDYDHPVAAEIRKGTWVANIELQDGFRLDAYKHI 236
 DB 151 --DTKYSNGRGHRDPTGGGFDAPDIDHINFRVQRELSTAMINWLTDLGFGWRDLDFAKGY 208

QY 237 KFSFLRDMVNHVREKTKEMFVAEYWONDGLAENLYNKTNNHNSVFPDPLHYOFHAAS 296
 DB 209 SAAMAKRYVN-----SKRPFVVGELYDRROLAWVAGVGPAPAFPFRTGVLQEA- 262
 QY 297 TGGGGYMRKLLNGT-----VSKRPLKSVTFVDNHDTPQGSLESTVQTFKPE-----L 346
 DB 263 VQG---DLGMRGSDGKAPGMIGMPEKVTVPIDNHD-----GSTRLMPPSPDKWQ 313
 QY 347 AVATILRESGYPOVFYGDYVTKGDSOREIPAL-----KHRIE-----ILKARQYAY 396
 DB 314 GYATILV-HGCIPIFDHFDMK--LKQITLALATVRSNGIHPCSTDLILKA----- 364
 QY 397 GAQHDYVDHHDIVGWTRSGSVANSGLALITDGGCAKMTVGRQAGE 447
 DB 365 -----EGDLVYAKIGKGVITRIG-----SRYNIGD 389
 RESULT 14
 CDGT_BACCI STANDARD; PRT; 718 AA.
 AC P30920;
 DT 01-JUN-1993 (Rel. 26, Created)
 DT 01-JUN-1993 (Rel. 26, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Cyclodextrin glucanotransferase precursor (EC 2.4.1.19)
 DE (Cyclodextrin-glycosyltransferase) (CGTase).
 OS Bacillus firmus.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1397;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=8;
 RX MEDLINE=91103970; PubMed=1368573;
 RA Nitschke U., Heeger K., Bender H., Schulz G.E.;
 RT "Molecular cloning, nucleotide sequence and expression in *Escherichia*
 RT coli of the beta-cyclodextrin glycosyltransferase gene from *Bacillus*
 RT circulans strain no. 8";
 RL Appl. Microbiol. Biotechnol. 33:542-546(1990).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
 RC STRAIN=8;
 RX MEDLINE=91171298; PubMed=1826034;
 RA Klein C., Schulz G.E.;
 RT "Structure of cyclodextrin glycosyltransferase refined at 2.0-A
 RT resolution.";
 RL J. Mol. Biol. 217:737-750(1991).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (3.4 ANGSTROMS).
 RC STRAIN=8;
 RX MEDLINE=90064533; PubMed=2531228;
 RA Hofmann B.E., Bender H., Schulz G.E.;
 RT "Three-dimensional structure of cyclodextrin glycosyltransferase from
 RT *Bacillus circulans* at 3.4-A resolution.";
 RL J. Mol. Biol. 209:793-800(1989).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
 RC STRAIN=8;
 RX MEDLINE=98226626; PubMed=9558324;
 RA Schmidt A.K., Cottaz S., Driguez H., Schulz G.E.;
 RT "Structure of cyclodextrin glycosyltransferase complexed with a
 RT derivative of its main product beta-cyclodextrin.";
 RL Biochemistry 37:5909-5915(1998).
 RN [5]
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
 RC STRAIN=8;
 RX MEDLINE=98409292; PubMed=9738912;
 RA Parsiegla G., Schmidt A.K., Schulz G.E.;
 RT "Substrate binding to a cyclodextrin glycosyltransferase and
 RT mutations increasing the gamma-cyclodextrin production";
 RL Eur. J. Biochem. 253:710-717(1998).
 CC -1- CATALYTIC ACTIVITY: Degrades starch to cyclodextrins by formation
 CC of a 1,4-alpha-D-glucosidic bond.

```
CC -1- COFACTOR: Binds 2 calcium ions per subunit.
CC -1- SUBUNIT: Monomer.
CC -1- MISCELLANEOUS: COTASE MAY CONSIST OF TWO PROTEIN DOMAINS. THE ONE
CC IN THE AMINO-TERMINAL SIDE CLEAVES THE ALPHA-1,4-GLUCOSIDIC BOND
CC IN STARCH, AND THE OTHER IN THE C-TERMINAL SIDE CATALYZES OTHER
CC ACTIVITIES, INCLUDING THE RECONSTITUTION OF AN
CC ALPHA-1,4-GLUCOSIDIC LINKAGE FOR CYCLIZING THE
CC MALTOOLIGOSACCHARIDE PRODUCED.
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
CC DR EMBL; X68326; CAA48401.1; -.
CC DR PIR; S23674; ALBSCG.
CC DR PDB; 1CGT; 31-JAN-94.
CC DR PDB; 1CGU; 31-JAN-94.
CC DR PDB; 3CGT; 27-MAY-98.
CC DR PDB; 4CGT; 12-AUG-98.
CC DR PDB; 5CGT; 12-AUG-98.
CC DR PDB; 6CGT; 14-OCT-98.
CC DR PDB; 7CGT; 12-AUG-98.
CC DR PDB; 8CGT; 14-OCT-98.
CC DR PDB; 9CGT; 14-OCT-98.
CC DR InterPro; IPR006588; Alp_amy1_cat_sub.
CC DR InterPro; IPR006046; Alpha_amy1_C.
CC DR InterPro; IPR006047; Alpha_amy1_cat.
CC DR InterPro; IPR002044; CBD_4.
CC DR InterPro; IPR006046; Glyco_hydro_13.
CC DR InterPro; IPR007110; IG_1ike.
CC DR InterPro; IPR002909; IPT_TIG.
CC DR Pfam; PF00128; alpha-amy1ase; 1.
CC DR Pfam; PF02806; alpha-amy1ase_C; 1.
CC DR Pfam; PF02806; CBM_20; 1.
CC DR Pfam; PF01833; TIG; 1.
CC DR PRINTS; PR00110; ALPHAMYLASE.
CC DR ProDom; PD001568; CBD_4; 1.
CC DR SMART; SM00642; Amyy_1.
CC DR SMART; SM00632; Amyy_C; 1.
CC DR transferase; Glycosyltransferase; Calcium-binding; Signal;
CC 3D-structure.
CC KW SIGNAL.
CC FT CHAIN 1 34 CYCLOMALTODEXTRIN GLUCANOTRANSFERASE.
CC FT DOMAIN 35 718 A1.
CC FT DOMAIN 35 172 B.
CC FT DOMAIN 173 236 A2.
CC FT DOMAIN 237 440 C.
CC FT DOMAIN 441 528 D.
CC FT DOMAIN 529 614 E.
CC FT DOMAIN 615 718 E.
CC FT DISULFID 77 84
CC FT ACT_SITE 258 258
CC FT ACT_SITE 291 291
CC FT ACT_SITE 362 362
CC FT METAL 61 61 CALCIUM 2. (VIA CARBONYL OXYGEN).
CC FT METAL 63 63 CALCIUM 2.
CC FT METAL 66 66 CALCIUM 2.
CC FT METAL 67 67 CALCIUM 2.
CC FT METAL 85 85 CALCIUM 2. (VIA CARBONYL OXYGEN).
CC FT METAL 87 87 CALCIUM 2.
CC FT METAL 173 173 CALCIUM 1.
CC FT METAL 224 224 CALCIUM 1. (VIA CARBONYL OXYGEN).
CC FT METAL 233 233 CALCIUM 1.
CC FT METAL 267 267 CALCIUM 1. (VIA CARBONYL OXYGEN).
CC FT TURN 37 38
CC FT TURN 40 41
CC FT TURN 43 44
CC FT TURN 47 48
CC FT STRAND 51 53

FT HELIX 56 59
FT HELIX 64 66
FT STRAND 70 72
FT STRAND 73 73
FT TURN 75 76
FT TURN 80 81
FT STRAND 83 83
FT HELIX 88 96
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FT TURN 493 498

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 Best Local Similarity 23.6%; Pred. No. 7.3e-14;
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 DB 85 GGDWGLINKINDYFSDLGVTALWISQPVENIFATINYSGVNTAYHGWABDFKKTNP 144
 QY 67 FHOQGVTRKTKGTKELOSALKSLSRDINVGVDVINHGGAATEDVTAVEVDP--AD 124
 DB 145 Y-----FGTMADPOMLITTAHAKGIKIIDFAPNHTS-----PAMETDTSFAE 167
 QY 125 RNRVLSGEHLIKAMTHFHPGSGTYSDFKMWYHFDGTDWDSRKLNRITYKQKAWDW 184
 DB 188 NGRIVDNGTLVGYYT-----NDTNGYFHHNGSDFS----- 218
 QY 185 EYSNENGDNDYLMYADIDYDHPVAAE-----IKRWGTWYANELQLDGFLDAVKHIFE 238
 DB 219 --SLENGIYKNL-YDLADFNHNNATIDKYFKDAIKLM-----LDMGVDSIRVDAYKHMPL 270
 QY 239 SFRLDWNHVRKTKGEMFTVAEYQNDLGALENYLNTKFNHVSFVPLHYQFHAA--- 295
 DB 271 GMQKSMWSSI--YAHKPVFTFGWF--LGSASADADNTDFANKSGMSLDFRNSAVRN 325
 QY 296 ---STQGGGYDMKELINGTVVSKHPLK-SVTFVDNHDTPQGSLESTVQTFKPIAVAFI 351
 DB 326 VERDNTSNYYALDSMTNSTATIDYQVNDQVTFIDHMDREFT--SAVNRRLDQALLAFT 383
 QY 352 LFRESGYPQVEYG-DWYGTGK--DSOREIPALK-----HKIEPLKARKQYAYGA 398
 DB 384 LT-SRQVPAIYGTGEYLYLGNQDPDRACMPSPFSSTTAFNVISKLAPLRKSNPAIAYGS 442
 QY 399 QHDYFDHDIWGTREGSSVA-----NSGIALITGPQGA 435
 DB 443 TQQRWINDVYVERKFGKSVAVAVNRNLSTASITGLSTLPTGS 489

RESULT 15
 CDBT_BACSC STANDARD; PRT; 718 AA.
 ID CDBT_BACSC STANDARD; PRT; 718 AA.
 AC P31747;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Cyclomaltodextrin glucanotransferase precursor (EC 2.4.1.19)
 GN (Cyclodextrin-glycosyltransferase) (Cgtase).
 OS Cgt.
 OS Bacillus sp. (strain 6.6.3).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 ON NCBI_TaxId=29335;
 RX [1]
 RP SEQUENCE FROM N.A.
 RA Ahmetsajanov N.A.
 RL Submitted (MAY-1992) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: Degrades starch to cyclodextrins by formation
 of a 1,4-alpha-D-glucosidic bond.
 CC -1- COFACTOR: Binds 2 calcium ions per subunit (By similarity).
 CC -1- SUBUNIT: Monomer.
 CC -1- MISCELLANEOUS: CGTASE MAY CONSIST OF TWO PROTEIN DOMAINS: THE ONE
 IN THE AMINO-TERMINAL SIDE CLEAVES THE ALPHA-1,4-GLUCOSIDIC BOND
 IN STARCH, AND THE OTHER IN THE C-TERMINAL SIDE CATALYZES OTHER
 ACTIVITIES, INCLUDING THE RECONSTITUTION OF AN
 ALPHA-1,4-GLUCOSIDIC LINKAGE FOR CYCLIZING THE
 MALTOOLIGOSACCHARIDE PRODUCED.
 CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
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DR EMBL; X66106; CAA46901.1; -.
 DR PIR; S21532; ALBSG6.
 DR HSSP; P30920; 1CGT.
 DR InterPro; IPR006589; Alp_amy1_cat_sub.
 DR InterPro; IPR006048; Alpha_amy1_C.
 DR InterPro; IPR006047; Alpha_amy1_cat.
 DR InterPro; IPR002044; CBD_4.
 DR InterPro; IPR006046; Glyco_hydro_13.
 DR InterPro; IPR007110; Ig-1like.
 DR InterPro; IPR002909; IPT_TIG.
 DR Pfam; PF00128; alpha-amy1ase; 1.
 DR Pfam; PF02806; alpha-amy1ase_C; 1.
 DR Pfam; PF00686; CBM_20; 1.
 DR Pfam; PF01833; TIG; 1.
 DR PRINTS; PR00110; ALPHAMYLASE.
 DR ProDom; PD001568; CBD_4; 1.
 DR SMART; SM00642; Amy; 1.
 DR SMART; SMO0632; Amy; C; 1.
 KW Transferase; Glycosyltransferase; Calcium-binding; signal.
 FT SIGNAL 1 34
 FT CHAIN 35 718
 FT DOMAIN 35 172
 FT DOMAIN 173 236
 FT DOMAIN 237 440
 FT DOMAIN 441 528
 FT DOMAIN 529 614
 FT DOMAIN 615 718
 FT ACT_SITE 263 263
 FT ACT_SITE 291 291
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 FT METAL 61 61
 FT METAL 63 63
 FT METAL 66 66
 FT METAL 67 67
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 FT METAL 233 233
 FT METAL 267 267
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 FT SEQUENCE 718 AA; 78014 MW; 7644096D402707E5 CRC64;

Query Match 10.9%; Score 291.5; DB 1; Length 718;
 Best Local Similarity 23.0%; Pred. No. 8e-14;
 Matches 118; Conservative 91; Mismatches 180; Indels 123; Gaps 24;

QY 19 GQHWRLON--DSAYLAHGTAVWIPPA-----YKG-TSQADVGYGAYDYLDE 66
 DB 85 GGDWGLINKINDYFSDLGVTALWISQPVENIFATINYSGVNTAYHGWABDFKKTNP 144
 QY 67 FHOQGVTRKTKGTKELOSALKSLSRDINVGVDVINHGGAATEDVTAVEVDP--AD 124
 DB 145 Y-----FGTMADPOMLITTAHAKGIKIIDFAPNHTS-----PAMETDTSFAE 167
 QY 125 RNRVLSGEHLIKAMTHFHPGSGTYSDFKMWYHFDGTDWDSRKLNRITYKQKAWDW 184
 DB 188 NGRIVDNGTLVGYYT-----NDTNGYFHHNGSDFS----- 218
 QY 185 EYSNENGDNDYLMYADIDYDHPVAAE-----IKRWGTWYANELQLDGFLDAVKHIFE 238
 DB 219 --SLENGIYKNL-YDLADFNHNNATIDKYFKDAIKLM-----LDMGVDSIRVDAYKHMPL 270
 QY 239 SFRLDWNHVRKTKGEMFTVAEYQNDLGALENYLNTKFNHVSFVPLHYQFHAA--- 295
 DB 271 GMQKSMWSSI--YAHKPVFTFGWF--LGSASADADNTDFANKSGMSLDFRNSAVRN 325

Tue May 4 14:34:45 2004

us-10-644-187-2.rsp

Page 17

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QY 296 ---STGGGYDMRKLNGTVVSKHPLK-SVTFVNDHDTQGGLESTVQTWEKPLAVFI 351
Db 326 VFRDNTSNMYALDSMINSFATDYQVNDQVTFIDNHMDRFT--SAVNNRRLEQALAFI 383
QY 352 LTRBSGYPOVFXG-DWYGTG---DSGREIPALK-----HKIEPILKARKQYAYGA 398
Db 384 LT-SRGVPALYYGTBOYLTONGDPDNKAPSPFSKSTTAPNVISKLAPLKKSNPALAYGS 442
QY 399 QHDFDHHDIVGWTRGDSSTA-----NSGLAALITDGGGAKRMVGRQNAGET 448
Db 443 TQQRMINNDYVYERKFKGSVAVAVVNRNLSTPANITGLSTSLPTGSYTDVLGGVING-- 500
QY 449 WHDITGNRSEPVVINSRGWGEFHVNGGSVSIY 480
Db 501 -NNITSSNGS--VNS-----FTLAGATAVW 523
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Job time : 12.4645 secs

Tue May 4 14:34:44 2004

us-10-644-187-2.rpx

Page 1

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 3, 2004, 20:45:43 ; Search time 13.7346 Seconds
(without alignments)
3382.735 Million cell updates/sec

Title: US-10-644-187-2
Perfect score: 2666
Sequence: 1 ANLNGTLWQFEWYMPNDQ.....SEGWGEFHWGSGVSIYQR 483

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues
Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78: *
1: PIR1: *
2: PIR2: *
3: PIR3: *
4: PIR4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2654	99.5	512	1	ALBSL
2	2184	81.9	514	1	ALBSN
3	1879	70.5	518	1	A27705
4	1786.5	67.0	549	1	A54541
5	1780.5	66.8	549	1	A24549
6	1776.5	66.6	549	1	A24436
7	1715	64.3	548	1	ALBSF
8	1262	47.3	493	2	S15713
9	1244	46.7	492	2	AH2079
10	1233	46.2	484	2	G95160
11	1228	46.1	484	2	P98026
12	1108	41.6	491	2	C86781
13	1091.5	40.9	495	2	G98247
14	1090	40.9	495	2	AD3038
15	1050	39.8	484	1	B45738
16	1035	39.5	484	2	AD0751
17	1047	39.3	495	1	A45738
18	1047	39.3	495	2	B90962
19	1028	38.6	495	2	B85810
20	524	19.7	217	2	A19506
21	340	12.8	1196	2	A29130
22	321	12.0	826	2	B96720
23	311.5	11.7	421	2	S10514
24	310	11.6	504	2	A55861
25	304	11.4	440	2	S14958
26	302.5	11.3	482	2	S31478
27	300	11.3	437	2	S14956
28	298	11.2	713	2	S09196
29	294	11.0	713	1	ALBSG1

30	292.5	11.0	413	1	ALMTW3	alpha-amylase (EC
31	292	11.0	718	1	ALBSGC	cyclomaltohextrin
32	291.5	10.9	418	1	ALBSG6	cyclomaltohextrin
33	290.5	10.9	437	2	UC7138	alpha-amylase (EC
34	290	10.9	437	2	UT0946	alpha-amylase 3E -
35	289	10.8	438	2	S14957	alpha-amylase (EC
36	288	10.8	712	1	ALBSG3	cyclomaltohextrin
37	286	10.7	713	2	A58800	alpha-amylase (EC
38	284.5	10.7	423	2	T09942	alpha-amylase (EC
39	281	10.5	435	2	S12625	alpha-amylase (EC
40	280	10.5	435	2	UC7137	cyclomaltohextrin
41	279	10.5	713	1	ALBSG7	cyclomaltohextrin
42	277.5	10.4	710	1	S63598	cyclomaltohextrin
43	276.5	10.4	718	1	ALBSMX	alpha-amylase (EC
44	275.5	10.3	439	2	T02956	alpha-amylase (EC
45	271.5	10.2	528	1	ALBSK	alpha-amylase (EC

ALIGNMENTS

RESULT 1
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alpha-amylase (EC 3.2.1.1) precursor [validated] - Bacillus licheniformis
N.Alternate names: 1,4-alpha-D-glucan glucanohydrolase
C.Species: Bacillus licheniformis
C.Date: 30-Jun-1987 #sequence revision 24-Apr-1998 #ext change 15-Sep-2000
C.Accession: A91997; B24549; A91796; A21663; I39772; J26151; S53788; A00644
R.Yunki, T.; Nomura, T.; Teshima, H.; Tsuboi, A.; Yamagata, H.; Tsukagoshi, N.; Uchida, S.
J. Biochem. 98, 1147-1156, 1985
A.Title: Complete nucleotide sequence of a gene coding for heat- and pH-stable alpha-amylase deduced from the DNA sequences.
A.Reference number: A91997; MUID:86111694; PMID:2418011
A.Accession: A91997
A.Molecule type: DNA
A.Residues: 1-162; 'R', 164-512 <YU>
A.Cross-references: GB:X03236; NID:g39551; PIDN:CAA26981.1; PID:g39552
R.Experimental source: NCIB 8061
R.Stephens, W.A.; Orlepp, S.A.; Ollington, J.F.; McConnell, D.J.
J. Bacteriol. 158, 369-372, 1984
A.Title: Nucleotide sequence of the 5' region of the Bacillus licheniformis alpha-amylase
A.Reference number: A91796; MUID:84185455; PMID:6609154
A.Accession: A91796
A.Molecule type: DNA
A.Residues: 1-104 <STR>
A.Cross-references: GB:K01984; NID:g142432; PIDN:AAA22193.1; PID:g142433
R.Sibakov, M.; Palva, I.
Eur. J. Biochem. 145, 567-572, 1984
A.Title: Isolation and the 5'-end nucleotide sequence of Bacillus licheniformis alpha-amylase
A.Reference number: A21663; MUID:86076654; PMID:6334606
A.Accession: A21663
A.Molecule type: DNA
A.Residues: 1-3; 'H', 5-12; 'P', 14-47; 'R', 49-61; 'V', 63; 'D', 65-67; 'VA', 70-71; 'S', 73-80; 'D', 8
A.Experimental source: Chromosomal DNA of ATCC 14580
A.Note: The authors translated the codon CGT for residue 48 as Gly and GAC for residue 6
R.Boyd, B.M.; Chambliss, G.H.; McConnell, D.J.
J. Bacteriol. 171, 2435-2442, 1989
A.Title: Bacillus licheniformis alpha-amylase gene, amyA, is subject to promoter-independent
A.Reference number: I39773; MUID:89213924; PMID:2540150
A.Accession: I39773
A.Status: translated from GB/EMBL/DBJ
A.Molecule type: DNA
A.Residues: 1-29 <LMO>
A.Cross-references: GB:M26412; NID:g341477; PIDN:AAA22237.1; PID:g516590

R.Jorgensen, P.L.; Hansen, C.K.; Poulsen, G.B.; Diderichsen, B.
 Gene 96, 37-41, 1990
 A>Title: In vivo genetic engineering: homologous recombination as a tool for plasmid con
 A'Reference number: 139772; PMID:91092499; PMID:2265757
 A'Accession: 139772
 A>Status: translated from GB/EMBL/DBJ
 A'Molecule type: DNA
 A'Residuals: 1-32, '1' <JOR>
 A'CROSS-references: GB:M62637; NID:G142498; PIDN:AAA2232.1; PID:G142499
 R.Kuhn, H.; Fietzek, P.P.; Lampen, J.O.
 J. Bacteriol. 149, 372-373, 1982
 A>Title: N-terminal amino acid sequence of Bacillus licheniformis alpha-amylase: compar
 A'Reference number: A26151; PMID:82098050; PMID:6172418
 A'Accession: A26151
 A'Molecule type: protein
 A'Residuals: 30-37, 'E', '39-41', 'X', '43-47' <KUH>
 R.Machius, M.; Wiegand, G.; Huber, R.
 J. Mol. Biol. 246, 545-559, 1995
 A>Title: Crystal structure of calcium-depleted Bacillus licheniformis alpha-amylase at 2
 A'Reference number: S53788; PMID:95182462; PMID:7877175
 A'Accession: S53788
 A'Molecule type: protein
 A'Residuals: 'D', '220-227' <MAC>
 A>Note: sequence represents amino end of an internal fragment created by a single enzyma
 R.Machius, M.; Wiegand, G.; Huber, R.
 submitted to the Brookhaven Protein Data Bank, July 1995
 A'Reference number: A65206; PDB:1BPL
 A'Accession: A65206
 A'Contents: annotation: X-ray crystallography, 2.2 angstroms, residues 32-210, 222-511
 A>Note: These structural studies suggest 163 is Leu rather than Arg
 R.Song, H.K.; Huang, K.Y.; Chang, C.; Suh, S.W.
 submitted to the Brookhaven Protein Data Bank, October 1996
 A'Reference number: A66860; PDB:1VVS
 A'Accession: A66860
 A'Contents: annotation: X-ray crystallography, 1.7 angstroms, residues 32-210, 222-511
 C'Genetics:
 A'Gene: amyL
 A'Function: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
 A'Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
 A'Pathway: glycogen/starch degradation
 C'Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology
 C'Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; polysac
 F:1-39/Domain: signal sequence #status predicted <SIG>
 F:30-512/Product: alpha-amylase #status experimental <MNT>
 F:327-360/Domain: alpha-amylase core homology <AMY>
 F:133, 229, 264/Binding site: calcium (Asn, Asp, His) #status experimental
 F:260, 290, 357/Active site: Asp, Glu, Asp #status experimental
 Query Match 99.5%; Score 2654; DB 1; Length 512;
 Best Local Similarity 99.4%; Pred. No. 9, 8e-181;
 Matches 480; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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 DB 390 VFYGMVYTKGSGSOREIPALKKIPIPLKARKQYAYGAOHYFQDHDIWGTREGSSVA 449
 QY 421 NSGLALITDGGGAKRMVYGRQNGETWHDITGRSEPPVINSQWGEFHYNGGSVSIY 480
 DB 450 NSGLALITDGGGAKRMVYGRQNGETWHDITGRSEPPVINSQWGEFHYNGGSVSIY 509
 QY 481 VQR 483
 DB 518 VQR 512
 RESULT 2
 ALBNS
 alpha-amylase (EC 3.2.1.1) precursor - Bacillus amyloliquefaciens
 A'Alternate names: 1,4-alpha-D-glucan glucanohydrolase
 C'Species: Bacillus amyloliquefaciens
 C'Date: 30-Nov-1980 #sequence revision 30-Jun-1987 #text change 18-Jun-1999
 A'Accession: A92389; A90307; I39756; I39763; A00843
 R.Takkinen, K.; Petersson, R.F.; Kalkkinen, N.; Palva, I.; Soderlund, H.; Kaariainen, L.
 J. Biol. Chem. 258, 1007-1013, 1983
 A>Title: Amino acid sequence of alpha-amylase from Bacillus amyloliquefaciens deduced fr
 A'Reference number: A92389; PMID:83108808; PMID:6185474
 A'Accession: A92389
 A'Contents: PUB110
 A'Molecule type: DNA
 A'Residuals: 1-514 <TK>
 A'CROSS-references: GB:J01542; GB:J01543; GB:M12033; GB:M12034; NID:G142428; PIDN:AAA221;
 R.Chung, H.S.; Friedberg, F.
 Biochem. J. 185, 387-395, 1980
 A>Title: Sequence of the N-terminal half of Bacillus amyloliquefaciens alpha-amylase.
 A'Reference number: A90307; PMID:80241725; PMID:6156671
 A'Accession: A90307
 A'Molecule type: protein
 A'Residuals: 32-53, 'I', '55-63', 'U', '65-78', 'D', '80-83', 'S', '85-222' <CH>
 R.Palva, I.; Petersson, R.F.; Kalkkinen, N.; Lehtovaara, P.; Savas, M.; Soderlund, H.;
 Gene 15, 43-51, 1981
 A>Title: Nucleotide sequence of the promoter and NH2-terminal signal peptide region of t
 A'Reference number: I39756; PMID:82051296; PMID:6170539
 A'Accession: I39756
 A>Status: translated from GB/EMBL/DBJ
 A'Molecule type: DNA
 A'Residuals: 1-96 <RES>
 A'CROSS-references: EMBL:V00092; NID:G39297; PIDN:CAA23430.1; PID:G39298
 R.Ruohonen, L.; Hackman, P.; Lehtovaara, P.; Knowles, J.K.C.; Karasenn, S.
 Gene 59, 161-170, 1987
 A>Title: Efficient secretion of Bacillus amyloliquefaciens alpha-amylase cells by its ow
 A'Reference number: I39763; PMID:88137952; PMID:2830166
 A'Accession: I39763
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A'Molecule type: DNA
 A'Residuals: 1-39 <RE2>
 A'CROSS-references: GB:M18424; NID:G142430; PIDN:AAA2192.1; PID:G142431
 C'Function:
 A'Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
 A'Pathway: glycogen/starch degradation
 C'Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology
 C'Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation
 F:1-51/Domain: signal sequence #status predicted <SIG>
 F:32-514/Product: alpha-amylase #status predicted <MNT>
 F:329-362/Domain: alpha-amylase core homology <AMY>
 F:133, 231, 266/Binding site: calcium (Asn, Asp, His) #status predicted
 F:262, 292, 359/Active site: Asp, Glu, Asp #status predicted
 Query Match 81.9%; Score 2184; DB 1; Length 514;
 Best Local Similarity 80.3%; Pred. No. 2, 3e-147;
 Matches 388; Conservative 44; Mismatches 49; Indels 2; Gaps 1;

QY 63 DLGSEFHQKGVRTKTKKGGELQSAIKSLHARDINVVGDVYINHKSGADATIEDVTAAYVDP 122
Db 92 DLGSEFOQKGVTRITRYGKSELDQALGSLHSHKNVGVDDVVLNKAAGADATIEDVTAAYVDP 151
QY 123 ADNRKRVISGEHLIAWTHFHPPGSGSTYSDPKMWHFHDGTDMDESKLRIRYK--QOK 180
Db 152 ANRNGEISEEYQIKAMWDFRFPGRGNTYSDPKMWHFHDGADWDESKIRIFKFRGECK 211
QY 181 AMWDEVSNENGNVYDLYMADIDYDHPVAAIKRMGMWYANELQDSEFRLDAVHITKESF 240
Db 212 AMWDEVSESENNYLYLWADVDYDHPVAAETKRMGLWYANELSLDGERLDAAGHILFESF 271
QY 241 LRDVWNRHREKTKGEMFVAEYWMQNDLGALNNYINKTNFNHSEVSDVPLHYQFHAASQTQG 300
Db 272 LRDVWQAARQATKGEMFVAEYWMQNAKLENTINKTSEFNGSVDPDLPHFWLQAASQGG 331
QY 301 GYDKRKLLNGTVYVSGKPEKSVTFVNDHDTQGGCSIESVQVWFPEFLAYAFILTRSGYPO 360
Db 332 GYDKRRLLDGTVVSHPEKAVTFVENHDTQGGCSIESVQVWFPEFLAYAFILTRSGYPO 391
QY 361 VFYGMVGTQKQDSOREIPALKHKIEPIKAKROYAGQAFYPPHNDIVLWTRGDSGSA 420
Db 392 VFYGMVGTGKTSPEIEISLKDNIETPIIKAKREYAYGGQHYYIDHPVIGWTRGDSAA 451
QY 421 NSGLAALITDGGAKRMVYVGQNNAGETWHDITGNRSEPVVINSGEWGEFHVNGGSVIX 480
Db 452 KSGLAALITDGGGSGKRMVYAGKNAGETWYDITGNRSPITVXIGSDGWEFHVNDGSVIX 511
QY 481 VOR 483
Db 512 VOR 514

RESULT 3
A27705
alpha-amyLase (EC 3.2.1.1) precursor - *Bacillus* sp.
N|Alternate names: 1,4-alpha-D-glucan glucanohydrolase; G6-amyLase
C|Species: *Bacillus* sp.
C|Date: 31-Mar-1989 #sequence_revision 18-Aug-1995 #text_change 18-Jun-1995
C|Accession: A27705
R|Tsuchimoto, A.; Kimura, K.; Ishii, Y.; Takano, T.; Yamane, K.
B|Biochem. Biophys. Res. Commun. 151, 25-31, 1988
A|Title: Nucleotide sequence of the maltotetraose-producing amyLase gene from an alkalophile
A|Reference number: A27705; MUID:88162814; PMID:3258152
A|Accession: A27705
A|Molecule type: DNA
A|Residues: 1-518 <TSU>
A|Cross-references: GB:M18862; NID:G142496; PID:AAA2221.1; PID:G142497
A|Experimental source: Chromosomal DNA of strain 707
A|Note: amino end of mature protein also determined
C|Comment: This is the smallest of five starch-hydrolyzing enzymes from this organism.
C|Function:
A|Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A|Pathway: glycogen/starch degradation
C|Superfamily: alpha-amyLase, amyLolifaciens type; alpha-amyLase core homology
C|Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation
F|1-33/Domain: signal sequence #status predicted <Sig>
F|34-518/Product: alpha-amyLase #status experimental <MAP>
F|336-369/Domain: alpha-amyLase core homology <AMY>
F|339,238,273/Binding site: calcium (Asn, Asp, His) #status predicted
F|269,299,366/Active site: Asp, Glu, Asp #status predicted

Query Match	70.5%;	Score 1879;	DB 1;	Length 518;
Best Local Similarity	67.8%;	Pred. 1e-125;		
Matches 329;	Conservative	67;	Mismatches 79;	Indels 10;
				Gaps 4

QY	4	NGTLMQGFENYMPDQGHWRRLONDSAVYLEHGGTAVWIPPAKYGTQADVGAYVLYLD	63
		::: :::	
Db	39	NGTMMQGFENWLPDQGHWRRLNDSANLKSQGTAVWIPPAWMAQAQNDVGAYVLYLD	98
QY	64	LGEEHQGIVATKTKGTGELQSAFKSLHSRDLINYEGDIVIHKKGAQATEDEVTAVEYDPA	123
		::: :::	

```

Db      99  LGEPRQKOTVPTKYCTRSQLQAAVTS LKNNGI QVYGDVYMNKKGADATEMVAEYVFN 158
QY      124  DNRNVI SEHLLI KANTHFHFPGRGSTYSD FKKMWHTFDGTDMDESKL -NR1YKFO-- GK 180
           :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db      159  NRNCEVTGEYLT EATVRFPD FPGRGNTHS FKKRWYHFFDVAWMDQSRLLNR1YKFRGHK 218
           :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
QY      181  AMDWVSXENGVYD LMYADIDYDHPDVAET KRMGTWYANELQDGFRLDAVXHI KFSF 240
           :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db      219  AMDWVVDJENGVYD LMYADIDMDHEEYVNE LRNGWVNTNLGLDGFRLDAVXHI KXSF 278
           :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
QY      241  LRDWNVNREKTKEMFTVAEYMONDLGAL ENYLNKTNFNHSYEDVPLHYQFHAATQGG 300
           :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db      279  TRDWNVNRSATGKNMFAVEAFWKNDLGAI ENYLTQTNMNHSEYEDVPLHNLNLYASKSGG 338
           :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
QY      301  GYDERK LNGTVYSKGLSVTFVNDHDTPQGSLESTQVWKPLAVALTLTREGSPXQ 360
           :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db      339  NYDMNNIFNGTVYQHPSHAVTFVNDHDSQPEBALHSFVEEMWKPLAVALTLTREGSPYS 398
           :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
QY      361  VYEGDMYG--TKGDSORZ:PALKHKIEPI LKARKQYAYGAOHDPFHHDIVGWTREGDSS 418
           :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db      399  VYEGDYIGLPTHG-----VPARSKIDPIL EAKQKAYAGQONQYLDHNNIIIGWTRREGNTA 453
           :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
QY      419  VANSGLAALITDGP GAKMYYGRONAGETWHDITGNRSFPPVINSNGMGEFHNNGGSVS 478
           :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db      454  HNSGLATIMSDGAGSKMMFVGRNKGQVMSDITGNRTVTIVINADGWNQFSVNGGSVS 513
           :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
QY      479  IYVQR 483
           :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db      514  IYVNRK 518
           :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::

```

RESULT 4
A54541
alpha-amylase (BC 3.2.1.1) precursor - *Bacillus stearothermophilus* (strain DM1792)
Maltinertase names: 1,4-alpha-D-glucan glucanohydrolase
C:Species: *Bacillus stearothermophilus*
C:Date: 28-Oct-1994 #sequence_rev18 18-Aug-1995 #text_change 13-Jun-1997
C:Accession: A54541
R:Jorgensen, P.L.; Poulsen, G.B.; Diderichsen, B.
FEBS Microbiol. Lett. 77, 271-276, 1991
A:Title: Cloning of a chromosomal alpha-amylase gene from *Bacillus stearothermophilus*.
A:Reference number: A54541
A:Accession: A54541
A:Molecule type: DNA
A:Residues: 1-549 <TOR>
A:Cross-references: GB:X59476
A:Experimental source: chromosomal DNA of strain DM1792
C:Comment: Alpha-amylase genes have been found on plasmids and in multiple copies on the
C:Genetics:
A:Start codon: GTG
C:Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: alpha-amylase, amyloliofaciens type; alpha-amylase core homology
C:Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; polysacc
F:1-34/Domian: signal sequence #status predicted <SIG>
F:35-569/Product: alpha-amylase #status predicted <MAT>
F:325-368/Domian: alpha-amylase core homology <AMY>
F:139,237/272/Binding site: calcium (Asp, Asp, His) #status predicted
F:268,298,365/Active site: Asp, Glu, Asp #status predicted

Query Match	67.0%;	Score 1786.5;	DB 1;	Length 549;
Best Local Similarity	64.7%;	Pred. No. 4e-119;		
Matches 314;	Conservative 68;	Mismatches 98;	Indels 5;	Gaps 2

QY	1	A	N	I	N	G	T	L	M	O	F	E	M	Y	K	N	D	S	O	H	R	L	N	D	S	A	I	A	E	H	I	T	A	V	M	I	P	P	R	A	K	G	T	S	O	A	D	V	G	C	A	D	60	
DB	36	A	P	E	N	G	T	M	O	Y	F	E	W	Y	L	P	D	D	G	I	L	M	T	K	V	N	E	N	N	S	L	S	I	T	A	L	M	I	P	P	R	A	K	G	T	S	R	S	V	G	V	A	D	95
QY	61	L	V	L	G	E	F	H	O	K	G	T	V	T	K	T	G	K	G	E	L	S	A	I	K	S	I	S	H	R	D	I	N	V	G	D	V	A	I	N	H	K	G	A	D	E	D	V	A	V	E	120		
DB	96	L	V	L	G	E	F	H	O	K	G	T	V	T	K	T	G	K	A	O	L	S	A	I	K	S	A	A	H	A	G	M	G	V	A	D	V	P	D	H	G	A	D	G	E	T	W	A	V	E	155			

Qy	121	PAADRNRTISEHLLIKAMTHFHPGQSTYSDPKMWHYHPGQTWDESRKLNRYKFO--	178
Db	156	NPSRNOICSTYQIQAMTKFDFPGRGHTYSSFKMRYHHPGQVUMDSRKLSRYKRG	215
Qy	179	GKAMDWEVSNGNYDILMYADIDYDHDVAAIKRWGTYANBLQDLGRDAVKIKF	238
Db	216	GKAMDWEVDTENGNYDILMYADILMDHPEVATLKNMGKWVNTTINDIGRLDAVKIKF	275
Qy	239	SFLDQWVNAHAEKYGKEKFTVAEYQNDLGLENVLYLKTNPNSHVEDVPLHYQHA	298
Db	276	SFPEDWLSYVNSQTKPLFTVGEYMSYDINLHNHYITKTQDMSLFDAPLHNKRYT	335
Qy	299	GGGYDMRLKNGTYVASKPLKSYTFVNDHDTQPOCSLESTQVTFKPLAAYAFIL	358
Db	336	GGADMRRLMTNITLMKQPLAVTFVNDHDTFPGQALQSWDPFKPLAAYAFILTR	395
Qy	359	PQVEYGDMYGTGKDSQREIPALKKIEBILKARQAYAGACHDYFDHDIWGTREG	418
Db	396	PCVFEGDYTG---PQVNIPLKSKIDPILLARDAVGTGHYDLHSDITGWTREG	452
Qy	419	VANGSLALLIDGREGAGKMYVGRONAGETMHDITGRSEPVVINSBGWGFHN	478
Db	453	KPGSLALLIDGPGSKMYTVGRQAHGKVPYDLGNKSDVTYNSGQWGEFKN	512
Qy	479	IYVOR 483	
Db	513	VWVPR 517	

RESULT 5

alpha-amylase[EC 3.2.1.1] precursor - *Bacillus stearothermophilus* (strain NZ-3)
 A:Alternate names: 1,4-alpha-D-glucan glucanohydrolase
 C:Species: *Bacillus stearothermophilus*
 C:Date: 30-Jun-1988 #sequence_revision 18-Aug-1995 #text_change 18-Jun-1999
 A:Accession: A24549; 139501; 139770
 R:Giray, G.L.; Mainier, S.E.; Rey, M.W.; Lamsa, M.H.; Kindle, K.L.; Carmona, C.; Reguadt,
 J. *Bacteriol.* 166, 635-643, 1986
 A:Title: Structural genes encoding the thermophilic alpha-amylases of *Bacillus stearothermophilus*
 A:Reference number: A91817; MUID:86195857; PMID:3009417
 A:Accession: A24549
 A:Molecule type: DNA
 A:Residues: 1-549 <GRA>
 A:Cross-references: GB:M1255; NID:G142512; PIDN:AAA22241.1; PID:G142513
 A:Experimental source: genomic DNA of strain NZ-3
 J:Sato, H.; Nishida, H.; Isoro, K.
 J. *Bacteriol.* 170, 1034-1040, 1988
 A:Title: Evidence for movement of the alpha-amylase gene into two phylogenetically distant
 A:Reference number: 139501; MUID:88139156; PMID:3257753
 A:Accession: 139501
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 536-549 <RES>
 A:Cross-references: GB:M25577; NID:G142476; PIDN:AAA22225.1; PID:G142478
 A:Experimental source: strain DY-5
 A:Accession: 139770
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 536-549 <RES>
 A:Cross-references: GB:M25578; NID:G142484; PIDN:AAA22228.1; PID:G142486
 A:Experimental source: strain 799
 C:Comment: Alpha-amylase genes have been found on plasmids and in multiple copies on the
 C:Genetics:
 A:Start Codon: GTG
 A:Function:
 A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
 A:Pathway: glycogen/starch degradation
 C:Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology
 C:Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; polysaccharide
 F1-3-549/Product: signal sequence #status predicted <Sig>
 F1-235-366/Domains: alpha-amylase #status predicted <MT>
 F1-235-366/Domains: alpha-amylase core homology <MT>
 F1-139,237,272/Binding site: calcium (Asp, Asp, His) #status predicted

F;268,298,365/Active site: Asp, Glu, Asp #status predicted

Query Match	66.8%;	Score 1780.5;	DB 1;	Length 549;
Best Local Similarity	64.7%;	Pred. No. 1.1e-118;		
Matches 314;	Conservative 67;	Mismatches 99;	Indels 5;	Gaps 2;

```

0Y 1 ANNGTLMQYFPMWYVNGGMRRLQDSDSYLAEHGTAWIPBPKGYSQADVGAGAD
36 APFNGTMQYFEMWLPDDGLMTKYABANNLSSIGTALMLBPAPKGRSRSDVGAVD
0Y 61 LYNLSEFHNGKGVTRKYGTEKGELOSATKSLHSRNLNYGDDVYNHHGSGADATEDYTAEBV
Db 96 LYNLSEFNKGKGVTRKYGTEKQYLOALQALAGMOYADVDFDHKGADGTEWDAVEV
0Y 121 DPADRNRVYSGEHLIKAMTHFHPGSGSTYSDFKMWHFDPGTDWDESSKRLNRYKQO--
156 NPSDRNQELSGTYQIQAMTKFDFNGRGTYGVSFCRWYHEDDGVDMDESRKLSRYKFGI
0Y 179 GKAMDVEVSENGANTDYLMYADIDYDEHDVAAGYKRGTYANELDODGRDADVHILFE
216 GKAMDVEVTEENGANDYLYMADLMDHDEVTLEKMGKXYVATVTINIDGRDLDAVHILFE
0Y 239 SFPLRDMVHREKTEGKEMETVAEYONDIGALENYLTKTFNHSVDFDVLHYOFHAASQ
276 SFEPDLASVYRQOTKRPLETGEWMSYDINLHNYIKINGTMSLFDAPLHNKFYASKS
0Y 299 GSGYDKRLKLVGTVSKHPLKSVTFVDNHDQPOGOSIESTVQYTFKFLAYAFILITRESY
336 GGFDFDSTLMNNYLMKDDPTLAVTFVDHNDHDEPOALQSWDWFKFLAFAFLTRQBSY
0Y 359 POAFYDMVTGKQDSOREIPALKKTEIPLKARQOYVGAQHDYFHHIDVGTREGDSS
396 PCFYFYDYGTL---FQYNIPLSKMIDPLLIARDVAYGQHYLDHSDILGWTREGVTE
0Y 419 VANSGLAALITDGPQKAKMYVGRONAGETWHDITGNRSEPVYINSGNWEEFHNNGSJS
453 KPSGSLAALITDGPQGSKMVYGRQHAQKAVFYDITGNRSDTYVINSQGWEEFVYNGGSVS
0Y 479 IYVQR 483
513 VWVPR 517

```

RESULT 6

A24436
 Alpha-amyLase (EC 3.2.1.1) precursor - *Bacillus stearothermophilus* plasmid pAT5
 N:Alternate names: 1,4-alpha-D-glucan Glucanohydrolase
 C:Species: *Bacillus stearothermophilus*
 C>Date: 05-Jun-1987 #sequence_revision 18-Aug-1995 #text_change 18-Jun-1999
 C/Accession: A24436, 139777
 R:NakaJima, R.; Imanaka, T.; Aiba, S.
 J. Bacteriol. 163, 401-406, 1985
 A:Reference number: A24436; MUID:85234394; PMID:3924857
 A:Accession: A24436
 A:Molecule type: DNA
 A:Residues: 1-549 <NA>
 A/Cross-references: GB:M11450
 A/Experimental source: plasmid pAT5
 A/Note: amino end of the mature protein also determined
 R:Jorgensen, P.L.; Hansen, C.K.; Poulsen, G.B.; Diderichsen, B.
 Gene 96, 37-41, 1990
 A/Title: In vivo genetic engineering: homologous recombination as a tool for plasmid con-
 A/Reference number: 139772; MUID:91092499; PMID:2265757
 A/Accession: 139777
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-45 <RES>
 A/Cross-references: GB:M62638; NID:g142514; PIDN:AAA22242.1; PID:g142515
 C/Comment: Alpha-amyLase genes have been found on plasmids and in multiple copies on the
 C/genetics:
 A:Gene: amyS
 A:genome: plasmid
 A/Start codon: GTG

C/Function: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A/Description: glycoylase/starch degradation
A/Pathway: glycoylase/starch degradation
C/Superfamily: alpha-amylose, amylopectinase type; alpha-amylose core homology
C/Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; polysac
F/1-34/Domain: signal sequence #status predicted <SIG>
F/1-34/Product: alpha-amylose #status experimental <MAT>
F/235-549/Domain: alpha-amylose core homology <AMY>
F/235-549/Product: alpha-amylose core homology <AMY>
F/139-237/Binding site: calcium (Asp, Asp, His) #status predicted
F/268,298,365/Active site: Asp, Glu, Asp #status predicted

Query Match 66.6%; Score 1776.5; DB 1; Length 549;
Best Local Similarity 64.7%; Pred. No. 2,1e-118; Indels 5; Gaps 2;
Matches 314; Conservative 66; Mismatches 100;
QY 1 ANLNGTMOYFEMWMPNDGQWRLONDSAYLAHGTAVWIPPAKGTSDQADVGAYD 60
DB 36 APFNGTMOYFEMWLPDGLMTKVAEANNLSLGLTALMPPAKGTSRSDVGAYD 95
QY 61 LYDGEFHQKGTVRKTKYGTGELQSAIKSLHSRDINYGVDVINHGKADATEDVTAVEY 120
DB 96 LYDGEFHQKGTVRKTKYGTGELQSAIKSLHSRDINYGVDVINHGKADATEDVTAVEY 155
QY 121 DPADNRVTSGEHLIKAMTHFHPGSGTSDCFKMWYHPDGTMDPSRKLRIYKFO-- 178
DB 156 NPSDRNOEISGTQYQAMTKFDFPGRGNTYSSFKRWYHFDGVDMSRKLRIYKFO 215
QY 179 GKAWMEVSNENGNVDYLMYADIDYHDPVAEIKRWGTWYANLQDGFRLDAVKIKF 238
DB 216 GKAWMEVSNENGNVDYLMYADIDYHDPVAEIKRWGTWYANLQDGFRLDAVKIKF 275
QY 239 SPLRWNVNHRKTKGEMFTVAEYQNDLGALNTKNTNNSVFPVPLHYOFAASTQ 298
DB 276 SFPDMLSVRSQTKPLFTVGEYWSYDINKLHNTKNTNNSVFPVPLHYOFAASTQ 335
QY 299 GGGYDMRKLTNGTVSKHPLKSVTFVNDHTQPGQSLSTVQTFKPLAVALITRESGY 358
DB 336 GGGYDMRKLTNGTVSKHPLKSVTFVNDHTQPGQSLSTVQTFKPLAVALITRESGY 395
QY 359 POVYFGMTGKGSQSEIPALKEIPILKARKQYAGAOHYFDHDIWGTREDDSS 418
DB 396 PCVYFGDYGI--PQYNIPLKSKIDPLIARQYAGAOHYFDHDIWGTREDDSS 452
QY 419 VANSGLAALITDGPAGAKMYVGRONAGETWHDITGRSEPVVINSGEWGFHNGSGVS 478
DB 453 KPGSGLAALITDGPAGAKMYVGRONAGETWHDITGRSEPVVINSGEWGFHNGSGVS 512
QY 479 IYVQR 483
DB 513 VWVPR 517

RESULT 7

ALBP
Alpha-amylose (EC 3.2.1.1) precursor - Bacillus stearothermophilus (strain DY-5) plasmid
N/Alternate names: 1,4-alpha-D-glucan glucanohydrolase
C/Species: Bacillus stearothermophilus
C/Date: 30-Jun-1987 #sequence revision 30-Jun-1987 #text change 16-Feb-1997
C/Accession: A91999; B91999; A00845
R/Ihara, H.; Sasaki, T.; Tsuboi, A.; Yamagata, H.; Tsukagoshi, N.; Uda, S.
J. Biochem. 98, 95-103, 1985
A/Title: Complete nucleotide sequence of a thermophilic alpha-amylose gene: homology bet
A/Reference number: A91999; MUID:86008166; PMID:3876333
A/Accession: A91999
A/Molecule type: DNA
A/Residues: 1-548 <1H1>
A/Cross-references: GB:X02769
A/Experimental source: plasmid PH1300 from strain DY-5
A/Accession: B91999
A/Molecule type: protein
A/Residues: 35-48 <1H2>
A/Experimental source: strain DY-5
R/Tsukagoshi, N.; Iritani, S.; Sasaki, T.; Takemura, T.; Ihara, H.; Idota, Y.; Yamagata,

J. Bacteriol. 164, 1182-1187, 1985
A/Title: Efficient synthesis and secretion of a thermophilic alpha-amylose by protein-pr
A/Reference number: A91804; MUID:86059211; PMID:2999073
A/Contents: PBAM101
A/Accession: A91804
A/Molecule type: DNA
A/Residues: 1-59, 'Q', 31-75, 'W', 77-122 <TSU>
A/Comment: Alpha-amylose genes have been found on plasmids and in multiple copies on the
C/Genetics:
A/Genome: plasmid
A/Start codon: GTG
C/Function:
A/Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A/Pathway: glycoylase/starch degradation
C/Superfamily: alpha-amylose, amylopectinase type; alpha-amylose core homology
C/Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; polysac
F/1-34/Domain: signal sequence #status predicted <SIG>
F/1-34/Product: alpha-amylose #status experimental <MAT>
F/235-549/Domain: alpha-amylose core homology <AMY>
F/139-237/Binding site: calcium (Asp, Asp, His) #status predicted
F/268,298,365/Active site: Asp, Glu, Asp #status predicted

Query Match 64.3%; Score 1715; DB 1; Length 548;
Best Local Similarity 63.1%; Pred. No. 4.8e-114; Indels 6; Gaps 3;
Matches 306; Conservative 67; Mismatches 106;
QY 1 ANLNGTMOYFEMWMPNDGQWRLONDSAYLAHGTAVWIPPAKGTSDQADVGAYD 60
DB 36 APFNGTMOYFEMWLPDGLMTKVAEANNLSLGLTALMPPAKGTSRSDVGAYD 95
QY 61 LYDGEFHQKGTVRKTKYGTGELQSAIKSLHSRDINYGVDVINHGKADATEDVTAVEY 120
DB 96 LYDGEFHQKGTVRKTKYGTGELQSAIKSLHSRDINYGVDVINHGKADATEDVTAVEY 155
QY 121 DPADNRVTSGEHLIKAMTHFHPGSGTSDCFKMWYHPDGTMDPSRKLRIYKFO-- 178
DB 156 NPSDRNOEISGTQYQAMTKFDFPGRGNTYSSFKRWYHFDGVDMSRKLRIYKFO 215
QY 179 GKAWMEVSNENGNVDYLMYADIDYHDPVAEIKRWGTWYANLQDGFRLDAVKIKF 238
DB 216 GKAWMEVSNENGNVDYLMYADIDYHDPVAEIKRWGTWYANLQDGFRLDAVKIKF 275
QY 239 SPLRWNVNHRKTKGEMFTVAEYQNDLGALNTKNTNNSVFPVPLHYOFAASTQ 298
DB 276 SFPDMLSVRSQTKPLFTVGEYWSYDINKLHNTKNTNNSVFPVPLHYOFAASTQ 335
QY 299 GGGYDMRKLTNGTVSKHPLKSVTFVNDHTQPGQSLSTVQTFKPLAVALITRESGY 358
DB 336 GGGYDMRKLTNGTVSKHPLKSVTFVNDHTQPGQSLSTVQTFKPLAVALITRESGY 394
QY 359 POVYFGMTGKGSQSEIPALKEIPILKARKQYAGAOHYFDHDIWGTREDDSS 418
DB 396 PCVYFGDYGI--PQYNIPLKSKIDPLIARQYAGAOHYFDHDIWGTREDDSS 451
QY 419 VANSGLAALITDGPAGAKMYVGRONAGETWHDITGRSEPVVINSGEWGFHNGSGVS 478
DB 452 KPGSGLAALITDGPAGAKMYVGRONAGETWHDITGRSEPVVINSGEWGFHNGSGVS 511
QY 479 IYVQR 483
DB 512 VWVPR 516

RESULT 8

S15713
Alpha-amylose (EC 3.2.1.1) - Bacillus circulans
C/Species: Bacillus circulans
C/Date: 18-Feb-1994 #sequence revision 10-Nov-1995 #text change 22-Jun-1999
C/Accession: S15713
R/Marcel, T.
submitted to the EMBL Data Library, May 1991
A/Reference number: S15713
A/Accession: S15713

A:Molecule type: DNA
 A:Residues: 1-493 <NMR>
 A:Cross-references: EMBL:X60779; NID:G939411; PIDN:CAA43194.1; PID:G939412
 C:Genetics:
 A:Gene: amyE
 C:Function:
 A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
 A:Pathway: glycogen/starch degradation
 C:Superfamily: alpha-amylose, amyloliquefaciens type; alpha-amylose core homology
 C:Keywords: glycosidase; hydrolase; polysaccharide degradation
 F:200-333/Domain: alpha-amylose core homology <AMY>

Query Match 47.3%; Score 1262; DB 2; Length 493;
 Best Local Similarity 47.6%; Pred. No. 5.9e-82;
 Matches 230; Conservative 75; Mismatches 166; Indels 12; Gaps 3;

```

QY      4 NGTLMQYFEMWMPNDQGHRRRLONDSAYLAEGITAWIPPAKGTSGADVGAYDLYD 63
DB      4 NHTMMQFPEHMLADGDHMKRLAEMAEPLAKAGIDITWVBPVTKAVSAEDTGVGYDLYD 63
QY      64 LGEPHQKGTVTRTKYGTKEGLOSAIKSLHSRDINYYGCVVINHKGADATEDVTAAYVDA 123
DB      64 LGEPDQKGTVTRTKYGTKEGLOSAIKSLHSRDINYYGCVVINHKGADATEDVTAAYVDA 123
QY      124 DNRVITSGEHLIKAWTHFHPRGSTYSDFKMHYFEDGTDMDSEKLNRIYKFG--KA 181
DB      124 DRIKEISPEIEEMWTKETFPGRGDQYSSFKMSEHNGTDFPAREERTGVFRIGENKK 183
QY      182 WDMEVSNENGYDYDLYMADIDYDHPDVAAEIKWGTAYANELQDGFRLDAVXHKISPL 241
DB      184 WNEVVDPEFGYDYLMPANIDYRNMIDWGMKILDTLQCGGFRDAIKHINHEI 243
QY      242 RDVNVHREKTKGKMFVAEYQNDLGALENYLNKTNFNHSVDPVPLHQTGHAAGTGGG 301
DB      244 KEFAEITRRKGQDFYVGEFMSNLDACREPLDTVDYQIDLDVLAHKLHSAKSGD 303
QY      302 YDMKRLNGTVVSKPLKSVTFVDNHDTPQGSLESTVQTFKPLAYATILTRBSGPGV 361
DB      304 FDLKIPDDTLVGHFPHAVTVDNHDSPHEALLESIGDMFERSAYATILLRBGYPV 363
QY      362 FYGDMYGTGK---DSQRETPALKHTEPLKARKQYAYAGADYDHDHDYGTMRBGS 417
DB      364 FYGYIYGGEPEYDGGKEI-----DLILSARCNKAYGEQDYFDHANTTIGWRRGYE 417
QY      418 SVANSGLAALITDGPQAKMYVGRQVAGETWHDITGNSEPVINSEMGCFHYNGSV 477
DB      418 EIESSGCAVVISNGDDGKRMFGEHRAAGEVWVDLTFVSCDDQTIEEDMATFHYCGGV 477
QY      478 SIY 480
DB      478 SVM 480

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RESULT 9

AH2079
 alpha-amylose [imported] - Nostoc sp. (strain PCC 7120)

C:Species: Nostoc sp. PCC 7120
 C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
 C:Accession: AH2079
 F:Kaneke, T.; Nakamura, Y.; Molk, C.P.; Kuritz, T.; Sasamoto, S.; Matanabe, A.; Irituguhi, Nakazaki, N.; Shimo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
 DNA Res. 8, 205-213, 2001
 A:Title: Complete Genome Sequence of the filamentous Nitrogen-fixing Cyanobacterium *Anabaena* sp. PCC 7120
 A:Reference number: AB1807; MUID:21595285; PMID:1175840
 A:Accession: AH2079
 A:Status: Preliminary
 A:Molecule type: DNA
 A:Residues: 1-492 <KUR>
 A:Cross-references: GB:BA000019; PIDN:BAW73889.1; PID:g17131281; GSPDB:GN00179
 A:Experimental source: strain PCC 7120
 C:Genetics:
 A:Gene: alr2190

C:Superfamily: alpha-amylose, amyloliquefaciens type; alpha-amylose core homology

Query Match 46.7%; Score 1244; DB 2; Length 492;
 Best Local Similarity 47.5%; Pred. No. 1.1e-80;
 Matches 234; Conservative 84; Mismatches 161; Indels 14; Gaps 6;

```

QY      1 ANNGTLMQYFEMWMPNDQGHRRRLONDSAYLAEGITAWIPPAKGTSGADVGAY 59
DB      2 AQKNGTLMQYFEMWMPNDQGHRRRLONDSAYLAEGITAWIPPAKGTSGADVGAY 61
QY      60 DLYDLGEPHQKGTVTRTKYGTKEGLOSAIKSLHSRDINYYGCVVINHKGADATEDVTA 119
DB      62 DLPDLGEPDQKGTVTRTKYGTKEGLOSAIKSLHSRDINYYGCVVINHKGADATEDVTA 121
QY      120 VDPAENRNVITSGEHLIKAWTHFHPRGSTYSDFKMHYFEDGTDMDSEKLNRIYK 177
DB      122 FPODDLINPQKGLQDITKITHNFPKQKTSNFMHMHFDVADYINSGDSITVLL 181
QY      178 QGRAMDVSNENGYDYDLYMADIDYDHPDVAAEIKWGTAYANELQDGFRLDAVXHK 237
DB      182 EGNKFDYVALKXGNFAYLMGCDLDFQENWVAGETVYGMKCLDTTKVDGRDAIKHIS 241
QY      238 FSLIRVMVHVRKTKGKMFVAEYQNDLGALENYLNKTNFNHSVDPVPLHQTGHAAG 297
DB      242 TWFPFADYIYGAAYEDWGDGNRYNIFMPSHWIILDKLYARKHAYGPQYNYIDHWMTI 301
QY      298 QGGYDMKRLNGTVVSKPLKSVTFVDNHDTPQGSLESTVQTFKPLAYATILTRBSG 357
DB      302 SGQYDMKRLNGTVVSKPLKSVTFVDNHDTPQGSLESTVQTFKPLAYATILTRBSG 361
QY      358 YPQYFGDMYGTGK---DSQRETPALKHTEPLKARKQYAYAGADYDHDHDYGTMR 409
DB      362 YPQYFGDMYGTGK---DSQRETPALKHTEPLKARKQYAYAGADYDHDHDYGTMR 421
QY      410 GWTREBDSVANSGLAALITDGPQAKMYVGRQVAGETWHDITGNSEPVINSEMGCF 469
DB      422 GWTREBDSVANSGLAALITDGPQAKMYVGRQVAGETWHDITGNSEPVINSEMGCF 478
QY      470 FHYNGSVISLYG 482
DB      479 FRLGGSVSVWVQ 491

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RESULT 10

G95160
 alpha-amylose [imported] - Streptococcus pneumoniae (strain TIGR4)

C:Species: Streptococcus pneumoniae
 C:Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 24-Aug-2001
 C:Accession: G95160
 F:Teitelin, R.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heidrich, J.D.; Umayam, L.A.; White, O.; Salberg, S.T.; Lewis, M.R.; Radune, D.; Holtzapple, I.; Hickey, E.K.; Holt, I.E.
 Science 293, 498-506, 2001
 A:Authors: Teitelin, R.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heidrich, J.D.; Umayam, L.A.; White, O.; Salberg, S.T.; Lewis, M.R.; Radune, D.; Holtzapple, I.; Hickey, E.K.; Holt, I.E.
 A:Title: Complete Genome Sequence of a virulent isolate of *Streptococcus pneumoniae*.
 A:Reference number: A95000; MUID:2157209; PMID:11463916
 A:Accession: G95160
 A:Status: Preliminary
 A:Molecule type: DNA
 A:Residues: 1-484 <KUR>
 A:Cross-references: GB:AE005672; PIDN:AAK75480.1; PID:g14972868; GSPDB:GN00164; TIGR:SP4
 A:Experimental source: strain TIGR4
 C:Genetics:
 A:Gene: SPI382
 C:Superfamily: alpha-amylose, amyloliquefaciens type; alpha-amylose core homology

Query Match 46.2%; Score 1233; DB 2; Length 484;
 Best Local Similarity 48.6%; Pred. No. 6.6e-80;
 Matches 234; Conservative 72; Mismatches 167; Indels 8; Gaps 4;

```

QY      4 NGTLMQYFEMWMPNDQGHRRRLONDSAYLAEGITAWIPPAKGTSGADVGAYDLYD 63
DB      3 NGTLMQYFEMWMPNDQGHRRRLONDSAYLAEGITAWIPPAKGTSGADVGAYDLYD 62

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QY 64 LGFHQKGTVRKTKYKSGELQSAIKSLHSRDINVDVYINHGKAGATEDVTAVEVPA 123
DB 63 LGFNGKGTVRKTKYKSGELQSAIKSLHSRDINVDVYINHGKAGATEDVTAVEVPA 122
QY 124 DNRNVISGEHLIKAMTHFHPGRGSTYSDFKMWHYFPGDSTDWDESKLRIRYKFGQ--KA 181
DB 123 DRIVEIGEPTINGWISFTFDGQDTYNGFHHMHWFHTGDDAKSKSGIILIQDNKG 182
QY 182 WDME--VSNENGVYDLMVADIDYDHPVAALIKKWTYANELQDGRDLAVYKIKS 239
DB 183 WANEELVDNENGVYDLMVADIDYDHPVAALIKKWTYANELQDGRDLAVYKIKS 242
QY 240 FLRDVNVHVEKTKEMFTVAEYQNDLGALENVYLNKTNFNSVFPVPLHYQFHAASDQ 299
DB 243 FMRNFIRDMKEXKGDDDYVGEFWMNDKXANLDYLEKTEHFDLVDRHLQNLFEASQAG 302
QY 300 GGYDMRKLLNGTVVSKHPLKSVTFVDNHDTPQGSLESTVQTFKPLAVAFILTRSGYP 359
DB 303 ANYDLRGIFDLSLVEKPDKAVTFVDNHDTPQGSLESTVQTFKPLAVAFILTRSGYP 362
QY 360 QVFYGDYGGISGQYAOQ--DFKELIDRLAIRKOLAYGEQNDYFDHANCIGWRSAGEN- 419
DB 363 CVFYGDYGGISGQYAOQ--DFKELIDRLAIRKOLAYGEQNDYFDHANCIGWRSAGEN- 419
QY 420 ANSGLAALITDPGAKRMVYGRONAGETWHDITGNRSEPVVINSGEGBFHYNGSVSI 479
DB 420 -QSPIAVLISNDQNSKSMFVGQEWMTQTFVDLIGHQGVITIDEGYGGFVPSARSVS 478
QY 480 Y 480
DB 479 W 479

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RESULT 11

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F98026
Alpha-amylase (EC 3.2.1.1) precursor (imported) - Streptococcus pneumoniae (strain R6)
C/Species: Streptococcus pneumoniae
C/Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 02-Nov-2001
C/Accession: F98026
R/Hoskins, J.A.; Albom Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; Dehoff, B.S.; E
R.; R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.D.; Lu, J.; Matsushima, P.; McAhren, S.; M
J.; P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A/Authors: Yang, Y., Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A/Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A/Reference number: A97872; MUID:21429245; PMID:11544234
A/Accession: F98026
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-484 <KIR>
A/Cross-references: GB:AE007317; PIDN:AAU0043.1; PID:G15458876; GSPDB:GN00174
C/Genetics:
A/Gene: amy
C/Superfamily: alpha-amylase, amyloliquefaciens type, alpha-amylase core homology
C/Keywords: glycosidase; hydrolase

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Query Match 46.1%; Score 1228; DB 2; Length 484;
Best Local Similarity 48.2%; Pred. No. 1.5e-79;
Matches 232; Conservative 75; Mismatches 166; Indels 8; Gaps 4;
QY 4 NGTLMQYFEWYMPNDGQHRRLQNDASAVLAHGITAVIIPRAYKTSQA-DVGYGAYDLYD 63
DB 3 NGTLMQYFEWYLPDHDGHTRLAENAPHLAHLGISHWMPAFKATKXGVGYVDLFD 62
QY 64 LGFHHQKGTVRKTKYKSGELQSAIKSLHSRDINVDVYINHGKAGATEDVTAVEVPA 123
DB 63 LGFNGKGTVRKTKYKSGELQSAIKSLHSRDINVDVYINHGKAGATEDVTAVEVPA 122
QY 124 DNRNVISGEHLIKAMTHFHPGRGSTYSDFKMWHYFPGDSTDWDESKLRIRYKFGQ--KA 181
DB 123 DRIVEIGEPTINGWISFTFDGQDTYNGFHHMHWFHTGDDAKSKSGIILIQDNKG 182

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QY 182 WDME--VSNENGVYDLMVADIDYDHPVAALIKKWTYANELQDGRDLAVYKIKS 239
DB 183 WANEELVDNENGVYDLMVADIDYDHPVAALIKKWTYANELQDGRDLAVYKIKS 242
QY 240 FLRDVNVHVEKTKEMFTVAEYQNDLGALENVYLNKTNFNSVFPVPLHYQFHAASDQ 299
DB 243 FMRNFIRDMKEXKGDDDYVGEFWMNDKXANLDYLEKTEHFDLVDRHLQNLFEASQAG 302
QY 300 GGYDMRKLLNGTVVSKHPLKSVTFVDNHDTPQGSLESTVQTFKPLAVAFILTRSGYP 359
DB 303 ANYDLRGIFDLSLVEKPDKAVTFVDNHDTPQGSLESTVQTFKPLAVAFILTRSGYP 362
QY 360 QVFYGDYGGISGQYAOQ--DFKELIDRLAIRKOLAYGEQNDYFDHANCIGWRSAGEN- 419
DB 363 CVFYGDYGGISGQYAOQ--DFKELIDRLAIRKOLAYGEQNDYFDHANCIGWRSAGEN- 419
QY 420 ANSGLAALITDPGAKRMVYGRONAGETWHDITGNRSEPVVINSGEGBFHYNGSVSI 479
DB 420 -QSPIAVLISNDQNSKSMFVGQEWMTQTFVDLIGHQGVITIDEGYGGFVPSARSVS 478
QY 480 Y 480
DB 479 W 479

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RESULT 12

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C66781
Alpha-amylase (imported) - Lactococcus lactis subsp. lactis (strain IL1403)
C/Species: Lactococcus lactis subsp. lactis
C/Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
C/Accession: C66781
R/Bolotin, A.; Winkler, P.; Manger, S.; Jallion, O.; Malarre, K.; Weissenbach, J.; Ehrli
Genome Res. 11, 731-753, 2001
A/Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis se
A/Reference number: A66625; MUID:21235186; PMID:11337471
A/Accession: C66781
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-491 <STD>
A/Cross-references: GB:AE005176; PID:G12724224; PIDN:AK05349.1; GSPDB:GN00146
A/Experimental source: strain IL1403
C/Genetics:
A/Gene: amyL
C/Superfamily: alpha-amylase, amyloliquefaciens type, alpha-amylase core homology

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Query Match 41.6%; Score 1108; DB 2; Length 491;
Best Local Similarity 41.7%; Pred. No. 5e-71;
Matches 204; Conservative 93; Mismatches 168; Indels 24; Gaps 7;
QY 6 TLMQYFEWYMPNDGQHRRLQNDASAVLAHGITAVIIPRAYKTSQA-DVGYGAYDLYD 64
DB 3 TLMQYFEWYLPDHDGHTRLAENAPHLAHLGISHWMPAFKATKXGVGYVDLFD 62
QY 65 LGFHQKGTVRKTKYKSGELQSAIKSLHSRDINVDVYINHGKAGATEDVTAVEVPA 123
DB 63 LGFNGKGTVRKTKYKSGELQSAIKSLHSRDINVDVYINHGKAGATEDVTAVEVPA 122
QY 124 DNRNVISGEHLIKAMTHFHPGRGSTYSDFKMWHYFPGDSTDWDESKLRIRYKFGQ 181
DB 123 DRIVEIGEPTINGWISFTFDGQDTYNGFHHMHWFHTGDDAKSKSGIILIQDNKG 182
QY 182 WDME--VSNENGVYDLMVADIDYDHPVAALIKKWTYANELQDGRDLAVYKIKS 239
DB 183 WANEELVDNENGVYDLMVADIDYDHPVAALIKKWTYANELQDGRDLAVYKIKS 242
QY 240 FLRDVNVHVEKTKEMFTVAEYQNDLGALENVYLNKTNFNSVFPVPLHYQFHAASDQ 299
DB 243 FMRNFIRDMKEXKGDDDYVGEFWMNDKXANLDYLEKTEHFDLVDRHLQNLFEASQAG 302
QY 300 GGYDMRKLLNGTVVSKHPLKSVTFVDNHDTPQGSLESTVQTFKPLAVAFILTRSGYP 359
DB 303 ANYDLRGIFDLSLVEKPDKAVTFVDNHDTPQGSLESTVQTFKPLAVAFILTRSGYP 362
QY 420 ANSGLAALITDPGAKRMVYGRONAGETWHDITGNRSEPVVINSGEGBFHYNGSVSI 479
DB 420 -QSPIAVLISNDQNSKSMFVGQEWMTQTFVDLIGHQGVITIDEGYGGFVPSARSVS 478
QY 480 Y 480
DB 479 W 479

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QY 362 FYGDMYCTKDSQREIPALXKIEPI-----LKRKOYVGAQHDYFDHDIYGMTRE 414
DB 360 FWDLYG-----IPS--HNVNPGVDMIRMTALRKNSEPLRNDYFDHDIIGMTNI 409
QY 415 GDSVSVANGSLAIIITDGPAGAKMYVGRONAGETWHDITGNSEPVINSBGMGEFHYNG 474
DB 410 LKIDNKEYGLSCITLTKNGSSKMIIDKXAGKVYIDLGRHEIITLIDQNGAFYVND 469
QY 475 GSVSYIVQR 483
DB 470 GSVSVWVWK 478

RESULT 13

Cytoplasmic alpha-amylase (1,4-alpha-D-glucan glucohydrolase) [imported] - Agrobacterium tumefaciens
C/Species: Agrobacterium tumefaciens
C/Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 18-Nov-2002
C/Accession: G98247
R/Gooder, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A/Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens
A/Reference number: A97359; PMID:21608551; PMID:11743194
A/Accession: G98247
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-506 <KUR>
A/Cross-references: GB:AE007870; PIDN:AAK89505.1; PID:g15159379; GSPDB:GN00170
C/Genetics:
A/Map position: linear chromosome
A/Suprafamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology

Query Match 40.9%; Score 1091.5; DB 2; Length 506;
Best Local Similarity 44.3%; Pred. No. 7.7e-70;
Matches 219; Conservative 80; Mismatches 178; Indels 17; Gaps 6;
QY 2 NLNG-TLMQYFEMVMPNDGQWRLQNDASVLAHSGITAVWIPRAYKGSQA-DVGYGAY 59
DB 11 NMAGRTILOFHHMYDDGGLMEVAKESLAKWGITVWMLPRAKGAAGYSVGYDTY 70
QY 60 DLYDLGEFHQXGVRTKYGKGLQSAIKSLSRDINVGDVVNHKSGADATEDVNAVE 119
DB 71 DLEDFLGEFFDQKGVATKYGPRALAEAGKTLKONGIRVHDVVLNKGADKEKVRVRR 130
QY 120 VDPADRRRVISGEHLIKAMTHFHPGRGSTYSPFKMHWHPDGTWDSRLKRIYKQG 179
DB 131 VNPDDRDIIDEDFPALAVYRFFPRNGKSKFTWDLKCSGVHIEPTEDGIFRLVYN 190
QY 180 K---AMDWEVSNENGVYDLYADIDYHPDVAEIKKMGTVANELQDGFRLDAVKA 235
DB 191 EYGDGENNEVDENGFYLMGADVEFRRAVYBELKTYGWMLEQYQVQDGFRLDAKH 250
QY 236 IKESFLADWVNHVREKTKGEMFTVAEYQNDLGALENYLNTKPNHSAVDFVLYHQFPA 295
DB 251 IPAMFFPDVGHARETVDPDLFVYAEYHFDLEALKSYELVDKQMLFDVALHHSFDDA 310
QY 296 STGGGVDKRLKNGVYKPKLSTYFVNDHDTQGSLESTVQTWFKPLAYAFILTRE 355
DB 311 SKGGSDPDMKSIDGSLVAVPDHATVLDNHTQGLSELPVPMFEPPLAYAILLRE 370
QY 356 SGYQVYFGDMYGTK-----GDSOREIPALKKHIEPILKAKQYVGAQHDYFDHND 407
DB 371 EGVPCVYFPDLFGSTYTDGNDGNEKIDIPALE-CLPKLEARSFRANPGDTDFDAS 429
QY 408 IVGMTRGDSVANGSLAIIITDGPAGAKMYVGRONAGETWHDITGNSEPVINSBGM 467
DB 430 CIAFIRHGTADA--PGCVVMSNGEPKQADLGPERRASVVRDPLGRHEHITLDESCK 487
QY 468 GEFVANGSVSYIV 481
DB 488 GTFPTNGGSVYVWV 501

RESULT 14

AD3038
alpha-amylase amya [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C/Species: Agrobacterium tumefaciens
C/Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C/Accession: AD3038
R/Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.; Karp, P.; Romero, P.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClellan, S.; Science 294, 2317-2323, 2001
A/Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, J.; ster, B.W.
A/Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A/Reference number: AB2577; PMID:21608550; PMID:11743193
A/Accession: AD3038
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-495 <KUR>
A/Cross-references: GB:AE008689; PIDN:AAL44722.1; PID:g17742354; GSPDB:GN00187
A/Experimental source: strain C58 (Dupont)
C/Genetics:
A/Map position: linear chromosome
A/Suprafamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology

Query Match 40.9%; Score 1090; DB 2; Length 495;
Best Local Similarity 44.4%; Pred. No. 9.6e-70;
Matches 217; Conservative 79; Mismatches 177; Indels 16; Gaps 5;
QY 6 TLMQYFEMVMPNDGQWRLQNDASVLAHSGITAVWIPRAYKGSQA-DVGYGAYLXDL 64
DB 5 TLDQFHHMYDPDGGGLMEVAKESLAKWGITVWMLPRAKGAAGYSVGYDTYDFDL 64
QY 65 GEFHOKGVRTKYGKGLQSAIKSLSRDINVGDVVNHKSGADATEDVNAVEVDPAD 124
DB 65 GEPDQGVATKYGPRALAEAGKTLKONGIRVHDVVLNKGADKEKVRVRRVDPD 124
QY 125 RNRVSGEHLIKAMTHFHPGRGSTYSPFKMHWHPDGTWDSRLKRIYKQG---- 180
DB 125 RTDIDDEDPALAVYRFFPRNGKSKFTWDLKCSGVHIEPTEDGIFRLVNEGDD 184
QY 181 AMDWEVSNENGVYDLYADIDYHPDVAEIKKMGTVANELQDGFRLDAVKAHIFSF 240
DB 185 ENNEEVDQNGNFDYLMGADVEFRRAVYBELKTYGWMLEQYQVQDGFRLDAKHIFAMF 244
QY 241 LADWVNHVREKTKGEMFTVAEYQNDLGALENYLNTKPNHSAVDFVLYHQFPA 300
DB 245 FPDVGHARETVDPDLFVYAEYHFDLEALKSYELVDKQMLFDVALHHSFDDASQ 304
QY 301 GYDNRKLNGVYKPKLSTYFVNDHDTQGSLESTVQTWFKPLAYAFILTRESGYPQ 360
DB 305 DDMKSIDGSLVAVPDHATVLDNHTQGLSELPVPMFEPPLAYAILLREBVCPC 364
QY 361 VFYQVYGTGK-----GDSOREIPALKKHIEPILKAKQYVGAQHDYFDHNDIYGMT 412
DB 365 VFYFDPFGSTYTDGNDGNEKIDIPALE-CLPKLEARSFRANPGDTDFDASCAFI 423
QY 413 REGDSVANGSLAIIITDGPAGAKMYVGRONAGETWHDITGNSEPVINSBGMGEFHY 472
DB 424 RGTATADA--PGCVVMSNGEPKQADLGPERRASVVRDPLGRHEHITLDESCKTFPT 481
QY 473 NGGSVSYIV 481
DB 482 NGGSVSVWV 490

RESULT 15

B45738
alpha-amylase (EC 3.2.1.1), cytosolic - Salmonella typhimurium
N/Alternate names: 1,4-alpha-D-glucan glucohydrolase
C/Species: Salmonella typhimurium

C>Date: 07-Apr-1994 #sequence_revision 18-Aug-1995 #text_change 18-Jun-1999
C/Accession: B45738
R/Raha, M.; Kawagishi, I.; Mueller, V.; Kihara, M.; Macnab, R.M.
J. Bacteriol. 174, 6644-6652, 1992
A/Title: Escherichia coli produces a cytoplasmic alpha-amylase, amYA.
A/Reference number: A45738; MUID:93015717; PMID:1400215
A/Accession: B45738
A/Molecule type: DNA
A/Residues: 1-494 <RAH>
A/Cross-references: GB:L01643; NID:G154043; PIDN:AAA27110.1; PID:G154045
C/Genetics:
A/Gene: amYA
C/Function:
A/Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A/Pathway: glycogen/starch degradation
C/Superfamily: alpha-amylase, amyloliquefactors type; alpha-amylase core homology
C/Keywords: cytosol; glycosidase; hydrolase; polysaccharide degradation
F:202-335/Domain: alpha-amylase core homology <AMY>
F:239,265,332/Active site: His, Glu, Asp #status predicted

Query Match 39.8%; Score 1060; DB 1; Length 494;
Best Local Similarity 42.4%; Pred. No. 1.3e-67;
Matches 208; Conservative 88; Mismatches 179; Indels 16; Gaps 6;
QY 4 NGTLMQYFEWYMPNDGQHWRLQNDASVLAHGIITAVITPAYKTSQA-DVGYGAYDLY 62
DB 3 NPTLQYFHYYPDGLWSELAEKADGINDIGINWMLPACKAGSGYSGYDTYDLF 62
QY 63 DLGFEHOKGTIVRTYGTGKLSQSKLSHRDINVDYVYINHGADATEDVTAVEVD 122
DB 63 DLGFEHOKGTIVRTYGTGKLSQSKLSHRDINVDYVYINHGADATEDVTAVEVD 122
QY 123 ADNRKRVSGEHLIKAWTHFHPGSGSTYSDFKWHYHFDGTDWDESKLRIRYK---FQ 178
DB 123 DRRQGLDNDIIECGWTRTYFPAPAAGYSNFIMDYHCFSGIDHIENPEDGIFKIVNDY 182
QY 179 GKAWMEVSNENGYDYLMTADIDYHPDYAAETKMGTYANELQLDGFRLDAVKHIF 238
DB 183 GDCWNPDQVDEBMGNFDYLMGNENIDFRNHAVTEETIKYWARVMWQTHCDGFRLDVAKH 242
QY 239 SFLBDMVNHVREKTKGEMFTVAEYWNQDGLAENYLNKTNFNSVFDVPLHYQFAASTQ 298
DB 243 WFKYEMIEHVOAVAPKPLFVIAETWSHEVDKLTITIDVDKTYLFDAPLQMKFHEASRQ 302
QY 299 GGGYDMKRLNGTVSKHPLKSVTFVNDHTOPGQSLESTVQTFKPLAYAFILTRBSGY 358
DB 303 GAEDYDMHIFGTLVEADPFHATVLANHDTPQLALEAVEPWFKPLAYALILLRENGV 362
QY 359 PQVFEYGMVGT-----KEDSOR-ELPALKHKEIFLKAKQYAGAGCHDYFDHDIYG 410
DB 363 PSVTFYDLYGASYSDESGENGETCRVDMEVLI-NQDLRLILARQRFHAGIQTLFEDHPNCL 421
QY 411 WTRGDSVANSGLAALITDGPAGAKMYGRQNAGETWHDITGNRSEPVVINSEGWGEF 470
DB 422 FSRGTEE--NPGCVVTLISNGDGEKTLILGDNVANKTRDFSGNRDEYVVTNDQGEATF 479
QY 471 HVNGGSVSIYV 481
DB 480 FCNAGSVSVWV 490

Search completed: May 3, 2004, 20:54:04
Job time : 14.7346 secs

R. Jorgensen, P.L.; Hansen, C.K.; Poulsen, G.B.; Diderichsen, B.
 Gene 96, 3-41, 1990
 A>Title: In vivo genetic engineering: homologous recombination as a tool for plasmid con
 A/Reference number: 139772; PMID:1092499; PMID:2265757
 A/Accession: 139772
 A>Status: translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-34, 1-100
 A/Cross-references: GB:M62637; NID:G142498; PIDN:AAA2232.1; PID:G142499
 R:Kuhn, H.; Fietzek, P.P.; Lampen, J.O.
 J. Bacteriol. 149, 372-373, 1982
 A>Title: N-terminal amino acid sequence of Bacillus licheniformis alpha-amylase: compari
 A/Reference number: 126151; PMID:82098050; PMID:6172418
 A/Accession: A26151
 A/Molecule type: protein
 A/Residues: 30-37, 'E', 'D', '41', 'X', '43-47' <KUH>
 R:Wachius, M.; Wiegand, G.; Huber, R.
 J. Mol. Biol. 246, 545-558, 1995
 A>Title: Crystal structure of calcium-depleted Bacillus licheniformis alpha-amylase at 2
 A/Reference number: 553788; PMID:95182462; PMID:7877175
 A/Accession: 553788
 A/Molecule type: protein
 A/Residues: 'D', '220-227' <MAC>
 A/Note: sequence represents amino end of an internal fragment created by a single enzyme
 R:Wachius, M.; Wiegand, G.; Huber, R.
 submitted to the Brookhaven Protein Data Bank, July 1995
 A/Reference number: A65206; PMID:1181
 A/Contents: annotation; X-ray crystallography, 2.2 angstroms, residues 32-210/222-511
 A/Note: these structural studies suggest 163 is less rather than Arg
 R:Song, H.K.; Huang, K.Y.; Chang, C. Sh, S.W.
 submitted to the Brookhaven Protein Data Bank, October 1996
 A/Reference number: A66860; PMID:1181
 A/Contents: annotation; X-ray crystallography, 1.7 angstroms, residues 32-210/222-511
 C/Genetics:
 A:Gene: amyL
 A/Function:
 A/Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
 A/Pathway: glycogen/starch degradation
 C/Superfamily: alpha-amylase, amylioliquefaciens type; alpha-amylase core homology
 C/Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; polysac
 F:1-29/DNA: signal sequence #status predicted <SIG>
 F:30-512/Product: alpha-amylase #status experimental <MPT>
 F:227-360/DNA: alpha-amylase core homology <MPT>
 F:113,229,264/Binding site: calcium (Asn, Asp, His) #status experimental
 F:260,290,357/Active site: Asp, Glu, Asp #status experimental

Query Match 99.5%; Score 2654; DB 1; Length 512;
 Best Local Similarity 99.4%; Pred. No. 9.8e-181;
 Matches 480; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ANNGTLMQFFWYMPDQGHRLQNDASLYLAHNGITAVMIPRAKGSQADVGAYD 60
 DB 30 ANNGTLMQFFWYMPDQGHRLQNDASLYLAHNGITAVMIPRAKGSQADVGAYD 89
 QY 61 LYDGEFHQKGTATKTKGELQSAIKSLHSRDINVGVDVNHGSGADATEDVAVAV 120
 DB 90 LYDGEFHQKGTATKTKGELQSAIKSLHSRDINVGVDVNHGSGADATEDVAVAV 149
 QY 121 DPADNRVIGSEHLIKATWTFHFGSGSTSDFKMTHYHFGDGDWDSKRLRIYFQOK 180
 DB 121 DPADNRVIGSEHLIKATWTFHFGSGSTSDFKMTHYHFGDGDWDSKRLRIYFQOK 180
 QY 150 DPADNRVIGSEHLIKATWTFHFGSGSTSDFKMTHYHFGDGDWDSKRLRIYFQOK 209
 DB 150 DPADNRVIGSEHLIKATWTFHFGSGSTSDFKMTHYHFGDGDWDSKRLRIYFQOK 209
 QY 181 AMWSEVSENGNDYLYADIDHDPVAAEIKRMGTWANEOLQGFRLDAVKHAFSEF 240
 DB 210 AMWSEVSENGNDYLYADIDHDPVAAEIKRMGTWANEOLQGFRLDAVKHAFSEF 269
 QY 241 LRDVAVHVRKTKGEMTVAEWMNDIGALENTLAKTNENHAFVDPVLAHQFPAASGOG 300
 DB 270 LRDVAVHVRKTKGEMTVAEWMNDIGALENTLAKTNENHAFVDPVLAHQFPAASGOG 319
 QY 301 GYDMKRLNTVSKELKAVTFDNDHDPGOSLESTVOTWTFKALYAFILTRREGYRQ 360
 DB 330 GYDMKRLNTVSKELKAVTFDNDHDPGOSLESTVOTWTFKALYAFILTRREGYRQ 389

QY 361 VFYGDWYTKGDSOREIPALKEKLEPILKARQVAYGAOHYFDHHDYVGMTREGDSVA 420
 DB 390 VFYGDWYTKGDSOREIPALKEKLEPILKARQVAYGAOHYFDHHDYVGMTREGDSVA 449
 QY 421 NSGLAALITDPCGAKRMVYGRONAGETWHDNGNSEEPVINSBEMGEFHNKGSVSIX 480
 DB 450 NSGLAALITDPCGAKRMVYGRONAGETWHDNGNSEEPVINSBEMGEFHNKGSVSIX 509
 QY 481 VQR 483
 DB 518 VQR 512

RESULT 2
 ALBNS
 alpha-amylase (EC 3.2.1.1) precursor - Bacillus amylioliquefaciens
 M/Alternate names: 1,4-alpha-D-glucan glucanohydrolase
 C/Species: Bacillus amylioliquefaciens
 C/Date: 30-Nov-1980 #sequence, revision 30-Jun-1987 #ext_change 18-Jun-1999
 C/Accession: A92389; A90307; 139756; 139763; A00643
 R:Takkinen, K.; Petersson, R.F.; Kalkkinen, N.; Palva, I.; Soderlund, H.; Kaariainen,
 J. Biol. Chem. 258, 1007-1013, 1983
 A>Title: Amino acid sequence of alpha-amylase from Bacillus amylioliquefaciens deduced f
 A/Reference number: A92389; PMID:83108808; PMID:6185474
 A/Accession: A92389
 A/Contents: PUB110
 A/Molecule type: DNA
 A/Residues: 1-514 <TRK>
 A/Cross-references: GB:U01542; GB:U01543; GB:M12033; GB:M12034; NID:G142428; PIDN:AAA22
 R:Chung, H.S.; Friedberg, F.
 Biochem. J. 185, 387-395, 1980
 A>Title: Sequence of the N-terminal half of Bacillus amylioliquefaciens alpha-amylase.
 A/Reference number: A90307; PMID:80241725; PMID:6156671
 A/Accession: A90307
 A/Molecule type: Protein
 A/Residues: 32-53, 'I', '55-63', 'L', '65-78', 'D', '80-83', 'S', '85-222' <CH>
 R:Palva, I.; Petersson, R.F.; Kalkkinen, N.; Lehtovaara, P.; Sarvas, M.; Soderlund, H.
 Gene 15, 43-51, 1981
 A>Title: Nucleotide sequence of the promoter and NH2-terminal signal peptide region of
 A/Reference number: 139756; PMID:8051256; PMID:6170539
 A/Accession: 139756
 A>Status: translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-96 <RBS>
 A/Cross-references: EMBL:V00092; NID:G39297; PIDN:CAA23430.1; PID:G39298
 R:Ruhonen, L.; Hackman, P.; Lehtovaara, P.; Knowles, J.R.C.; Karanen, S.
 Gene 59, 161-170, 1987
 A>Title: Efficient secretion of Bacillus amylioliquefaciens alpha-amylase cells by its o
 A/Reference number: 139763; PMID:86137952; PMID:2690166
 A/Accession: 139763
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-39 <RBS>
 A/Cross-references: GB:M18424; NID:G142430; PIDN:AAA22192.1; PID:G142431
 C/Function:
 A/Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
 A/Pathway: glycogen/starch degradation
 C/Superfamily: alpha-amylase, amylioliquefaciens type; alpha-amylase core homology
 C/Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation
 F:1-11/DNA: signal sequence #status predicted <SIG>
 F:32-514/Product: alpha-amylase #status predicted <MPT>
 F:229-362/DNA: alpha-amylase core homology <MPT>
 F:113,231,266/Binding site: calcium (Asn, Asp, His) #status predicted
 F:262,292,359/Active site: Asp, Glu, Asp #status predicted

Query Match 81.3%; Score 2184; DB 1; Length 514;
 Best Local Similarity 80.3%; Pred. No. 2.3e-147;
 Matches 388; Conservative 44; Mismatches 49; Indels 2; Gaps 1;

QY 3 INGTLMQFFWYMPDQGHRLQNDASLYLAHNGITAVMIPRAKGSQADVGAYD 62
 DB 32 INGTLMQFFWYMPDQGHRLQNDASLYLAHNGITAVMIPRAKGSQADVGAYD 91

QY 63 DGEFHOKGTATRTKGTGKELGSAIKSLHSRDLNIVGVYVNHKGADATEMVAEYVNP 122
DB 92 DGEFHOKGTATRTKGTGKELGSAIKSLHSRDLNIVGVYVNHKGADATEMVAEYVNP 151
QY 123 ADNRVTSGEHLIKAMTHFHPGRGTSYSDPKMWHYFDGTMDSEKRLNRYKFE--QOK 180
DB 152 ARNNGTSEYQKAMTDFRFPGRGNTYSDPKMWHYFDGTMDSEKRLNRYKFE--QOK 211
QY 181 AMDEVSSENGNDYLMYADIDYDHPVAEIKRWGTWANELODGFPLDAVKIKFSF 240
DB 212 AMDEVSSENGNDYLMYADIDYDHPVAEIKRWGTWANELODGFPLDAVKIKFSF 271
QY 241 LRDVNVHREKTEKEMFTVAEYVNDLGALENTLNTHSVFVPLHYQFHAASQGG 300
DB 272 LRDVNVHREKTEKEMFTVAEYVNDLGALENTLNTHSVFVPLHYQFHAASQGG 331
QY 301 GYDMRKLNGTVSKPLSVTFVNDHDPQGSLESTVQTFKPLAVAFILTRREGYPQ 360
DB 332 GYDMRKLNGTVSKPLSVTFVNDHDPQGSLESTVQTFKPLAVAFILTRREGYPQ 391
QY 361 VFYGDWYGTGDSQREIPALKEIPILKARKOYAGAOHDYFDHDIYGMTREGSSVA 420
DB 392 VFYGDWYGTGDSQREIPALKEIPILKARKOYAGAOHDYFDHDIYGMTREGSSVA 451
QY 421 NSGLAALITDGPAGAKMYVGRONAGETWHDITGNRESEPVINSBGWGFHNVGGSVA 480
DB 452 NSGLAALITDGPAGAKMYVGRONAGETWHDITGNRESEPVINSBGWGFHNVGGSVA 511
QY 481 VOR 483
DB 512 VOR 514

RESULT 3

A:alpha-amyase (EC 3.2.1.1) precursor - Bacillus sp.
N:Alternate names: 1,4-alpha-D-glucan glucanohydrolase; G6-amyase
C:Species: Bacillus sp.
C>Date: 31-Mar-1989 #sequence_revision 18-Aug-1995 #next_change 18-Jun-1999
C:Accession: A27705
R:Tsukamoto, A.; Kilmura, K.; Ishii, Y.; Takano, T.; Yamane, K.
Biochem. Biophys. Res. Commun. 151, 25-31, 1988
A:Title: Nucleotide sequence of the maltobiose-oxidizing amyase gene from an alkalophilic
A:Reference number: A27705; PMID:88162814; PMID:3258152
A:Accession: A27705
A:Molecule type: DNA
A:Residues: 1-518 <TSU>
A:Cross-references: GB:M18662; NID:G142496; PID:AAA2231.1; PID:G142497
A:Experimental source: Chromosomal DNA of strain 707
A:Note: amino end of mature protein also determined
C:Comment: This is the smallest of five starch-hydrolyzing enzymes from this organism.
C:Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: alpha-amyase, amyloliquefaciens type; alpha-amyase core homology
C:Keywords: extracellular protein; glycosylase; hydrolase; polysaccharide degradation
F:1-33/Domain: signal sequence #status predicted <Sig>
F:34-518/Product: alpha-amyase #status experimental <Mat>
F:123-369/Domain: alpha-amyase core homology <AMY>
F:139,238,272/Binding site: calcium (Asp, Asp, His) #status predicted
F:269,299,366/Active site: Asp, Glu, Asp #status predicted

Query Match 70.5%; Score 1879; DB 1; Length 518;
Best Local Similarity 67.8%; Pred. No. 1e-125;
Matches 329; Conservative 67; Mismatches 79; Indels 10; Gaps 4;

QY 4 NGLIMQYFEMYNNDGQHRRLONDSAYLAEGITRAVWIPPAKGTSGADVGYAYDIYD 63
DB 39 NGIMQYFEMYNNDGQHRRLONDSAYLAEGITRAVWIPPAKGTSGADVGYAYDIYD 98
QY 64 LGEFHOKGTATRTKGTGKELGSAIKSLHSRDLNIVGVYVNHKGADATEMVAEYVNP 123

DB 99 LGEFHOKGTATRTKGTGKELGSAIKSLHSRDLNIVGVYVNHKGADATEMVAEYVNP 158
QY 124 DNRVTSGEHLIKAMTHFHPGRGTSYSDPKMWHYFDGTMDSEKRLNRYKFE--QOK 180
DB 159 ARNNGTSEYQKAMTDFRFPGRGNTYSDPKMWHYFDGTMDSEKRLNRYKFE--QOK 211
QY 181 AMDEVSSENGNDYLMYADIDYDHPVAEIKRWGTWANELODGFPLDAVKIKFSF 240
DB 212 AMDEVSSENGNDYLMYADIDYDHPVAEIKRWGTWANELODGFPLDAVKIKFSF 278
QY 241 LRDVNVHREKTEKEMFTVAEYVNDLGALENTLNTHSVFVPLHYQFHAASQGG 300
DB 272 LRDVNVHREKTEKEMFTVAEYVNDLGALENTLNTHSVFVPLHYQFHAASQGG 338
QY 301 GYDMRKLNGTVSKPLSVTFVNDHDPQGSLESTVQTFKPLAVAFILTRREGYPQ 360
DB 332 GYDMRKLNGTVSKPLSVTFVNDHDPQGSLESTVQTFKPLAVAFILTRREGYPQ 398
QY 361 VFYGDWYGTGDSQREIPALKEIPILKARKOYAGAOHDYFDHDIYGMTREGSSVA 428
DB 392 VFYGDWYGTGDSQREIPALKEIPILKARKOYAGAOHDYFDHDIYGMTREGSSVA 453
QY 421 NSGLAALITDGPAGAKMYVGRONAGETWHDITGNRESEPVINSBGWGFHNVGGSVA 480
DB 452 NSGLAALITDGPAGAKMYVGRONAGETWHDITGNRESEPVINSBGWGFHNVGGSVA 513
QY 481 VOR 483
DB 514 VOR 518

RESULT 4

A:alpha-amyase (EC 3.2.1.1) precursor - Bacillus stearothermophilus (strain DN1792)
N:Alternate names: 1,4-alpha-D-glucan glucanohydrolase
C:Species: Bacillus stearothermophilus
C>Date: 28-Oct-1994 #sequence_revision 18-Aug-1995 #next_change 13-Jun-1997
C:Accession: A54541
R:Jorgensen, P.L.; Poulsen, G.B.; Diderichsen, B.
FEMS Microbiol. Lett. 7, 271-276, 1991
A:Title: Cloning of a chromosomal alpha-amyase gene from Bacillus stearothermophilus.
A:Reference number: A54541
A:Accession: A54541
A:Molecule type: DNA
A:Residues: 1-549 <QOR>
A:Cross-references: GB:X59476
A:Experimental source: Chromosomal DNA of strain DN1792
A:Comment: Alpha-amyase genes have been found on plasmids and in multiple copies on cl
A:Genetics:
A:Start codon: GCG
C:Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: alpha-amyase, amyloliquefaciens type; alpha-amyase core homology
C:Keywords: extracellular protein; glycosylase; heat-stable protein; hydrolase; polysac
F:1-34/Domain: signal sequence #status predicted <Sig>
F:35-549/Product: alpha-amyase #status predicted <Mat>
F:125-368/Domain: alpha-amyase core homology <AMY>
F:139,237,272/Binding site: calcium (Asp, Asp, His) #status predicted
F:268,298,365/Active site: Asp, Glu, Asp #status predicted

Query Match 67.0%; Score 1780.5; DB 1; Length 549;
Best Local Similarity 64.7%; Pred. No. 1e-119;
Matches 314; Conservative 68; Mismatches 98; Indels 5; Gaps 2;

QY 1 ANGLIMQYFEMYNNDGQHRRLONDSAYLAEGITRAVWIPPAKGTSGADVGYAYDIYD 60
DB 36 APNGIMQYFEMYNNDGQHRRLONDSAYLAEGITRAVWIPPAKGTSGADVGYAYDIYD 95
QY 61 LGEFHOKGTATRTKGTGKELGSAIKSLHSRDLNIVGVYVNHKGADATEMVAEYVNP 120
DB 96 LGEFHOKGTATRTKGTGKELGSAIKSLHSRDLNIVGVYVNHKGADATEMVAEYVNP 155

SQ SEQUENCE 514 AA; 59403 MW; 3DE66B3FB5CDE7E CRC64;
 Query Match 81.9%; Score 2184; DB 1; Length 514;
 Best Local Similarity 80.3%; Pred. No. 9.8e-153;
 Matches 388; Conservative 44; Mismatches 49; Indels 2; Gaps 1;

3 LAGTLMQYFEMWYNDGQHRRLONDSAYLAHGTTAVIPPAKYGTSQADVGAYDLY 62
 32 VNGTLMQYFEMWYNDGQHRRLONDSAYLAHGTTAVIPPAKYGTSQADVGAYDLY 91
 63 DLGEFQKGTVTRKYGTSKGLSALSKLSHSDINIVYGVYINHGKADATEDVAVENP 122
 92 DLGEFQKGTVTRKYGTSKGLSALSKLSHSDINIVYGVYINHGKADATEDVAVENP 151
 123 ADNRVYSGEHLIKANTHFFPRGSTYSDPKMYTHFPGDMDSSRLNTLYF--GK 180
 152 ANNRQSTSEYQIKAWTDPRFPGKNTYSDPKMYTHFPGDMDSSRLNTLYF--GK 211
 181 AMDWEVSNENGNVYDLYADIDYDHPDVAALIKMGWYANLQDGFRLDAVGHKFSF 240
 212 AMDWEVSENGVYDLYADIDYDHPDVAALIKMGWYANLQDGFRLDAVGHKFSF 271
 241 LRMVNAHVSEKTKEMFTVAETWONDGALNENYLNKTNHSEVTPVPHYQFHAASRQGG 300
 272 LRMVNAHVSEKTKEMFTVAETWONDGALNENYLNKTNHSEVTPVPHYQFHAASRQGG 331
 301 GYDMRKLLNGTVVSKPELKVTFVNDHDTQPGQSLESTVQTFKELAYAFILTBESGYPO 360
 332 GYDMRKLLNGTVVSKPELKVTFVNDHDTQPGQSLESTVQTFKELAYAFILTBESGYPO 391
 361 VFGDWMYGTGDSQREIPALAKHIEPILKARKQYAGAOHYDHYDVTWMTREGDSSVA 420
 392 VFGDWMYGTGDSQREIPALAKHIEPILKARKQYAGAOHYDHYDVTWMTREGDSSVA 451
 421 NSGLAALITDGPAGARMYVGRONAGETWHDITGRSEPVINSGESEFVNGGSVSIY 480
 452 KSGLAALITDGPAGARMYVGRONAGETWHDITGRSEPVINSGESEFVNGGSVSIY 511
 481 VOR 483
 512 VOR 514

RESULT 3
 AMT6_BACS7
 ID AMT6_BACS7 STANDARD; PRT; 518 AA.
 AC P1957;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 10-OCT-2000 (Rel. 42, Last annotation update)
 DE Glucan 1,4-alpha-maltohexaosidase precursor (EC 3.2.1.98) (66-amy1ase)
 DE Maltotetraose-producing amy1ase (Exo-maltotetraohydrolase).
 OS Bacillus sp. (strain 707).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID:1416;
 RN [1]
 RE SEQUENCE FROM N.A. AND SEQUENCE OF 34-36.
 RX MEDLINE=88162814; PubMed=258152;
 RA Teukanoto A., Kimura K., Ishii Y., Takano T., Yamane K.;
 RA "Nucleotide sequence of the maltotetraose-producing amy1ase gene from
 RA an alkalophilic Bacillus sp. #707 and structural similarity to
 RA lignifying type alpha-amy1ases."
 RL Biochem. Biophys. Res. Commun. 151:35-31(1988).
 CC -1- CATALYTIC ACTIVITY: Hydrolysis of 1,4-alpha-D-glucosidic linkages
 CC in amylose polysaccharides so as to remove successive
 CC maltotetraose residues from the non-reducing chain ends.
 CC -1- COFACTOR: Binds 2 calcium ions and 1 sodium ion per subunit (By
 CC similarity).
 CC -1- PATHWAY: Starch degradation.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.

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 CC or send an email to license@ebi.ac.uk).

EMBL: M1862; AAA2231.1; -
 DR PIR: A27705; A27705.
 DR HSP: P06278; IY05.
 DR InterPro: IPR006589; Alp_amy1_cat_sub.
 DR InterPro: IPR006047; Alpha_amy1_cat.
 DR InterPro: IPR006046; Glyco_hydro_13.
 DR Pfam: PF00128; alpha-amy1ase; 1.
 DR PRINTS: PR00110; ALPHAMYLASE.
 DR SMART: SM00642; Amy; 1.
 KW Hydrolase; Glycosidase; Carbohydrate metabolism; Signal.
 FT SIGNAL 1 33
 FT CHAIN 34 518
 FT ACT SITE 289 269
 FT ACT SITE 271 273
 FT ACT SITE 366 366
 FT METAL 139 139
 FT METAL 196 196
 FT METAL 219 219
 FT METAL 221 221
 FT METAL 232 232
 FT METAL 238 238
 FT METAL 240 240
 FT METAL 242 242
 FT METAL 273 273
 SQ SEQUENCE 518 AA; 59009 MW; 3A961E21612682C4 CRC64;
 Query Match 70.5%; Score 1879; DB 1; Length 518;
 Best Local Similarity 67.8%; Pred. No. 2.3e-130;
 Matches 329; Conservative 67; Mismatches 79; Indels 10; Gaps 4;

4 NGTLMQYFEMWYNDGQHRRLONDSAYLAHGTTAVIPPAKYGTSQADVGAYDLY 63
 39 NGTLMQYFEMWYNDGQHRRLONDSAYLAHGTTAVIPPAKYGTSQADVGAYDLY 98
 64 LGFQKGTVTRKYGTSKGLSALSKLSHSDINIVYGVYINHGKADATEDVAVENP 123
 99 LGFQKGTVTRKYGTSKGLSALSKLSHSDINIVYGVYINHGKADATEDVAVENP 158
 124 DNRRVYSGEHLIKANTHFFPRGSTYSDPKMYTHFPGDMDSSRLNTLYF--GK 180
 159 NNQSVTSEYQIKAWTDPRFPGKNTYSDPKMYTHFPGDMDSSRLNTLYF--GK 218
 181 AMDWEVSNENGNVYDLYADIDYDHPDVAALIKMGWYANLQDGFRLDAVGHKFSF 240
 219 AMDWEVSENGVYDLYADIDYDHPDVAALIKMGWYANLQDGFRLDAVGHKFSF 278
 241 LRMVNAHVSEKTKEMFTVAETWONDGALNENYLNKTNHSEVTPVPHYQFHAASRQGG 300
 272 LRMVNAHVSEKTKEMFTVAETWONDGALNENYLNKTNHSEVTPVPHYQFHAASRQGG 338
 301 GYDMRKLLNGTVVSKPELKVTFVNDHDTQPGQSLESTVQTFKELAYAFILTBESGYPO 360
 339 GYDMRKLLNGTVVSKPELKVTFVNDHDTQPGQSLESTVQTFKELAYAFILTBESGYPO 398
 361 VFGDWMYGTGDSQREIPALAKHIEPILKARKQYAGAOHYDHYDVTWMTREGDSSVA 428
 399 VFGDWMYGTGDSQREIPALAKHIEPILKARKQYAGAOHYDHYDVTWMTREGDSSVA 453
 429 NSGLAALITDGPAGARMYVGRONAGETWHDITGRSEPVINSGESEFVNGGSVSIY 488
 454 NSGLAALITDGPAGARMYVGRONAGETWHDITGRSEPVINSGESEFVNGGSVSIY 513
 479 IYOR 483

Tue May 4 14:34:48 2004

us-10-644-187-4.rpt

Page 1

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 3, 2004, 20:44:58 ; Search time 34.1232 Seconds
(without alignments)

4438.289 Million cell updates/sec

Title: US-10-644-187-4
Perfect score: 2624
Sequence: 1 VNGTLMQYFEMWTPNDGQHW.....KIGSDGWEFHVNDGSVSIY 480

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1017041 segs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SPTREMBL.25:*

1: sp_archaea:*\n2: sp_bacteria:*\n3: sp_fungi:*\n4: sp_human:*\n5: sp_invertebrate:*\n6: sp_mammal:*\n7: sp_mhc:*\n8: sp_organelle:*\n9: sp_phage:*\n10: sp_plant:*\n11: sp_protist:*\n12: sp_virus:*\n13: sp_vertebrate:*\n14: sp_unclassified:*\n15: sp_rvtnus:*\n16: sp_bacteriap:*\n17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2061	78.5	519	2	Q9ROT8
2	1947	74.2	513	16	Q81A54
3	1946	74.2	513	2	Q9A054
4	1914	72.9	513	16	Q81YU4
5	1836	70.0	516	2	Q82839
6	1767.5	67.3	549	2	Q9KMY6
7	1766.5	67.3	549	2	Q9KMY6
8	1762.5	66.7	521	2	P71034
9	1749.5	66.7	513	2	Q59222
10	1614.5	61.5	501	2	Q93149
11	1474.5	56.2	507	16	Q87H66
12	1359	51.8	481	16	Q89YF1
13	1253	46.4	493	2	Q03657
14	1217	46.4	484	16	Q97049
15	1212	46.2	484	16	Q8DPC8
16	1206.5	46.0	488	16	Q8B696

17	1206.5	46.0	488	16	Q8B0M2	Q8B0M2 streptococc
18	1205.5	45.9	486	16	Q8D708	Q8D708 streptococc
19	1197	45.6	492	16	Q8YU21	Q8YU21 anabaena sp
20	1190.5	45.4	484	2	O50583	O50583 streptococc
21	1182.5	45.1	486	2	O68875	O68875 streptococc
22	1177.5	44.9	485	2	O53786	O53786 streptococc
23	1127	42.9	491	16	O9CGS9	O9CGS9 lactococc
24	1057.5	40.3	529	3	Q877B1	Q877B1 aspergillus
25	1050	40.0	506	16	Q8U916	Q8U916 agrobacteri
26	1006	38.3	494	16	Q8Z5S5	Q8Z5S5 salmonella
27	1000	38.1	495	16	Q8F5I8	Q8F5I8 escherichia
28	999	38.1	495	16	Q8XB36	Q8XB36 escherichia
29	989	37.7	495	16	Q7UAB0	Q7UAB0 shigella fl
30	987	37.6	495	16	Q83R40	Q83R40 shigella fl
31	966	18.9	469	1	O50200	O50200 thermococc
32	944.5	18.8	461	1	Q8NKR5	Q8NKR5 thermococc
33	480.5	18.3	461	1	O33476	O33476 pyrococcus
34	480	18.3	457	1	O36477	O36477 thermococc
35	476.5	18.2	460	1	O3P9L0	O3P9L0 pyrococcus
36	476.5	18.2	460	1	O08452	O08452 pyrococcus
37	476.5	18.2	461	1	Q8NKR4	Q8NKR4 thermococc
38	476.5	18.2	473	17	Q8U319	Q8U319 pyrococcus
39	464.5	17.7	432	14	Q8JZK3	Q8JZK3 uncultured
40	351.5	13.4	826	10	Q9CRA6	Q9CRA6 arabidopsis
41	351.5	13.4	887	10	Q94A41	Q94A41 arabidopsis
42	334.5	12.7	906	10	Q8L0K4	Q8L0K4 oryza sativ
43	326	12.4	420	10	Q9ZP43	Q9ZP43 phaseolus v
44	324.5	12.4	421	10	Q7X9T1	Q7X9T1 phaseolus v
45	322	12.3	416	10	Q8LU06	Q8LU06 musa acumin

ALIGNMENTS

RESULT 1	ID	Q9ROT8	PRELIMINARY;	PRT;	519 AA.
AC	Q9ROT8				
DT	01-MAY-2000 (T-EMBLrel. 13, Created)				
DT	01-MAY-2000 (T-EMBLrel. 13, Last sequence update)				
DT	01-UN-2003 (T-EMBLrel. 24, Last annotation update)				
DE	Raw starch digesting amylase precursor.				
OS	Cytophaga sp.				
OC	Bacteria; Bacteroidetes; Sphingobacteria; Sphingobacteriales;				
OC	Flexibacteraceae; Cytophaga.				
OX	NCBI_Taxid=29535;				
PN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Uang C.L., Chen L.S., Chen M.Y.,				
RL	Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; AF067653; AAF00567.1; -				
DR	HSSP; P06278; IVUS.				
DR	GO; GO:0004556; P:alpha-amylase activity; IEA.				
DR	GO; GO:0005975; P:carbohydrate metabolism; IEA.				
DR	InterPro; IPR006047; Alpha amyl cat.				
DR	InterPro; IPR006589; Alp_aml_cat sub.				
DR	InterPro; IPR006046; Glyco_hydro_13.				
DR	Pfam; PF00128; alpha-amylase; 1.				
DR	PRINTS; PR00110; ALPHAAMYLASE.				
DR	SMART; SMC0642; Amy; 1.				
KW	Signal.				
FT	SIGNAL	1	57	POTENTIAL.	
FT	CHAIN	58	519	RAW STARCH DIGESTING AMYLASE.	
FT	SEQUENCE	519 AA;	58337 MW;	365884ADP98B163 CRC64;	
QY	Query Match	78.5%	Score 2061;	DB 2;	Length 519;
DB	Best Local Similarity	75.4%	Pred. No. 3,8e-134;		
	Matches 361;	Conserved 48;	Mismatches 70;	Indels 0;	Gaps 0;
	2 NGTLMQYFEMWTPNDGQHWRLONDAEHLSDISITAVWTIPYAKGIGSDGNGGYPDLVD 61				
	38 NGTLMQYFEMWTPNDGQHWRLONDAEHLSDISITAVWTIPYAKGIGSDGNGGYPDLVD 97				

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QY 62 LGFEQKGVTRTKYGTSELODAIGSLHSRNVQYGVVNLNKAAGADATEDYTAVERNPA 121
DB 98 LGFEQKGVTRTKYGTSELODAIGSLHSRNVQYGVVNLNKAAGADATEDYTAVERNPA 157
QY 122 NRNOETSEEVQIAQWDFRPPRGNGNTYSDPKMWHYFDGADWDESKIRIFKRGEGKA 181
DB 158 NRNOETSEEVQIAQWDFRPPRGNGNTYSDPKMWHYFDGADWDESKIRIFKRGEGKA 217
QY 182 WDEVSSENGNYDYLYMADYDHPDVVAETKKGIWYANELSLDGFRIIDAKHIFSEFL 241
DB 218 WDEVSSENGNYDYLYMADYDHPDVVAETKKGIWYANELSLDGFRIIDAKHIFSEFL 277
QY 242 RDVQAVROATGKEMFTVAEYQWNNAGLENTYKTSFNOSVDFVPLHFNLOAASSQGG 301
DB 278 RDVQAVROATGKEMFTVAEYQWNNAGLENTYKTSFNOSVDFVPLHFNLOAASSQGG 337
QY 302 YDMRRLIDGTIVSRHPEKATFEVNHDTOPGQSLSESTVOGTFKPLAVALITRESGYPOV 361
DB 338 YDMRRLIDGTIVSRHPEKATFEVNHDTOPGQSLSESTVOGTFKPLAVALITRESGYPOV 397
QY 362 FYGDMYTGKTSPEKIPSLKDNIEPLIKARKEVAYGPOHDYIHDPVIGMTRESGSSAK 421
DB 398 FYGDMYTGKTSPEKIPSLKDNIEPLIKARKEVAYGPOHDYIHDPVIGMTRESGSSAK 457
QY 422 SGLAALITDGPQSKMVAAGLKNAGETWYDITGNRSDTYKISDQGEFHVNDGSYSIY 480
DB 458 SGLAALITDGPQSKMVAAGLKNAGETWYDITGNRSDTYKISDQGEFHVNDGSYSIY 516

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RESULT 2

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ID 081A54 PRELIMINARY; PRT; 513 AA.
AC 081A54;
DT 01-JUN-2003 (TREMUREL. 24, Created)
DT 01-JUN-2003 (TREMUREL. 24, Last sequence update)
DE 01-OCT-2003 (TREMUREL. 25, Last annotation update)
DE 01-OCT-2003 (TREMUREL. 25, Last annotation update)
GN Bacillus cereus (strain ATCC 14579 / DSM 31).
OS Bacillus cereus (strain ATCC 14579 / DSM 31).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=228000;
RN [1]
RP SEQUENCE FROM N.A. Pubmed=12721630;
RX MEDLINE=22608415; PubMed=12721630;
RA Ivanova N., Sorokin A., Anderson I., Galleron N., Candellon B.,
RA Kapural V., Bhattacharya A., Rezak G., Mikhailova N., Lapidus A.,
RA Chu L., Mazur M., Goldman E., Larsen N., D'Souza M., Malinas T.,
RA Greckin Y., Pusch G., Haselkorn R., Ponstein M., Ehrlich S.D.,
RA Overbeek R., Kyrides N.,
RT "Genome sequence of Bacillus cereus and comparative analysis with
RT Bacillus anthracis."
RL Nature 423:87-91(2003).
DR EMBL: AE017009; AAP10417.1; -.
DR GO: GO:0004556; F:alpha-amylase activity; IEA.
DR GO: GO:0004556; F:alpha-amylase activity; acting on glycosyl bonds; IEA.
DR GO: GO:0004556; F:carbohydrate metabolism; IEA.
DR InterPro: IPR006589; Alp_amy1_cat_sub.
DR Pfam: PF00128; alpha-amylase; 1.
DR SMART: SM00642; Amy; 1.
KW Glycosidase; Hydrolase; Complete proteome
SQ SEQUENCE 513 AA; 58306 MW; 05C4611C4BF8F6 CRC64;

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Query Match 74.2%; Score 1947; DB 16; Length 513;
 Best Local Similarity 71.8%; Pred. No. 2.8e-126;
 Matches 344; Conservative 47; Mismatches 88; Indels 0; Gaps 0;

```

QY 2 NGTLMQYFMYTPNDGQWMLKNDLDAEHLSDIGITAWMTIPRAKGSOSDNGGPDYLD 61
DB 32 NGTLMQYFMYTPNDGQWMLKNDLDAEHLSDIGITAWMTIPRAKGSOSDNGGPDYLD 91
62 LGFEQKGVTRTKYGTSELODAIGSLHSRNVQYGVVNLNKAAGADATEDYTAVERNPA 121

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DB 92 LGFEQKGVTRTKYGTSELODAIGSLHSRNVQYGVVNLNKAAGADATEDYTAVERNPA 151
QY 122 NRNOETSEEVQIAQWDFRPPRGNGNTYSDPKMWHYFDGADWDESKIRIFKRGEGKA 181
DB 152 NRNOETSEEVQIAQWDFRPPRGNGNTYSDPKMWHYFDGADWDESKIRIFKRGEGKA 211
QY 182 WDEVSSENGNYDYLYMADYDHPDVVAETKKGIWYANELSLDGFRIIDAKHIFSEFL 241
DB 212 WDEVSSENGNYDYLYMADYDHPDVVAETKKGIWYANELSLDGFRIIDAKHIFSEFL 271
QY 242 RDVQAVROATGKEMFTVAEYQWNNAGLENTYKTSFNOSVDFVPLHFNLOAASSQGG 301
DB 272 RDVQAVROATGKEMFTVAEYQWNNAGLENTYKTSFNOSVDFVPLHFNLOAASSQGG 331
QY 302 YDMRRLIDGTIVSRHPEKATFEVNHDTOPGQSLSESTVOGTFKPLAVALITRESGYPOV 361
DB 332 YDMRRLIDGTIVSRHPEKATFEVNHDTOPGQSLSESTVOGTFKPLAVALITRESGYPOV 391
QY 362 FYGDMYTGKTSPEKIPSLKDNIEPLIKARKEVAYGPOHDYIHDPVIGMTRESGSSAK 421
DB 392 FYGDMYTGKTSPEKIPSLKDNIEPLIKARKEVAYGPOHDYIHDPVIGMTRESGSSAK 451
QY 422 SGLAALITDGPQSKMVAAGLKNAGETWYDITGNRSDTYKISDQGEFHVNDGSYSIY 480
DB 452 SGLAALITDGPQSKMVAAGLKNAGETWYDITGNRSDTYKISDQGEFHVNDGSYSIY 510

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RESULT 3

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ID 09A054 PRELIMINARY; PRT; 533 AA.
AC 09A054;
DT 01-JUN-2001 (TREMUREL. 17, Created)
DT 01-JUN-2001 (TREMUREL. 17, Last sequence update)
DE 01-JUN-2001 (TREMUREL. 24, Last annotation update)
DE 01-JUN-2001 (TREMUREL. 24, Last annotation update)
GN Alpha-amylase.
OS Bacillus megaterium.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1404;
RN [1]
RP SEQUENCE FROM N.A.
RA Kim Y.B., Lee B.N., Son H.J., Lee J.W., Kim B.J., Kim Y.-M.,
RA Park K.-H.,
RT "Cloning of maltopentase-producing amylase from Bacillus megaterium
RT KSM B-404."
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF220440; AAK00598.1; -.
DR HSP: P06279; IYTS.
DR GO: GO:0004556; F:alpha-amylase activity; IEA.
DR GO: GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro: IPR006589; Alp_amy1_cat_sub.
DR Pfam: PF00128; alpha-amylase; 1.
DR SMART: SM00642; Amy; 1.
SQ SEQUENCE 533 AA; 60557 MW; 789CCE06A19C0DDE CRC64;

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Query Match 74.2%; Score 1946; DB 2; Length 533;
 Best Local Similarity 72.0%; Pred. No. 3.5e-126;
 Matches 345; Conservative 44; Mismatches 90; Indels 0; Gaps 0;

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QY 2 NGTLMQYFMYTPNDGQWMLKNDLDAEHLSDIGITAWMTIPRAKGSOSDNGGPDYLD 61
DB 52 NGTLMQYFMYTPNDGQWMLKNDLDAEHLSDIGITAWMTIPRAKGSOSDNGGPDYLD 111
QY 62 LGFEQKGVTRTKYGTSELODAIGSLHSRNVQYGVVNLNKAAGADATEDYTAVERNPA 121
DB 112 LGFEQKGVTRTKYGTSELODAIGSLHSRNVQYGVVNLNKAAGADATEDYTAVERNPA 171
QY 122 NRNOETSEEVQIAQWDFRPPRGNGNTYSDPKMWHYFDGADWDESKIRIFKRGEGKA 181
DB 172 NRNOETSEEVQIAQWDFRPPRGNGNTYSDPKMWHYFDGADWDESKIRIFKRGEGKA 231
QY 182 WDEVSSENGNYDYLYMADYDHPDVVAETKKGIWYANELSLDGFRIIDAKHIFSEFL 241

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472 VNGSVSVWV 481
 481 CNGSVSVWV 490
 RESULT 7
 CDGT_BACSP STANDARD; PRT; 713 AA.
 ID CDGT_BACSP
 AC P30921
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUN-1993 (Rel. 26, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Cyclomaldextrin glucanotransferase precursor (EC 2.4.1.19)
 DE (Cyclomaldextrin-glucosyltransferase) (CGTase).
 CGT.
 GN Bacillus sp. (strain 17-1).
 OS Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OC NCBI_Taxid=1409;
 RX MEDLINE=90257592; PubMed=2534609;
 RA Kaneko T., Song K.B., Hamamoto T., Kudo T., Horikoshi K.
 RT "Construction of a chimeric series of Bacillus cyclomaldextrin
 RT glucanotransferases and analysis of the thermal stabilities and pH
 RT optima of the enzymes."
 RL J. Gen. Microbiol. 135:3447-3457 (1989).
 CC -1- CATALYTIC ACTIVITY: Degrades starch to cyclodextrins by formation
 CC of a 1,4-alpha-D-glucosidic bond.
 CC -1- COFACTOR: Binds 2 calcium ions per subunit (By similarity).
 CC -1- SUBUNIT: Monomer.
 CC -1- MISCELLANEOUS: CGTase may consist of two protein domains: THE ONE
 CC IN THE AMINO-TERMINAL SIDE CLEAVES THE ALPHA-1,4-GLUCOSIDIC BOND
 CC IN STARCH, AND THE OTHER IN THE C-TERMINAL SIDE CATALYZES OTHER
 CC ACTIVITIES, INCLUDING THE RECONSTITUTION OF AN
 CC ALPHA-1,4-GLUCOSIDIC LINKAGE FOR CYCLIZING THE
 CC MALTOOLIGOSACCHARIDE PRODUCED.
 CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC
 CC EMBL: M28053; AAA22310.1;
 DR HSP: P43379; 1CDG.
 DR InterPro: IPR006589; Alp_amy1_cat_sub.
 DR InterPro: IPR006048; Alpha_amy1_C.
 DR InterPro: IPR006047; Alpha_amy1_cat.
 DR InterPro: IPR020444; CBD_4.
 DR InterPro: IPR006046; Glyco_hydro_13.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR002909; IPT_TIG.
 DR Pfam: PF00128; alpha-amy1ase; 1;
 DR Pfam: PF02806; alpha-amy1ase_C; 1;
 DR Pfam: PF00686; CBM_20; 1;
 DR Pfam: PF01833; TIG; 1;
 DR PRINTS: PR00110; ALPHAMYLASE.
 DR PRODOM: PD001568; CBD_4; 1.
 DR SMART: SM00642; Amy; 1.
 DR SMART: SM00632; Amy; C; 1.
 DR Transferase; Glycosyltransferase; Calcium-binding; signal.
 KM SIGNAL
 FT CHAIN 1 27
 FT DOMAIN 28 713 CYCLOMALDEXTRIN GLUCANOTRANSFERASE.
 FT ACT_SITE 166 229 B.
 FT DOMAIN 166 229 A1.
 FT DOMAIN 230 433 B.
 FT DOMAIN 434 522 A2.
 FT DOMAIN 523 609 C.
 FT DOMAIN 610 713 D.
 FT ACT_SITE 256 256 E.
 BY SIMILARITY.

FT ACT_SITE 284 284 BY SIMILARITY.
 FT ACT_SITE 355 355 BY SIMILARITY.
 FT METAL 54 54 CALCIUM 2 (BY SIMILARITY).
 FT METAL 56 56 CALCIUM 2 (VIA CARBONYL OXYGEN) (BY
 FT METAL 59 59 SIMILARITY).
 FT METAL 60 60 CALCIUM 2 (BY SIMILARITY).
 FT METAL 78 78 CALCIUM 2 (BY SIMILARITY).
 FT METAL 80 80 CALCIUM 2 (VIA CARBONYL OXYGEN) (BY
 FT METAL 166 166 SIMILARITY).
 FT METAL 217 217 CALCIUM 1 (BY SIMILARITY).
 FT METAL 226 226 CALCIUM 1 (VIA CARBONYL OXYGEN) (BY
 FT METAL 260 260 SIMILARITY).
 FT DISULFID 70 77 BY SIMILARITY.
 FT SEQUENCE 713 AA; 77389 MW; D13AEFC507FA5E CRC64;
 Query Match 11.0%; Score 313; DB 1; Length 713;
 Best Local Similarity 24.7%; Pred. No. 8.6e-15;
 Matches 135; Conservative 82; Mismatches 188; Indels 142; Gaps 29;
 19 DGLT-----WTKVANEANN--LSSLGITMLMP--AYKTSRSDYGVYDL 62
 67 DGTCTNRLYGGDMOGIINKINDGYLTGCVTAIWISQPVENISVINYSGVNTAHHG 126
 63 YDLSEFNQKGVTRKSTKAQYLOAIOAHAAAGQYADVDFDKGA--DGTWVDAVE 120
 127 YWADFCK--TNAYGTITADFONLAAHAKNIKITIDFANHSPASLDQPSFAENGK 183
 121 VNSDSRQNEISGYIOQAWTKFDPFGRGNTYSFFKRWYHFGVDMDESKLSRYKRG 180
 184 LYNNGRRE--GGY-----TNTQHLNF--HNGGTFFS----- 211
 181 IGAADMEVDTEGNYDYLM-VADLMDHEVTELEKNKGYVTTNTIDGFRDAVKHI 239
 212 -----TTEGNIYKLVLDLADLNHNSTVDYIKAIKWL-D-IGIDGIRMDAYGEM 261
 240 KFSFPEMLSVRSQTKRPFYGEWYSYDINK--HYITKIDGMELFDPAPLNKPYT 297
 262 PFGWQKSMATVANNY-KVPTFGE--WELGVNVSLENHNPANVSGLIDRFPQKTRQ 318
 298 ASK--SGGAPDMRTMTNTL-----MKDPTLAIVTFVDNHDTE--PGALQSWDPWK 347
 319 VKQNTDNYGLKSMLSGASATDYAQMEDQ---VTEIDNHDMEFFHNSANRKLKEQ--- 371
 348 PLAYAFILTROEGPCYFGDYGYIROY-----NIIS-----LKSRIPL 387
 372 --ALAFILF--SRGPALY--YGTETQMGSGNDPNRARIPTSTTTAYOVSKTLAPL 424
 388 LIAEDVAVGTQHDYLDHSDILIGTRRGTE-----KFGSLALITDREGSKW 437
 425 KXSNPAIAYGTORRWANVDVLIYERKFGNNVAIVANRWNTSASITGLVSLPAGS-- 482
 438 MYVGQHQAKYFVLLTGN--RSDVTITNSDGWE--FKVNGSVSVV--VPRKTVSTIAR 492
 483 -----YTVLGLNLGNLITVSGSGSASIFTLAAGTAWQYTTATYAPLIGHV 531
 493 -PITTRP 498
 532 GPWMAKP 538
 RESULT 8
 AMVB_PABRO STANDARD; PRT; 1196 AA.
 ID AMVB_PABRO
 AC P21553;
 DT 01-MAY-1991 (Rel. 26, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Beta/alpha-amy1ase precursor [includes: Beta-amy1ase (EC 3.2.1.2);
 DE Alpha-amy1ase (EC 3.2.1.1)].